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OM protein - protein search, using sw model

Run on: November 14, 2003, 12:54:54 ; Search time 14.7143 Seconds
(without alignments)
41.151 Million cell updates/sec

Title: US-09-736-076-15

Perfect score: 49

Sequence: 1 MLGRPPE 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Genseq_19Jun03:*
- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
 - 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
 - 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
 - 4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
 - 5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
 - 6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
 - 7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
 - 8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
 - 9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
 - 10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
 - 11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
 - 12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
 - 13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
 - 14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
 - 15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
 - 16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
 - 17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
 - 18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
 - 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
 - 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
 - 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
 - 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
 - 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
 - 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	9	AAW74159	HJ loop peptide J-
2	49	100.0	9	AAU98315	Polo kinase serine
3	49	100.0	10	AAW74213	HJ loop peptide K0
4	49	100.0	10	AAU98357	Polo kinase SNK se
5	49	100.0	11	AAW74163	HJ loop peptide J-
6	49	100.0	11	AAU98329	Polo kinase serine
7	49	100.0	469	AAU994717	Human protein sequ
8	49	100.0	469	AAU994717	Amino acid sequenc
9	49	100.0	685	AAU00915	Human serum induci

10	49	100.0	685	20	AAW88432	Disease associated
11	49	100.0	685	23	ABP61474	Human NF-kB activa
12	49	100.0	753	23	ABP41992	Human ovarian anti
13	46	93.9	9	20	AAW74161	HJ loop peptide J-
14	46	93.9	9	23	AAU98317	Polo kinase serine
15	43	87.8	626	21	ABU35805	Protein involved i
16	43	87.8	769	22	ABU36057	Drosophila melanog
17	41	83.7	8	20	AAW74160	HJ loop peptide J-
18	41	83.7	416	8	AAU98316	Polo kinase serine
19	41	83.7	416	17	AAU92176	Sak serine-threon
20	41	83.7	464	17	AAU92214	SAK-b serine-threo
21	41	83.7	925	17	AAU92177	SAK-a serine-threo
22	41	83.7	925	23	ABU57273	Mouse ischaemic co
23	41	83.7	970	22	AAU78833	Human protein SEQ
24	41	83.7	970	22	AAU39244	Human polypeptide
25	41	83.7	980	22	AAU79817	Human protein SEQ
26	41	83.7	980	22	AAU41030	Human polypeptide
27	40	81.6	9	20	AAW74162	HJ loop peptide J-
28	40	81.6	9	23	AAU98318	Polo kinase serine
29	40	81.6	20	20	AAW74173	HJ loop peptide PO
30	40	81.6	20	23	AAU98306	Peptide sequence o
31	40	81.6	329	21	AAU56690	Human prostate can
32	40	81.6	528	23	ABP73734	Candida albicans e
33	40	81.6	531	23	AAU74656	Mammalian polo-lik
34	40	81.6	603	16	AAU74620	Human lung tumour
35	40	81.6	603	23	AAU79306	Mouse polo-like ki
36	40	81.6	603	23	AAU79308	Mouse polo-like ki
37	40	81.6	603	23	AAU79309	Mouse polo-like ki
38	40	81.6	603	23	AAU79310	Mouse polo-like ki
39	40	81.6	603	23	AAU79311	Mouse polo-like ki
40	40	81.6	603	23	AAU79312	Mouse polo-like ki
41	40	81.6	603	23	AAU79313	Mouse polo-like ki
42	40	81.6	603	23	AAU79314	Mouse polo-like ki
43	40	81.6	603	23	AAU79315	Mouse polo-like ki
44	40	81.6	603	23	AAU79316	Mouse polo-like ki
45	40	81.6	603	23	AAU79317	Mouse polo-like ki

ALIGNMENTS

RESULT 1

AAW74159

ID AAW74159 standard; peptide; 9 AA.

AC AAW74159;

XX 05-MAY-1999 (first entry)

DT HJ loop peptide J-42.

XX HJ loop peptide J-42.

DB HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;

XX haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;

KW inflammatory disorder; central nervous system disease; septic shock;

KW Parkinson's disease; hypertension.

XX Synthetic.

OS

XX

XX

XX

XX

XX

XX

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XX

PA YISS : YISSUM RES & DEV CO.
 XX Ben-Sasson SA;
 PF WPI: 1999-070142/06.
 XX
 XX New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders
 XX
 XX Disclosure; Fig 6; 70pp; English.
 XX
 CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 49; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPPE 9
 DB |||||
 2 MLLGRPPPE 10
 RESULT 4
 AAQ98157
 ID AAQ98157 standard; Peptide; 10 AA.
 AC AAQ98157;
 DT 05-MAY-1999 (first entry)
 DE HJ loop peptide J-46.
 XX HJ loop; serine/threonine kinase STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytotoxic; antidiabetic; anorectic; neurological;
 KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
 KW modulating STK activity; polo kinase; SNK; KC38H101.
 XX Unidentified.
 CS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl-yl"
 FT Modified-site 10 /note= "Benzyl Ester of Glutamic Acid, C-terminal amide"
 XX
 XX US2000049101-A1.
 XX 25 APR 2002.
 XX
 XX 13 DEC 2000; 2000US-0736076.
 XX

PR 21-MAY-1997; 97US-0861338.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA Ben-Sasson SA;
 PI WPI: 2002-462787/49.
 XX
 XX New peptide from the HJ loop of serine-threonine kinase, useful for
 PT treating e.g. cancer and for producing diagnostic antibodies -
 XX
 XX Disclosure; Fig 6; 41pp; English.
 XX
 CC The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase SNK
 CC serine-threonine kinase HJ loop peptide KC38H101. This sequence is one
 CC of the short peptides of the invention that selectively modulate the
 CC activity of STK.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 49; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPPE 9
 DB |||||
 2 MLLGRPPPE 10
 RESULT 5
 AAQ74163
 ID AAQ74163 standard; peptide; 11 AA.
 AC AAQ74163;
 DT 05-MAY-1999 (first entry)
 DE HJ loop peptide J-46.
 XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "acetylated"
 FT Modified-site 11 /note= "amidated"
 XX
 XX WC9853050-A2.
 XX
 XX 26-NOV-1998.
 XX
 XX 20-MAY-1998; 98WO-US-0319.
 XX
 XX 21-MAY-1997; 97US-0861338.
 XX
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA (YISS) YISSUM RES & DEV CO.
 XX Ben-Sasson SA;
 PF

ocular disorders such as diabetic retinopathy and benign hypertrophic diseases such as haemangiomas. The polynucleotides can be used as hybridisation probes for cDNA and genomic DNA or as primers for a nucleic acid amplification (PCR) reaction, to isolate full-length cDNAs and genomic clones encoding polypeptides of this invention and to isolate cDNA and genomic clones of other genes which have a high sequence similarity to the SNK coding sequence. The differences between cDNA and genomic sequences can be observed and therefore mutations detected. Any mutations may then be attributed to likely causative agents of disease. The nucleotide sequences are also useful for chromosome identification.

XX Sequence 685 AA;

Query Match 100.0%; Score 49; DB 20; Length 685;

Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 9; Conservative C; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9

DB 273 MLLGRPPPE 281

RESULT 10

AAW68432
ID AAW68432 standard; Protein; 685 AA.

XX AC AAW68432.

XX AC AAW68432.

XX 26 APR-1999 (first entry)

DE Disease associated protein kinase DAPK-1.

XX DAPK-1; disease associated protein kinase; human; diagnosis; therapy; adult respiratory distress syndrome; allergy; asthma; arteriosclerosis; bronchitis; emphysema; hyper eosinophilia; myocardial inflammation; pericardial inflammation; anaemia; rheumatoid arthritis; Addison's disease; AIDS; atherosclerosis; atopic dermatitis; dermatomyositis; diabetes mellitus; glomerulonephritis; gout; Grave's disease; lupus erythematosus; multiple sclerosis; myasthenia gravis; osteoarthritis; osteoporosis; pancreatitis; polycystic kidney disease; polymyositis; scleroderma; Sjogren's syndrome; autoimmune thyroiditis; cancer; infection; trauma; cell proliferation.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Binding-site 99..96 /note= "potential ATP binding site"

XX Peptide 566..511 /note= "presumed regulatory sequence common to

XX polo family protein kinases"

XX WC9558052-A2.

XX 21-DEC-1998.

XX 19 JUN-1998; 98MO-US:2813.

XX 19 JUN-1997; 97US-0678989.

XX (INCYT) INCYTE PHARM INC.

XX Bandman O, Corley NC, Goli SK, Guegler KJ, Hillman CL;

XX Lai P, Shan P;

XX WPI; 1999-080952/07.

XX N-PSDB; AAX06831.

XX New disease associated protein kinases used to stimulate cell

XX proliferation and to treat the immune response and cancer

XX

PS Claim 1; Page 54-56; 93pp; English.

XX This is the amino acid sequence of human disease associated protein kinase DAPK-1, as deduced from a consensus sequence (see AAX06831) of overlapping cDNA clones from libraries which are immortalised or cancerous and show inflammatory or immune responses. DAPK-1 shows 53% homology to human proliferation-related protein kinase PRK (GI 1488263). The invention provides DAPK-1 to DAPK-7 polypeptides (see AAW68432-38) and cDNA clones encoding them (see AAX06831-36 and AAX06882), as well as expression vectors, host cells, agonists, antagonists and antibodies. The invention further provides uses of such products in the diagnosis, prevention and treatment of diseases associated with cell proliferation, especially cancer or an immune response (claimed). Conditions that may be treated include adult respiratory distress syndrome, allergies, asthma, arteriosclerosis, bronchitis, emphysema, hyper eosinophilia, myocardial or pericardial inflammation, rheumatoid arthritis, Addison's disease, AIDS, anaemia, atherosclerosis, various diseases of the digestive system, atopic dermatitis, dermatomyositis, diabetes mellitus, glomerulonephritis, gout, Grave's disease, lupus erythematosus, multiple sclerosis, myasthenia gravis, osteoarthritis, osteoporosis, pancreatitis, polycystic kidney disease, polymyositis, scleroderma, Sjogren's syndrome, autoimmune thyroiditis, complications of cancer, extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal and helminthic infections, and trauma (disclosed).

XX Sequence 685 AA;

Query Match 100.0%; Score 49; DB 20; Length 685;

Best Local Similarity 100.0%; Pred. No. 0.97; Indels 0; Gaps 0;

Matches 9; Conservative C; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9

DB 273 MLLGRPPPE 281

RESULT 11

ABP61474

ID ABP61474 standard; Protein; 685 AA.

XX AC ABP61474;

XX 30-SEP-2002 (first entry)

XX Human NF-KB activating protein SEQ ID NO 101.

XX Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;

XX immunomodulator; cytostatic; antineoplastic; osteopathic; neurotropic;

XX neuroprotective; anti-HIV; autoimmune disease; cancer; infection;

XX bone disease; AIDS; neurodegenerative disease; ischaemic disorder.

XX Homo sapiens.

XX WO200253737-A1.

XX 11-JUL-2002.

XX 25-DEC-2001; 2001WO-JP11389.

XX 28-DEC-2000; 2000JP-0402288.

XX 26-MAR-2001; 2001JP-0089912.

XX 24-AUG-2001; 2001JP-0254018.

XX (ASAH) ASAH KASEI KOGYO KK.

XX Matsuda A, Honda G, Muramatsu S, Nagano Y;

XX WPI; 2002-583617/62.

XX N-PSDB; ABQ91962.

XX NF-approximatelykB activating gene and expressed protein, applicable in

PT diagnosis and screening inhibitors or promoters to control excessive
 PT activation or inhibition for treating e.g. inflammations, autoimmune
 PT diseases and cancer -
 XX
 XX Claim 1: Page 448-453; 841pp: Japanese.
 XX
 XX The invention relates to a purified protein (I), comprising one of 90
 XX fully defined sequences (ABP61424-ABP61513) or a protein based on any of
 XX the sequences but with some amino acids deleted, substituted or added and
 XX with a NF- κ B nuclear factor kappa B) activating effect. The protein and
 XX encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
 XX inhibitors or promoters to control excessive activation or inhibition
 XX and for treating e.g. inflammations, autoimmune diseases, cancers,
 XX infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
 XX disorders.
 XX
 XX Sequence 685 AA:
 SQ
 Query Match 100.0%; Score 49; DB 23; Length 685;
 Best Local Similarity 100.0%; Pred. No. 0.97;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPFE 9
 DB 273 MLLGRPPFE 281
 |||||
 |||||
 RESULT 12
 ID ABP41992
 ID ABP41992 standard; Protein; 753 AA.
 XX
 XX ABP41992;
 XX
 XX 22-AUG-2002 (first entry)
 XX
 XX Human ovarian antigen HAOSMO3, SEQ ID NO:3124.
 XX
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 XX ovarian cancer; breast cancer; tumour; reproductive system disorder;
 XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 XX PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 XX inflammatory condition; immune disorder; blood disorder;
 XX cardiovascular disorder; respiratory disorder; neurological disorder;
 XX gastrointestinal disorder; urinary system disorder; drug screening;
 XX gene therapy; chromosome mapping; forensic analysis;
 XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 XX anti-inflammatory; gynaecological; reproductive; chromosome 5.
 XX
 XX Homo sapiens.
 XX
 XX CS
 XX PN WO200200677:A1.
 XX
 XX 01-JAN 2002.
 XX
 XX 01-JUN-2001; 2001WO-US:8569.
 XX
 XX 01-JUN-2000; 2000US-209467P.
 XX
 XX (HUXA-) HUMAN GENOME SCI INC.
 XX
 XX Barse CE, Rosen CA;
 XX
 XX WPI: 2002-147878/19.
 XX
 XX N-TSDB; ABQ55069.
 XX
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 XX useful in the prevention, treatment and diagnosis of cancer (e.g.
 XX ovarian cancer), immune disorders, cardiovascular disorders and
 XX neurological diseases -
 XX
 XX Claim 11; SEQ ID NO 3124; 2922pp: English.
 XX
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-

CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 753 AA;
 SQ
 Query Match 100.0%; Score 49; DB 23; Length 753;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPFE 9
 DB 341 MLLGRPPFE 349
 |||||
 |||||
 RESULT 13
 ID AAW74161
 ID AAW74161 standard; peptide; 9 AA.
 XX
 XX AAW74161;
 XX
 XX 05-MAY-1999 (first entry)
 XX
 XX HJ loop peptide J-43.1.
 XX
 XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 XX haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 XX inflammatory disorder; central nervous system disease; septic shock;
 XX Parkinson's disease; hypertension.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Modified-site 1 /note= "acetylated"
 XX Modified-site 9 /note= "amidated"
 XX
 XX WO9853050-A2.
 XX
 XX 26-NOV-1998.
 XX
 XX 20-MAY-1998; 98WO-US10319.
 XX
 XX 21-MAY-1997; 97US-0861338.
 XX
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 XX (YISS) YISSUM RES & DEV CO.

XX PA Ben-Sasson SA;
 XX ER WPI: 1999-070142/06.
 XX
 XX New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders
 XX
 XX Claim 14: Fig 4; 70pp; English.
 PS
 XX This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis), cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.
 XX
 XX Sequence 9 AA:
 SQ
 Query Match 93.9%; Score 46; DB 20; Length 9;
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY : MLLGKPPPE 9
 DB : MLLGKPPPE 9
 ||| : |||
 1 MLLGKPPPE 9

RESULT 14
 AAU98317
 ID AAU98317 standard; Peptide; 9 AA.
 XX
 XX AAU98317;
 AC
 XX 13-AUG 2002 (first entry)
 DE
 DE Polo kinase serine-threonine kinase HJ loop peptide J-43.1.
 XX
 XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 KW anti-inflammatory; immunosuppressive; cardiac; haemostatic;
 KW modulating STK activity; polo kinase; J-43.1.
 XX
 XX Unidentified.
 OS
 CS Synthetic.

Key Location/Qualifiers
 FH Modified-site 1
 FT Modified-site 9 /note= "N-terminal acetyl"
 FT Modified-site 9 /note= "Benzyl ester of Glutamic acid, C-terminal amide"
 FT
 XX US2002049301-A1.
 FN
 XX 25-APR-2002.
 PC
 XX 13-DEC 2000; 2000US-0736076.
 XX
 XX 21 MAY 1997; 97US-0861338.
 FK

XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA Ben-Sasson SA;
 PI
 XX WPI: 2002-462787/49.
 DR
 XX New peptide from the HJ loop of serine-threonine kinase, useful for
 PT treating e.g. cancer and for producing diagnostic antibodies -
 PT
 XX Disclosure; Fig 4; 41pp; English.
 PS
 XX The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase
 CC serine-threonine kinase HJ loop peptide J-43.1. This sequence is one of
 CC the short peptides of the invention that selectively modulate the
 CC activity of STK.
 XX Sequence 9 AA:
 SQ
 Query Match 93.9%; Score 46; DB 23; Length 9;
 Best Local Similarity 88.9%; Pred. No. 9.3e+05;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGKPPPE 9
 DB 1 MLLGKPPPE 9
 ||| : |||
 1 MLLGKPPPE 9

RESULT 15
 AAB35805
 ID AAB35805 standard; Protein; 626 AA.
 XX
 XX AAB35805;
 AC
 XX 23-FEB-2001 (first entry)
 DT
 XX Protein involved in cell cycle regulation SEQ ID 46.
 DE
 XX Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
 KW cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
 KW cotton; rice; barley; millet.
 XX
 XX Zea mays.
 OS
 XX WO2000065040-A2.
 PN
 XX 02-NOV-2000.
 PD
 XX 13-APR-2000; 2000WO-US99975.
 PF
 XX 22-APR-1999; 99US-0130849.
 PR
 XX (PION-) PIONEER HI-BRED INT INC.
 PA
 XX Helentjaris TG, Habben JE, Sun Y;
 PI
 XX WPI: 2000-687333/67.
 DR
 DR N-PSDB; AAC83112.
 XX
 XX Nucleic acids useful for producing transgenic plants, preferably maize,
 PT with increased cell cycle gene activity, preferably activity of cyclin
 PT and/or cyclin-dependent kinase -
 PT
 XX Claim 16; Page 117-118; 122pp; English.
 PS

XX polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -
 CC AAB35806 which are involved in regulating the cell cycle. The protein and
 CC DNA sequences have been isolated from Zea mays (corn), and the invention
 CC also includes oligonucleotides AAC83114 - AAC83139 which are related to
 CC the cell cycle polynucleotides. The cell cycle polynucleotide sequences
 CC are useful for producing transgenic plants such as maize, soybean,
 CC sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and
 CC riller with increased levels of cell cycle gene activity, such as
 CC activity of cyclin and cyclin-dependent kinases. The DNA sequences are
 CC also useful as probes for detecting deficiencies in the level of mRNA in
 CC screening for desired transgenic plants, for detecting mutations in the
 CC gene, for monitoring upregulation of expression or changes in enzyme
 CC activity in screening assays of compounds for detecting any number of
 CC allelic variants, orthologs or paralogues of the gene, and site-directed
 CC mutagenesis in eukaryotic cells. The DNA sequences are also useful for
 CC recombinant expression of the encoded polypeptides and as immunogens for
 CC preparing and screening antibodies. A transgenic plant comprising an
 CC expression cassette including a cell cycle regulatory gene is useful for
 CC assaying enzyme agonists and antagonists, and as immunogens or antigens
 CC to obtain antibodies. The antibodies are useful in assaying expression
 CC levels of cell cycle regulatory proteins, for identifying and isolating
 CC nucleic acids from expression libraries, for identifying homologues of
 CC polypeptides from other species, and for purification of the proteins.
 XX
 SQ Sequence 626 AA;

Query Match 87.8%; Score 43; DB 21; Length 626;

Best Local Similarity 77.8%; Pred. No. 12;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9

Db 228 LLVGRPPFE 236

11111111

RESULT 16

ABE61067

ID ABE61067 standard; Protein: 769 AA.

AC ABE61067;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO :5993.

XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharm-aceutical.

XX Drosophila melanogaster.

XX WC200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2301WO-USC9231.

XX 23-MAR-2000; 2300US-191637P.

XX 11-JUL-2000; 2000US-0614-50.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656869/75.

XX N-PSDB; ABL07170.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

XX genes from Drosophila and for elucidating cell signalling and cell-cell

XX interactions .

XX Disclosure; SEQ ID NO :5993; 21pp + Sequence Listing; English.

XX

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABBS7737-ABBS72072).

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 769 AA;

Query Match 87.8%; Score 43; DB 22; Length 769;

Best Local Similarity 77.8%; Pred. No. 14;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9

Db 206 LLVGRPPFE 214

11111111

RESULT 17

AAW74160

ID AAW74160 standard; peptide; 8 AA.

XX AAW74160;

XX

DT C5-MAY-1999 (first entry)

XX

DE HJ loop peptide J-43.

XX

KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;

KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;

KW inflammatory disorder; central nervous system disease; septic shock;

KW Parkinson's disease; hypertension.

XX

OS Synthetic.

XX

PH Key Location/Qualifiers

FT Modified-site 1

FT Modified-site 8

FT Modified-site 8

FT Modified-site 8

FT Modified-site 8

XX WO98S3050-A2.

XX

PD 26-NOV-1998.

XX

PF 20-MAY-1998; 98WO-US10319.

XX

PR 21-MAY-1997; 97US-0861338.

XX

PA (CHIL-) CHILDRENS MEDICAL CENT.

PA (YISS) YISSUM RES & DEV CC.

XX

PI Ben-Sasson SA;

XX

DR WPI; 1999-070142/06.

XX

PT New peptides for modulating serine/threonine kinase activity -

PT comprise a sequence corresponding to the HJ loop of a

PT serine/threonine kinase, used for treating, e.g. cancers,

PT inflammatory disorders or autoimmune disorders

XX

PS Claim 14; Fig 4; 70pp; English.

XX

CC This sequence represents a peptide of the invention, and is a derivative

CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be

CC used for the treatment of disorders caused by overactivity or

CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic

CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,

CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.

XX Sequence 8 AA;

Query Match 83.7%; Score 41; DB 23; Length 8;

Best Local Similarity 87.5%; Pred. No. 9.3e+05;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPF 8

DB 1 MLLGRPPF 8

RESULT 18

AAR92176

AC AAR92176 standard; Peptide; 8 AA.

XX AAR92176;

XX AAR92176;

XX AAR92176;

DT 25-MAY-1996 (first entry)

DE Sak serine-threonine kinase N-terminus.

KW Sak; serine-threonine kinase; STK; cancer; diabetes; obesity;

KW central nervous system disorder; inflammatory disorder;

KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;

KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;

KW anti-inflammatory; immunosuppressive; cardiac; haemostatic;

KW modulating STK activity; polo kinase, J-43.

XX Unidentified.

XX Synthetic.

XX Key

XX Modified site 1 Location/Qualifiers

XX Modified-site 8 /note= "N-terminal: acetyl"

XX Modified-site 8 /note= "C-terminal amide"

XX US2002049301-A1.

XX 25 APR-2002.

XX 13-DEC-2000; 2000US-C736076.

XX 21-MAY-1997; 97US-C861338.

XX (CHILD); CHILDRENS MEDICAL CENT.

XX Ben-Sasson SA;

XX WPI; 2002-462787/49.

XX New peptide from the HJ loop of serine-threonine kinase, useful for

XX treating e.g. cancer and for producing diagnostic antibodies -

XX Disclosure; Fig 4; 41pp; English.

XX The present invention relates to new peptides derived from the HJ loop

XX of a serine/threonine kinase (STK). The peptides of the invention are

XX used to modulate STK activity, especially for treating cancer, diabetes,

XX obesity or a wide variety of central nervous system, inflammatory,

XX autoimmune or cardiovascular disorders, also haemorrhagic shock, and for

CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase
 CC serine-threonine kinase HJ loop peptide J-43. This sequence is one of
 CC the short peptides of the invention that selectively modulate the
 CC activity of STK.

XX Sequence 8 AA;

Query Match 83.7%; Score 41; DB 23; Length 8;

Best Local Similarity 87.5%; Pred. No. 9.3e+05;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPF 8

DB 1 MLLGRPPF 8

RESULT 19

AAR92176

ID AAR92176 standard; Protein; 416 AA.

XX AAR92176;

XX AAR92176;

DT 25-MAY-1996 (first entry)

DE Sak serine-threonine kinase N-terminus.

KW Sak; serine-threonine kinase; STK; agonist; antagonist;

KW proliferative disease; cancer; tumour; antisense; transgenic animal;

KW therapy.

XX Mus musculus.

XX CA2150789-A.

XX 03-DEC-1995.

XX 01-JUN-1995; 95CA-2150789.

XX 02-JUN-1994; 94US-0252995.

XX (MOUN) MOUNT SINAI HOSPITAL CORP.

XX Dennis JW, Fode C, Heffernan M;

XX WPI; 1996-129817/14.

XX N-PSDB; AAT08710.

XX Nucleic acid encoding Sak serine-threonine kinase - useful for

XX identifying modulators potentially useful in treatment or prevention

XX of proliferative disease.

XX Claim 3; Page 46-48; 73pp; English.

XX 2 Isoforms, sak-a and sak-b, of a novel serine/threonine kinase

XX have an identical N-terminal sequence (AAR92176) that contains the

XX kinase domain and that shows significant homology to the polo

XX subfamily. The C-terminal sequences (each contg. 3 PEST regions)

XX of the 2 isoforms differ (see AAR92177 and AAR92214). Sak-a and Sak-b

XX are associated with mitotic and meiotic cell division, and may be

XX involved in cell proliferation. They can be obtd. in recombinant

XX form by expression of encoding sequences (see AAT08710-12) and used

XX to test for inhibitory or stimulatory cpds. that may be useful

XX in the treatment/diagnosis of proliferative disorders, such as

XX cancer and viral (esp. HIV) infection.

XX Sequence 416 AA;

Query Match 83.7%; Score 41; DB 17; Length 416;

Best Local Similarity 66.7%; Pred. No. 18;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLIGRPPE 9

DB 204 LLIGRPPE 212

RESULT 20

AAR92214

ID AAR92214 standard; Protein: 464 AA.

XX AC

XX AAR92214;

XX AC

XX 25-MAY-1996 (first entry)

XX DT

XX SAK-b serine-threonine kinase.

XX DE

XX SAK-b; serine-threonine kinase; STK; agonist; antagonist;

KW proliferative disease; cancer; tumour; antisense; transgenic animal;

KW therapy.

XX KW

XX Mus musculus.

XX OS

XX Key Location/Qualifiers

XX FH

XX Key

XX Domain

XX 1..416

XX /label= N-terminal domain

XX /note= "contains the kinase domain"

XX FT

XX Domain

XX 417..464

XX /label= C-terminal domain

XX /note= "contains 3 PEST regions"

XX FT

XX CA2150789-A.

XX FN

XX 03-DEC-1995.

XX PE

XX 01-JUN-1995; 95CA-2150789.

XX PF

XX 02 JUN-1994; 94US-0252995.

XX PR

XX (MOJN) MOUNT SINAI HOSPITAL CORP.

XX PA

XX Dennis JW, Fode C, Heffernan M;

XX PI

XX WPI; 1996-129817/14.

XX DR

XX N-PSDB; AAT08711.

XX DR

XX Nucleic acid encoding Sak serine-threonine kinase - useful for

PT identifying modulators potentially useful in treatment or prevention

PT of proliferative disease.

XX PS

XX Claim 6; Page 59-61; 73pp; English.

XX CC

XX 2 Isoforms, SAK-a (AAR92177) and SAK-b (AAR92214), of a novel

CC serine/threonine kinase are associated with mitotic and meiotic cell

CC division and are characterized by having a kinase domain at the

CC N-terminus and 3 PEST sequences (rich in Pro, Ser, Thr, Asp, Glu) at

CC the C-terminus. The N-terminal regions of the 2 isoforms are

CC identical (see AAR92176). SAK-a and SAK-b can be obtd. in recombinant

CC form by expression of encoding sequences (see AAT08711-12), and used

CC to test for inhibitory or stimulatory cpds. useful in the

CC treatment/diagnosis of proliferative disorders such as cancer and

CC and viral (esp. HIV) infection, or used to raise antibodies.

XX SQ

XX Sequence 464 AA;

XX Query Match

XX Best Local Similarity 83.7%; Score 41; DB 17; Length 464;

XX Mismatches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

XX DB

XX 1 MLIGRPPE 9

XX 204 LLIGRPPE 212

RESULT 21

AAR92177

ID AAR92177 standard; Protein: 925 AA.

XX AC

XX AAR92177;

XX DT

XX 25-MAY-1996 (first entry)

XX DE

XX SAK-a serine-threonine kinase.

XX XX

XX SAK-a; serine-threonine kinase; STK; agonist; antagonist;

KW proliferative disease; cancer; tumour; antisense; transgenic animal;

KW therapy.

XX KW

XX Mus musculus.

XX OS

XX Key

XX Domain

XX 1..416

XX /label= N-terminal domain

XX /note= "contains the kinase domain"

XX FT

XX Domain

XX 417..925

XX /label= C-terminal domain

XX /note= "contains 3 PEST regions"

XX FT

XX CA2150789-A.

XX FN

XX 03-DEC-1995.

XX PD

XX 01-JUN-1995; 95CA-2150789.

XX PF

XX 02-JUN-1994; 94US-0252995.

XX PR

XX (MOJN) MOUNT SINAI HOSPITAL CORP.

XX PA

XX Dennis JW, Fode C, Heffernan M;

XX PI

XX WPI; 1996-129817/14.

XX DR

XX N-PSDB; AAT08711.

XX DR

XX Nucleic acid encoding Sak serine-threonine kinase - useful for

PT identifying modulators potentially useful in treatment or prevention

PT of proliferative disease.

XX PS

XX Claim 5; Page 50-55; 73pp; English.

XX CC

XX 2 Isoforms, SAK-a (AAR92177) and SAK-b (AAR92214), of a novel

CC serine/threonine kinase are associated with mitotic and meiotic cell

CC division and are characterized by having a kinase domain at the

CC N-terminus and 3 PEST sequences (rich in Pro, Ser, Thr, Asp, Glu) at

CC the C-terminus. The N-terminal regions of the 2 isoforms are

CC identical (see AAR92176). SAK-a and SAK-b can be obtd. in recombinant

CC form by expression of encoding sequences (see AAT08711-12), and used

CC to test for inhibitory or stimulatory cpds. useful in the

CC treatment/diagnosis of proliferative disorders such as cancer and

CC and viral (esp. HIV) infection, or used to raise antibodies.

XX SQ

XX Sequence 925 AA;

XX Query Match

XX Best Local Similarity 83.7%; Score 41; DB 17; Length 925;

XX Mismatches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

XX QY

XX 1 MLIGRPPE 9

XX 204 LLIGRPPE 212

XX DB

XX 1 MLIGRPPE 9

XX 204 LLIGRPPE 212

XX RESULT 22

XX ABB57273

XX ID

XX ABB57273 standard; Protein: 925 AA.

XX AC

XX ABB57273;

XX 07-MAR-2002 (first entry)
 XX Mouse ischaemic condition related protein sequence SEQ ID NO:766.
 XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
 XX Mus musculus.
 XX NC200188:88-A2.
 XX 22-NOV-2001.
 XX 18-MAY-2001; 2001WC-JP-4192.
 XX 18-MAY-2000; 2000JP-0145977.
 XX (JYMI-) UNIV NIHOON SCHOOL JURIDICAL PERSON.
 XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX WP1: 2002-034733/04.
 XX N-PSDB; AB199713.
 XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or
 PT by determining the expression profile of a gene group comprising these
 PT genes -
 XX Claim 2: Page 1893-1897; 2690pp; English.
 XX The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (i) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (i). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (AB199713 to AB199912, encoding
 CC the protein sequences in AB57020 to AB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The
 CC expression levels or expression profiles produced by these genes are
 CC used as an indicator when screening for ischaemic condition-improving
 CC drugs or therapeutics for ischaemic diseases. AB199713 and AB199914
 CC represent PCR primers for a mouse ischaemic condition related sequence,
 CC which are used in the exemplification of the present invention.
 XX Sequence 925 AA;
 XX Query Match 83.7%; Score 41; DB 23; Length 925;
 XX Best Local Similarity 66.7%; Pred. No. 41;
 XX Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 XX 1 MLLGRPPPE 9
 XX : : : : :
 XX 204 LLIGRPPFD 212
 XX RESULT 23
 XX AAM78833
 XX ID AAM78833 standard; Protein: 970 AA.
 XX AC AAM78833;
 XX 06-NOV-2001 (first entry)
 XX Human protein SEQ ID NO 1435.
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.

OS Homo sapiens.
 XX NC200157190-A2.
 XX 09-AUG-2001.
 XX 05-FEB-2001; 2001WO-US04098.
 XX 03-FEB-2000; 2000US-0496914.
 XX 27-APR-2000; 2000US-0560875.
 XX 20-JUN-2000; 2000US-0598075.
 XX 19-JUL-2000; 2000US-0620325.
 XX 01-SEP-2000; 2000US-0654936.
 XX 15-SEP-2000; 2000US-0663561.
 XX 20-OCT-2000; 2000US-0693325.
 XX 30-NOV-2000; 2000US-0728422.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Dranac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
 XX WP1: 2001-476283/51.
 XX N-PSDB; AAK51966.
 XX Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX Claim 20: Page 3782-3784; 6221pp; English.
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAH80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX Sequence 970 AA;
 XX Query Match 83.7%; Score 41; DB 22; Length 970;
 XX Best Local Similarity 66.7%; Pred. No. 43;
 XX Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 XX 1 MLLGRPPPE 9
 XX : : : : :
 XX 204 LLIGRPPFD 212
 XX RESULT 24
 XX AAM39244
 XX ID AAM39244 standard; Protein: 970 AA.
 XX AC AAM39244;
 XX 22-OCT-2001 (first entry)
 XX Human polypeptide SEQ ID NO 2389.
 XX Human; neutropenic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

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XX OS Homo sapiens.
XX PN WO200153312-A1.
XX PD 26-JUL-2001.
XX PF 26-FEB-2000; 2000WO-US34263.
XX PR 21-JAN-2000; 2000US-3488725.
XX PR 25-APR-2000; 2000US-0552317.
XX PR 09-JUL-2000; 2000US-0598042.
XX PR 19-JUL-2000; 2000US-0620312.
XX PR 23-AUG-2000; 2000US-0653450.
XX PR 14-SEP-2000; 2000US-0662291.
XX PR 29-OCT-2000; 2000US-0693036.
XX PR 19-NOV-2000; 2000US-0727344.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX PI Wang C, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX PR WPI: 2001-442253/47.
XX PR N-PSDB: AA158420.
XX PT Novel nucleic acids and polypeptides, useful for treating disorders
XX PT such as central nervous system injuries -
XX PS Example 4: SEQ ID NO 2389; 1007app; English.
XX CC The invention relates to human nucleic acids (AA157798-AA161369) and
XX CC the encoded polypeptides (AA136642-AA142213) with neurotropic,
XX CC immunosuppressant and cytostatic activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC of the invention may be used to treat diseases of the peripheral nervous
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localised neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX CC utilisation of the activities such as: immune system suppression,
XX CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukaemia and
XX CC CNS disorders.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification.
XX SQ Sequence 970 AA;
Query Match 83.7%; Score 41; DP 42; Length 970;
Best Local Similarity 66.7%; Pred. No. 43;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY : MLGRRPPPF 9
: : : : :
Db 204 LLGRRPPFD 212
RESULT 25
AAM798:7
ID AAM79817 standard; Protein: 980 AA.
XX AC AAM79817;
XX XX
XX DT 06-NOV-2001 (first entry)
XX DE Human protein SEQ ID NO 3463.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;

XX OS Homo sapiens.
XX PN WO200157190-A2.
XX PD 09-AUG-2001.
XX PF 05-FEB-2001; 2001WO-US04098.
XX PR 03-FEB-2000; 2000US-0496914.
XX PR 27-APR-2000; 2000US-0560875.
XX PR 20-JUN-2000; 2000US-0598075.
XX PR 19-JUL-2000; 2000US-0620325.
XX PR 01-SEP-2000; 2000US-0654936.
XX PR 15-SEP-2000; 2000US-0663561.
XX PR 20-OCT-2000; 2000US-0693325.
XX PR 30-NOV-2000; 2000US-0728422.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
XX PI Zhao QA, Wang D, Zhang J, Ren F, Chen R, Wang ZW;
XX PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
XX PR WPI: 2001-476283/51.
XX PR N-PSDB: AAK52950.
XX PT Nucleic acids encoding polypeptides with cytokine-like activities,
XX PT useful in diagnosis and gene therapy -
XX PS Claim 20; Page 345; 6221pp; English.
XX CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity relating to
XX CC cytokine, cell proliferation or cell differentiation or which may induce
XX CC production of other cytokines in other cell populations. The
XX CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX CC peptide therapy. The polypeptides have various cytokine-like activities,
XX CC e.g. stem cell growth factor activity, haematopoiesis regulating
XX CC activity, tissue growth factor activity, immunomodulatory activity and
XX CC activin/inhibin activity and may be useful in the diagnosis and/or
XX CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX CC inflammation.
XX CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX CC (AAK80020) are omitted as the relevant pages from the sequence listing
XX CC were missing at the time of publication.
XX SQ Sequence 980 AA;
Query Match 83.7%; Score 41; DP 22; Length 980;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY : 1 MLGRRPPPF 9
: : : : :
Db 214 LLGRRPPFD 222
RESULT 26
AAM41030
ID AAM41030 standard; Protein: 980 AA.
XX AC AAM41030;
XX XX
XX DT 22-OCT-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 5961.
XX KW Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX KW peripheral nervous system; neuropathy; central nervous system; CNS;
XX KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

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KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WC200153312-A1.
 XX
 PD 26-JUN-2001.
 XX
 PF 24 DEC-2000; 2000WO-US34263.
 XX
 FR 21-JAN-2000; 2000JS-0488725.
 FR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 31 AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang C, Wang Z, Wehrman T, Xu C, Xue A, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB; AA160186.
 XX
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 XX such as central nervous system injuries -
 XX
 ES Example 2: SEQ ID NO 5961; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAW38642-AAW42213) with neurotropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 SQ Sequence 980 AA;
 Query Match 83.7%; Score 417; DB 22; Length 980;
 Best Local Similarity 66.7%; Pred. No. 44;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGRPPPF 9
 DB 214 LLIGRPPPD 222
 RESULT 27
 ID AAW74162 standard; peptide; 9 AA.
 XX
 AC AAW74162;
 XX
 DT 05-MAY-1999 (first entry)
 XX
 DE HJ loop peptide J-45.
 XX
 KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;

KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "acetylated"
 FT Modified-site 9 /note= "amidated"
 FT
 XX WO9853050-A2.
 PN
 XX 26-NOV-1998.
 PD
 XX 20-MAY-1998; 98WO-US10319.
 PF
 XX 21-MAY-1997; 97US-0861338.
 PR
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA (YISS) YISSUM RES & DEV CO.
 XX
 XX Ben-Sasson SA;
 XX
 DR WPI: 1999-070142/06.
 XX
 XX New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders
 XX
 PS Claim 14; Fig 4; 70pp; English.
 XX
 CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity of
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.
 XX
 SQ Sequence 9 AA;
 Query Match 81.6%; Score 40; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LGRPPPF 9
 DB 1 LGRPPPF 7
 RESULT 28
 ID AAU98318 standard; Peptide; 9 AA.
 XX
 AC AAU98318;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Polo kinase serine-threonin; kinase HJ loop peptide J-45.
 XX
 KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;

KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 KW antiinflammatory; immunosuppressive; cardiant; haemostatic;
 KW modulating STK activity; polo kinase; J-45.
 XX Unidentified.
 CS Synthetic.
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminal acetyl"
 FT FT Misc difference 7
 FT FT Modified-site 9 /note= "benzyl ester of Glutamic acid"
 FT FT Modified-site 9 /note= "C-terminal amide"
 XX USPC2049301-A1.
 XX 23-APR-2002.
 XX 13-DEC-2003; 2003US-0736076.
 XX 21-MAY-1997; 97US-0861338.
 XX (CHILDRENS MEDICAL CENT.
 XX Ben-Sasson SA;
 XX MPI; 2002-462787/49.
 XX New peptide from the HJ loop of serine-threonine kinase, useful for
 FT treating e.g. cancer and for producing diagnostic antibodies -
 XX disclosure; Fig 4; 41pp; English.
 XX The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase
 CC serine-threonine kinase HJ loop peptide J-45. This sequence is one of
 CC the short peptides of the invention that selectively modulate the
 CC activity of STK.
 SQ Sequence 9 AA;
 Query Match 81.6%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9; 1e-05;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LGRPPPE 9
 DB 1 LGRPPPE 7
 RESULT 29
 ID AAW74:73 standard; peptide; 20 AA.
 XX AAW74:73;
 AC AAW74:73;
 DT 05-MAY-1999 (first entry)
 XX HJ loop peptide POLO.
 XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;

KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.
 OS Synthetic.
 PN WO9853050-A2.
 XX 26-NOV-1998.
 XX 20-MAY-1998; 99WO-US10319.
 XX 21-MAY-1997; 97US-0861338.
 XX (CHILDRENS MEDICAL CENT.
 XX (YISS) YISSUM RES & DEV CO.
 XX Ben-Sasson SA;
 XX MPI; 1999-070142/06.
 XX New peptides for modulating serine/threonine kinase activity -
 FT comprise a sequence corresponding to the HJ loop of a
 FT serine/threonine kinase, used for treating, e.g. cancers,
 FT inflammatory disorders or autoimmune disorders
 XX Claim 41; Fig 3b; 70pp; English.
 XX This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.
 SQ Sequence 20 AA;
 Query Match 81.6%; Score 40; DB 20; Length 20;
 Best Local Similarity 66.7%; Pred. No. 1.3;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGRRPPPE 9
 DB 3 LLVGKPPPE 11
 RESULT 30
 ID AAW98306 standard; Peptide; 20 AA.
 XX AAW98306;
 AC AAW98306;
 XX 13-AUG-2002 (first entry)
 XX Peptide sequence of HJ loop of serine-threonine kinase polo kinase.
 XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 KW antiinflammatory; immunosuppressive; cardiant; haemostatic;
 KW modulating STK activity; polo kinase.
 XX Unidentified.

PT for therapeutic intervention, by inactivating in the strain one allele
PT of a gene and placing other allele of the gene under conditional
XX expression -
XX
XX Claim 44: SEQ ID NO 7571; 167bp - Sequence Listing: English.
XX
XX The invention relates to constructing (M1) a strain of diploid fungal
XX cells in which both alleles of a gene are modified, comprising modifying
XX one allele by insertion or replacement by a cassette having an
XX expressible selectable marker and modifying other allele by
XX recombination, of a promoter replacement fragment with a heterologous
XX promoter, so that expression of the second allele is regulated by the
XX promoter. (M1) is useful for constructing a strain of diploid fungal
XX cells in which both alleles of a gene are modified. The diploid fungal
XX cells having both alleles modified are useful for identifying a gene that
XX is essential to the survival or growth of a fungus, a gene that
XX contributes to the virulence and/or pathogenicity of a fungus, a gene
XX that contributes to the resistance of a diploid fungus to an antifungal
XX agent, an antifungal agent that inhibits the growth of a diploid fungus
XX and for identifying a therapeutic agent for treatment of a mammalian
XX disease. (M1) is useful for identifying a compound which modulates the
XX activity of a gene product, preferably enzymatic activity, carbon
XX compound catabolism, biosynthetic, transporter, transcriptional,
XX translational, signal transduction, DNA replication and cell division
XX activity. The method is useful for identifying a compound having the
XX ability to inhibit growth or proliferation of *C. albicans* cells and for
XX treating infection by *C. albicans*. The present sequence is that of an
XX essential *Candida albicans* protein used in the method of the invention.
XX Note: The sequence data for this patent is not represented in the printed
XX specification but is based on sequence information supplied to Derwent by
XX the European Patent Office.
XX
XX Sequence 528 AA;

Query Match 81.6%; Score 40; DB 23; Length 528;
Best Local Similarity 66.7%; Pred. NO. 36;
Matches 6; Conservative 3; Mismatches 0; Gaps 0;

QY : MLGGRPFPE 9
Db 454 LLVGKPFPE 462

RESULT 33

AAU74656
ID AAU74656 standard; Protein; 531 AA.

XX AC AAU74656;

XX DT 09-APR-2002 (first entry);

XX CE Mammalian polo-like kinase (Plk).

XX KW Polo-like kinase; Plk; polo-box; cytosolic; neoplasm;
KW Hyperproliferative disorder; cytokinesis; solid tumour;
KW carcinoma; sarcoma; cancer; small cell carcinoma; adenocarcinoma;
KW Mullerian tumour; squamous cell carcinoma; protein.
XX OS Mammalia.

XX FH Key Location/Qualifiers
XX FT Misc-difference 130
XX FT Misc-difference 131 /label= Unknown
XX FT Misc-difference 132 /label= Unknown
XX FT Misc-difference 133 /label= Unknown
XX FT Misc-difference 134 /label= Unknown
XX FT Misc-difference 135 /label= Unknown
XX FT Misc-difference 136 /label= Unknown

FT Misc-difference 136 /label= Unknown
FT Misc-difference 137 /label= Unknown
FT Misc-difference 138 /label= Unknown
FT Misc-difference 139 /label= Unknown
FT Misc-difference 140 /label= Unknown
FT Misc-difference 141 /label= Unknown
FT Misc-difference 147 /label= Unknown
FT Misc-difference 148 /label= Unknown
FT Misc-difference 149 /label= Unknown
FT Misc-difference 150 /label= Unknown
FT Misc-difference 151 /label= Unknown
FT Misc-difference 152 /label= Unknown
FT Misc-difference 153 /label= Unknown
FT Misc-difference 154 /label= Unknown
FT Misc-difference 155 /label= Unknown
FT Misc-difference 156 /label= Unknown
FT Misc-difference 157 /label= Unknown
FT Misc-difference 158 /label= Unknown
FT Misc-difference 159 /label= Unknown
FT Misc-difference 160 /label= Unknown
FT Misc-difference 161 /label= Unknown
FT Misc-difference 162 /label= Unknown
FT Misc-difference 163 /label= Unknown
FT Misc-difference 164 /label= Unknown
FT Misc-difference 165 /label= Unknown
FT Region 410..439
FT /label= Polo-box
FT /note= "Core polo-box consensus sequence"
XX WO200190401-A2.
XX 29-NOV-2001.
XX 23-MAY-2001; 2001WO-US16903.
XX 23-MAY-2000; 2000US-206588P.
XX (HARD) HARVARD COLLEGE.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PA (USSH) US NAT INST OF HEALTH.
XX Lee KS, Song S, Erikson R;
XX WPI; 2002-106210/14.
XX Identifying polo-like kinase modulators by contacting eukaryotic cells
XX expressing polo-box peptides with test compounds and evaluating changes
XX in dominant negative cytokinesis-defective growth patterns .

XX Example 2; Fig 5; 57pp; English.

XX The invention describes a novel method of detecting compounds with

XX polo-like kinase (PLK) modulating activity. This comprises contacting

XX eukaryotic cells expressing polo-box or polo-box related peptides,

XX binding peptides comprising 25 contiguous residues from a polo-like

XX kinase C-terminal region, with a test compound. Ectopic expression of a

XX polo-box in a eukaryotic cell causes a severe cytokinetic defect in the

XX cell. These eukaryotic cells can also be tested with the test compound

XX used in the method of the invention. The polo-box related peptides and

XX polo-like kinase activity modulatory compounds can be used to inhibit or

XX enhance cellular proliferation and subsequently for treating

XX hyper-proliferative disorders including neoplasms, solid tumours,

XX carcinomas, sarcomas and cancers e.g. small cell carcinoma,

XX adenocarcinoma, Mullerian tumours and squamous cell carcinomas. This

XX is the amino acid sequence of a mammalian polo-like kinase (Plk),

XX uncontrolled expression of the Plk family is implicated in the

XX development of human cancers, discussed in the method of the invention.

XX

SQ Sequence 531 AA;

Query Match 81.6%; Score 40; DS 23; Length 531;

Best Local Similarity 66.7%; Pred. No. 36;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

2Y 1 MLLGRPPPE 9

Db 244 LLVGRPPPE 212

RESULT 34

AAU74620

ID AAR74620 standard; Protein; 603 AA.

AC AAR74620;

XX 25 MAR-2003 (updated)

XX 26-DEC-1995 (first entry)

DE Human lung tumour polo-like kinase.

XX Polo-like kinase; PLK; serine threonine kinase; human; lung tumour;

XX autoimmune disease; lymphocyte activity.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Binding-site 60..86

FT /label= AXP-binding_motif

FT Region 174..177

FT /note= "motif that is highly conserved in protein

FT kinases"

FT Region 194..196

FT /note= "motif that is highly conserved in protein

FT kinases"

PN DE4329:77-A1.

XX 02 MAR-1995.

XX 30 AUG-1993; 93DE-4329177.

XX 30-AUG-1993; 93DE-4329177.

XX (CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.

XX Holtrich U, Rubsamen-Waigmann H, Strebhardt K;

PI Rubsamen-Waigmann H;

XX WPI; 1995-099454/14.

DR N-FSDB; AAC88155.

XX

PT A polo-like serine threonine kinase-protein - isolated from

PT proliferating human tissue, useful in the determn of lymphocyte

PT activity, eg in auto-immune diseases

XX Claim 1; Page 8-10; 11pp; German.

XX A human lung tumour-derived cDNA (AA088155) was found to have high

XX homology with sequences from members of the serine/threonine kinase

XX family. Due to the strong homology with the Drosophila polo gene,

XX the protein encoded by the new cDNA (AAR74620) was designated a polo-

XX like kinase (PLK). PLK mRNA is expressed in proliferating cells such

XX as placenta, colon and tumours of the lung, oesophagus, gut and

XX intestine. Resting lymphocytes do not express the PLK gene but after

XX stimulation with phytohemagglutinin, PLK is expressed and can be

XX used as an indicator of lymphocyte stimulation.

XX (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 603 AA;

Query Match 81.6%; Score 40; DB 16; Length 603;

Best Local Similarity 66.7%; Pred. No. 41;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9

Db 244 LLVGRPPPE 252

RESULT 35

AAU79306

ID AAU79306 standard; Peptide; 603 AA.

AC AAU79306;

XX 02-JUL-2002 (first entry)

XX Mouse polo-like kinase (Plk).

XX Polo box; PBL; cytostatic; fungicide; protozoacide; antihelminthic;

XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;

XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;

XX cancer of the uterus; ovarian cancer; cervical cancer;

XX epithelial cancer; brain cancer; retina cancer; prostate cancer;

XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;

XX Epidermophyton; Microsporium; protozoan infection; helminthes infection;

XX arthropod infection; mouse; polo-like kinase; Plk.

XX Mus musculus.

XX US6358738-B1.

XX 19-MAR-2002.

XX 13-MAY-1999; 99US-0311311.

XX 13-MAY-1998; 98US-085296P.

XX (HARD) HARVARD COLLEGE.

XX Erikson RL, Lee KS;

XX WPI; 2002-314756/35.

XX Administering polo kinase inhibitors for the treatment of cancers and

XX fungal infections

XX Example 1; Column 59-64; 47pp; English.

XX The invention describes a method of inhibiting growth of an isolated

XX population of cells by inhibiting a cell polo kinase by administering a

XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a

XX carboxy terminal domain of the polo kinase which excludes the polo

XX kinase catalytic domain. The method is used for the treatment of cancer

CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of the polo-like kinase (Plk), a
 CC protein from which mitotic protein po-lo kinase inhibitory peptides are
 CC derived.
 XX
 SQ Sequence 603 AA;
 Query Match: 81.6%; Score 40; DB 23; Length 603;
 Best Local Similarity 66.7%; Pred. NO. 41;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPPE 9
 Db 244 LLVGKPPPE 252
 RESULT 36
 AAU79308
 ID AAU79308 standard; Peptide; 603 AA.
 XX
 AC AAU79308;
 XX
 DT 02 JUL-2002 (first entry)
 XX
 DE Mouse polo-like kinase (Plk) T21CD mutant.
 XX
 KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc difference 210 /note= "Wild type Thr substituted by Asp"
 FT
 XX US6358738-B1.
 XX
 PD 19-MAR-2002.
 XX
 PF 13-MAY-1999; 99US-0311311.
 XX
 PR 13-MAY-1998; 98US-085296P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Erikson RL, Lee KS;
 XX
 DR WPI; 2002-314756/35.
 XX
 PT Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections -
 XX
 PS Example 1; Page -; 47pp; English.
 XX
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.

CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information
 CC given in the invention.
 XX
 SQ Sequence 603 AA;
 Query Match: 81.6%; Score 40; DB 23; Length 603;
 Best Local Similarity 66.7%; Pred. NO. 41;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPPE 9
 Db 244 LLVGKPPPE 252
 RESULT 37
 AAU79309
 ID AAU79309 standard; Peptide; 603 AA.
 XX
 AC AAU79309;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Mouse polo-like kinase (Plk) T210E mutant.
 XX
 KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc difference 210 /note= "Wild type Thr substituted by Glu"
 FT
 XX US6358738-B1.
 XX
 PD 19-MAR-2002.
 XX
 PF 13-MAY-1999; 99US-0311311.
 XX
 PR 13-MAY-1998; 98US-085296P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Erikson RL, Lee KS;
 XX
 DR WPI; 2002-314756/35.
 XX
 PT Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections -
 XX
 PS Example 1; Page -; 47pp; English.
 XX
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.

CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information
 CC given in the invention.

XX
 XX
 SQ Sequence 603 AA;
 Query Match 81.6%; Score 40; DB 23; Length 603;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRPPPE 9
 : : : : :
 Db 244 LLVGKPPPE 252

RESULT 38
 AAU79310
 ID AAU79310 standard; Peptide; 603 AA.
 XX
 AC AAU79310;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Mouse polo-like kinase (Plk) E210V mutant.
 XX
 KW Polo box; PB1; cytostatic; fungicide; protozoicide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
 XX
 OS Mus musculus.
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Misc-difference 210 /note= "Wild type Thr substituted by Val"
 FT
 XX
 PN US6358738-B1.
 XX
 PD 19-MAR-2002.
 XX
 PF 13-MAY-1999; 99US-0311311.
 XX
 PR 13-MAY-1998; 98US-085296P.
 XX
 PA (HARD) HARVAEL COLLEGE.
 XX
 PI Erikson RL, Lee KS;
 XX
 DR WPI; 2002-314756/35.
 XX
 PT Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections
 XX
 PS Example 1; Page -; 47pp; English.

XX
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information

CC given in the invention.

XX
 SQ Sequence 603 AA;
 Query Match 81.6%; Score 40; DB 23; Length 603;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRPPPE 9
 : : : : :
 Db 244 LLVGKPPPE 252

RESULT 39
 AAU79311
 ID AAU79311 standard; Peptide; 603 AA.
 XX
 AC AAU79311;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Mouse polo-like kinase (Plk) E206V mutant.
 XX
 KW Polo box; PB1; cytostatic; fungicide; protozoicide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
 XX
 OS Mus musculus.
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Misc-difference 206 /note= "Wild type Glu substituted by Val"
 FT
 XX
 PN US6358738-B1.
 XX
 PD 19-MAR-2002.
 XX
 PF 13-MAY-1999; 99US-0311311.
 XX
 PR 13-MAY-1998; 98US-085296P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Erikson RL, Lee KS;
 XX
 DR WPI; 2002-314756/35.
 XX
 PT Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections
 XX
 PS Example 1; Page -; 47pp; English.

XX
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information
 CC given in the invention.

SQ Sequence 603 AA;
 Query Match 81.6%; Score 40; DB 23; Length 603;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 : : : : :
 Db 244 LLVGKPPPE 252

RESULT 40
 AAU79112
 ID AAU79312 standard; Peptide; 603 AA;
 XX
 AC AAU79312;
 XX
 DI 22-JUL 2002 (first entry)
 XX
 DE Mouse polo-like kinase (Plk) E206N mutant.
 XX
 KW Polo box; PB1; cytosolic; fungicide; protozoacide; antileishmanic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; Polo-like kinase; Plk; mutant; mtein.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 PH Key
 FT X:sc: difference 206 /note= "wild type Glu substituted by Asn"
 FT
 PE US6358738:B1.
 XX
 PD 19 MAR-2002.
 XX
 PF 12-MAY 1999; 98US-0311311.
 XX
 PR 11 MAY 1998; 98US 085296P.
 XX
 RA (HARD) HARVARD COLLEGE.
 XX
 PI Erikson RL. Lee KS;
 XX
 DR WPI: 2002-314756/35.
 XX
 PT Administering Polo kinase inhibitors for the treatment of cancers and
 PT fungal infections
 XX
 PS Example 1: Page -: 47pp; English.
 XX
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in: AAU79306 using information
 CC given in the invention.
 XX
 SQ Sequence 603 AA;

Query Match 81.6%; Score 40; DB 23; Length 603;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 : : : : :
 Db 244 LLVGKPPPE 252

Search completed: November 14, 2003, 13:25:19
 Job time : 34.7143 secs

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CM protein - protein search, using sw model

Run on: November 14, 2003, 13:23:00 ; Search time 11.8286 Seconds
(without alignments)
32.193 Million cell updates/sec

Title: US-09-736-076-15
Perfect score: 49
Sequence: 1 MLLGRPPFE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310838 residues

Total number of hits satisfying chosen parameters: 328/17

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2.6/prodata/1/aa/59-COMB pep:
3: /cgn2.6/prodata/1/aa/6A-COMB pep:
4: /cgn2.6/prodata/1/aa/6B-COMB pep:
5: /cgn2.6/prodata/1/aa/PCUS-COMB pep:
6: /cgn2.6/prodata/1/aa/backfiles1.pep:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	49	100.0	(9)	3	US-08-861-338-15
2	49	100.0	11	3	Sequence 15, Appl
3	49	100.0	272	1	Sequence 19, Appl
4	49	100.0	272	1	Sequence 12, Appl
5	49	100.0	272	2	Sequence 12, Appl
6	49	100.0	685	2	Sequence 1, Appl
7	49	100.0	685	3	Sequence 2, Appl
8	49	100.0	685	3	Sequence 1, Appl
9	46	93.9	9	3	Sequence 2, Appl
10	41	83.7	273	8	Sequence 17, Appl
11	41	83.7	273	3	Sequence 16, Appl
12	41	83.7	273	2	Sequence 10, Appl
13	41	83.7	416	1	Sequence 10, Appl
14	41	83.7	416	1	Sequence 2, Appl
15	41	83.7	464	1	Sequence 2, Appl
16	41	83.7	464	2	Sequence 6, Appl
17	41	83.7	925	1	Sequence 6, Appl
18	41	83.7	925	2	Sequence 4, Appl
19	40	81.6	9	3	Sequence 4, Appl
20	40	81.6	20	3	Sequence 18, Appl
21	40	81.6	272	1	Sequence 6, Appl
22	40	81.6	272	2	Sequence 14, Appl
23	40	81.6	603	3	Sequence 14, Appl
24	40	81.6	603	4	Sequence 2, Appl
25	39	79.6	264	2	Sequence 26, Appl
26	39	79.6	271	1	Sequence 17, Appl
27	39	79.6	271	2	Sequence 11, Appl

Sequence 12, Appl
Sequence 22, Appl
Sequence 28679, A
Sequence 13, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 1, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3742, Ap
Sequence 2, Appl
Sequence 10, Appl

39 79.6 303 4 US-09-739-455-12
39 79.6 303 4 US-09-739-455-22
38 77.6 259 4 US-09-252-931A-28679
31 38 275 1 US-08-252-995D-13
32 38 275 2 US-08-834-108-13
33 38 275 2 US-08-755-728-3
34 38 275 2 US-08-974-655-3
35 38 275 2 US-08-283-011-3
36 38 275 2 US-08-283-011-3
37 38 275 2 US-08-016-000-1
38 77.6 403 2 US-08-755-728-4
39 38 77.6 403 2 US-08-974-655-4
40 38 77.6 403 2 US-08-283-011-4
41 37 75.5 20 3 US-09-772-647-4
42 37 75.5 182 4 US-08-861-338-3
43 37 75.5 220 1 US-09-134-001C-3742
44 37 75.5 220 1 US-08-233-146-2
45 37 75.5 264 2 US-08-463-470-2
45 37 75.5 264 2 US-07-857-224B-10

ALIGNMENTS

RESULT 1
US-08-861-338-15
; Sequence 15, Application US/08861338
; Patent No 6174993
; GENERAL INFORMATION:
; APPLICANT: Ber-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861.338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Gamma Benzyl Ester of
; OTHER INFORMATION: Glutamic Acid-NH2"
US-08-861-338-15

Query Match 100.0%; Score 49; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGRPPPE 9
 Db 1 MLLGRPPPE 9

RESULT 2
 US-08-861-338-19
 ; Sequence 19, Application US/08861338
 ; Patent No. 6174993
 ; GENERAL INFORMATION:
 ; APPLICANT: Ben-Sasson, Shmuel A.
 ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/861-338
 ; FILING DATE: 21-MAY-1997
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brook, David E.
 ; REGISTRATION NUMBER: 22,592
 ; REFERENCE/DOCKET NUMBER: CMC-590
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (781) 861-6240
 ; TELEFAX: (781) 861-9540
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 1
 ; OTHER INFORMATION: /note= "N Acetyl Methionine"
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 9
 ; OTHER INFORMATION: /note= "Glutamic Acid Benzyl Ester"
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 11
 ; OTHER INFORMATION: /note= "Serine-NH2"
 ; US-08-861-338-19

Query Match 100.0%; Score 49; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.0e+04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGRPPPE 9
 Db 1 MLLGRPPPE 9

RESULT 3
 US-08-252-995D-12

; Sequence 12, Application US/08252995D
 ; Patent No. 5650501
 ; GENERAL INFORMATION:
 ; APPLICANT: Dennis, James W
 ; APPLICANT: Heffernan, Mike
 ; APPLICANT: Fode, Carol
 ; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BERESKIN & PARR
 ; STREET: 40 King Street West
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5H 3Y2
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/252,995D
 ; FILING DATE: 02-JUN-1994
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kurdydyk, Linda M
 ; REGISTRATION NUMBER: 34,971
 ; REFERENCE/DOCKET NUMBER: 3153-96
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 364-7311
 ; TELEFAX: (416) 361-1398
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 272 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; ORIGINAL SOURCE:
 ; ORGANISM: Mus musculus
 ; US-08-252-995D-12

Query Match 100.0%; Score 49; DB 1; Length 272;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGRPPPE 9
 Db 199 MLLGRPPPE 207

RESULT 4
 US-08-834-108-12
 ; Sequence 12, Application US/08834108
 ; Patent No. 5976893
 ; GENERAL INFORMATION:
 ; APPLICANT: Dennis, James W
 ; APPLICANT: Heffernan, Mike
 ; APPLICANT: Fode, Carol
 ; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BERESKIN & PARR
 ; STREET: 40 King Street West
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5H 3Y2
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-21C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7312
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; US-08-834-108-12

Query Match 100.0%; Score 49; DB 2; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
EB .99 MLLGRPPFE 207

RESULT 5
US-08-878-989-1
; Sequence 1, Application US/08878989
; Patent No. 5885803
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: La., Preeti
; APPLICANT: Goli, Surva K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,989
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:

US-09-736-076-15.ra1
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVENOB01
; CLONE: 39043
; US-08-878-989-1

Query Match 100.0%; Score 49; DB 2; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 273 MLLGRPPFE 281

RESULT 6
US-09-136-282-2
; Sequence 2, Application US/09136282
; Patent No. 6063609
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, KAREN
; APPLICANT: JACKSON, JEFFREY
; APPLICANT: HANSBURY, MICHAEL
; APPLICANT: NERURKAR, SANDHYA
; APPLICANT: ROSHAK, AMY
; APPLICANT: BOUZYK, MARK
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rattrer & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,282
; FILING DATE: 20-AUG-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,112
; FILING DATE: 20-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-136-282-2

Query Match 100.0%; Score 49; DB 3; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MLJGRPPE 9
      |||||
Db      273 MLJGRPPE 281

RESULT 7
US-09-272-796-1
; Sequence 1, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/878,999
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J. J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-032; US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVENOB01
; CLONE: 39043
US-09-272-796-1

Query Match      100.0%; Score 49; DB 3; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLJGRPPE 9
      |||||
Db      273 MLJGRPPE 281

RESULT 8
US-09-505-744-2
; Sequence 2, Application US/09505744
; Patent No. 6245544
; GENERAL INFORMATION:
; APPLICANT: Karen M. Andersor
```

```
; APPLICANT: Mark M. Bouzyk
; APPLICANT: Michael J. Hansbury
; APPLICANT: Jeffrey R. Jackson
; APPLICANT: Sandhya S. Nerurkar
; APPLICANT: Amy K. Roshak
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; FILE REFERENCE: GH-70231-D1
; CURRENT APPLICATION NUMBER: US/09/505,744
; CURRENT FILING DATE: 2000-02-16
; EARLIER APPLICATION NUMBER: C9/136,282
; EARLIER FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 60/056,112
; EARLIER FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 685
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-505-744-2

Query Match      100.0%; Score 49; DB 3; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLJGRPPE 9
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Db      273 MLJGRPPE 281

RESULT 9
US-08-861-338-17
; Sequence 17, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/861,338
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION:
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
```


Db 118 ITRPPFE 125

RESULT 27

S70964

pkns protein - Myxococcus xanthus

N:Alternate names: serine protein kinase homolog

C:Species: Myxococcus xanthus

C>Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 08-Oct-1999

C:Accession: S70964

R:Zhang, W.; Inouye, M.; Inouye, S.

Mol. Microbiol. 20, 435-447, 1996

A:Title: Reciprocal regulation of the differentiation of Myxococcus xanthus by Pkn5 and A:Reference number: S70964; MUID:96310390; PMID:8733241

A:Accession: S70964

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-380 <ZHA>

A:Cross-references: EMBL:U40656; NID:gl113924; PIDN:AA840049.1; PID:gl113925

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995

C:Genetics:

A:Gene: pkn5

Query Match 75.5%; Score 37; DB 2; Length 380;

Best Local Similarity 66.7%; Pred. No. 25;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 MLLGRPFFE 9

Db 314 LLSGRPPFD 322

RESULT 28

KIHJCA

protein kinase C (EC 2.7.1.1) alpha - human

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999

C:Accession: S09496

R:Finkenzeller, G.; Marne, D.; Hug, H.

Nucleic Acids Res. 18, 2183, 1990

A:Title: Sequence of human protein kinase C alpha.

A:Reference number: S09496; MUID:90245676; PMID:2336401

A:Accession: S09496

A:Molecule type: mRNA

A:Residues: 1-672 <FIN>

A:Cross-references: EMBL:X52479; NID:g35482; PIDN:CAA36718.1; PID:g35483

C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-specific inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters.

C:Comment: Binding to acidic phospholipids (phosphatidylinositol) in the cell membrane may C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.

C:Genetics:

A:Gene: GDB:PRKCA

A:Cross-references: GDB:128015; OMIM:176963

A:Map position: 17q22-17q23.2

C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C C1 region homology

C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding

F:19-29/Region: phospholipid binding #status experimental

F:22-27/Region: pseudophosphorylation motif

F:37-86/Domain: protein kinase C zinc-binding repeat homology <K21>

F:102-151/Domain: protein kinase C C2 region homology <K22>

F:152-264/Domain: protein kinase C C2 region homology <K22>

F:337-597/Domain: protein kinase C C2 region homology <KIN>

F:345-353/Region: protein kinase C C2 region homology

F:368/Active site: Lys #status predicted

F:631/638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 75.5%; Score 37; DB 1; Length 672;

Best Local Similarity 66.7%; Pred. No. 45;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 MLLGRPFFE 9

Db 531 MLAGQPPFD 539

RESULT 30

KIMSCA

protein kinase C (EC 2.7.1.1) alpha - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999

C:Accession: S07104; J30078

R:Megidish, T.; Mazurek, N.

Nature 342, 807-811, 1989

A:Title: A mutant protein kinase C that can transform fibroblasts.

A:Reference number: S07104; MUID:90098082; PMID:2601739

A:Accession: S07104

A:Molecule type: mRNA

A:Residues: 1-672 <MEG>

A:Cross-references: GB:X52685; GB:X51603; NID:g49938; PIDN:CAA36908.1; PID:g49939

A:Experimental source: strain Balb/c

R:Rose-John, S.; Dietrich, A.; Marks, F.

Gene 74, 465-471, 1988

A:Title: Molecular cloning of mouse protein kinase C (PKC) cDNA from Swiss 3T3 fibroblasts

A:Reference number: JS0078; MUID:8932737; PMID:2469625

A:Accession: JS0078

A:Molecule type: mRNA

A:Residues: 1-146, 'D', 148-217, 'N', 219-276, 'AH', 279-312, 'V', 314-466, 'N', 468-471, 'N', 473-474, 'N', 476-477, 'N', 479-480, 'N', 482-483, 'N', 485-486, 'N', 488-489, 'N', 491-492, 'N', 494-495, 'N', 497-498, 'N', 500-501, 'N', 503-504, 'N', 506-507, 'N', 509-510, 'N', 512-513, 'N', 515-516, 'N', 518-519, 'N', 521-522, 'N', 524-525, 'N', 527-528, 'N', 530-531, 'N', 533-534, 'N', 536-537, 'N', 539-540, 'N', 542-543, 'N', 545-546, 'N', 548-549, 'N', 551-552, 'N', 554-555, 'N', 557-558, 'N', 560-561, 'N', 563-564, 'N', 566-567, 'N', 569-570, 'N', 572-573, 'N', 575-576, 'N', 578-579, 'N', 581-582, 'N', 584-585, 'N', 587-588, 'N', 590-591, 'N', 593-594, 'N', 596-597, 'N', 599-600, 'N', 602-603, 'N', 605-606, 'N', 608-609, 'N', 611-612, 'N', 614-615, 'N', 617-618, 'N', 620-621, 'N', 623-624, 'N', 626-627, 'N', 629-630, 'N', 632-633, 'N', 635-636, 'N', 638-639, 'N', 641-642, 'N', 644-645, 'N', 647-648, 'N', 650-651, 'N', 653-654, 'N', 656-657, 'N', 659-660, 'N', 662-663, 'N', 665-666, 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RESULT 37

JO0548
Protein: kinase C (EC 2.7.1.1-) gamma - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
C:Accession: J03548; S20735; S29620
R:Bowers, B.C.; Parham, C.L.; Sikela, C.M.; Wehner, J.W.
Gene 123, 263-265, 1993
A:Title: Isolation and sequence of a mouse brain cDNA coding for protein kinase C-gamma
A:Reference number: JO0548; MUID:93154595; PMID:8428669
A:Accession: J03548
A:Molecule type: mRNA
A:Residues: 1-697 <BOX>
A:Cross-references: EMBL:X67129; NID:953696; PIDN:CAA47608.1; PID:953697
A:Experimental source: Brain
R:Seitges, M.; Proikas, T.; Stabel, S.
Submitted to the EMBL Data Library, April 1992
A:Description: Comparison of the mouse and rat protein kinase C gamma gene promoter.
A:Reference number: S20735
A:Accession: S20735
A:Molecule type: DNA
A:Residues: 1-67 <EI>
A:Cross-references: EMBL:X65720; NID:953694; PIDN:CAA46636.1; PID:953695
C:Genetics:
A:Introns: 57/2
C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C; Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding; F36-85/Domain: protein kinase C zinc-binding repeat homology <K21>
F:101-150/Domain: protein kinase C zinc-binding repeat homology <K21>
F:151-264/Domain: protein kinase C C2 region homology <K22>
F:343-614/Domain: protein kinase C C2 region homology <K2>
F:357-365/Region: protein kinase ATP-binding motif

Query Match 75.5%; Score 37; DB 2; Length 697;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9

Db 548 MLAGQPPFD 556

RESULT 39

<4664
Protein kinase C (EC 2.7.1.1-) gamma - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1988 #sequence_revision 13-May-1996 #text_change 23-Mar-2001
C:Accession: D24664; S31611; S36837
R:Cousens, L.; Parker, P.J.; Rhee, L.; Yang-Feng, T.L.; Chen, E.; Waterfield, M.D.; Fagan, S.C.
Science 233, 859-866, 1986
A:Title: Multiple, distinct forms of bovine and human protein kinase C suggest diversity
A:Reference number: A94291; MUID:86289426; PMID:3755548
A:Accession: D24664
A:Molecule type: mRNA
A:Residues: 1-313 'VS', 316, 'T', 318 <COU>
A:Note: The authors translated the codon GCA for residue 170 as Ser and AOC for residue 179.

R:Hug, H.
Submitted to the EMBL Data Library, September 1992
A:Description: Partial cDNA sequence of human protein kinase C zeta.
A:Reference number: S25605
A:Accession: S31611
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 162-697 <HUG>
A:Cross-references: EMBL:Z15114; NID:935496; PIDN:CAA78920.1; PID:935497
R:Kochs, G.; Hummel, R.; Meyer, D.; Hug, H.; Marne, D.; Sarre, T.F.
Eur. J. Biochem. 216, 597-606, 1993

A:Title: Activation and substrate specificity of the human protein kinase C alpha and zeta
A:Reference number: S36836; MUID:93387312; PMID:8375396
A:Accession: S36837
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA

A:Residues: 162-697 <KOC>

A:Cross-references: EMBL:Z15114; NID:935496; PIDN:CAA78920.1; PID:935497

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 19

C:Genetics:

A:Gene: GDB:PRKCG

A:Cross-references: GDB:128017; OMIM:176980

A:Map position: 19q13.4-19q13.4

C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein

C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/thr

F:36-85/Domain: protein kinase C zinc-binding repeat homology <K21>

F:101-150/Domain: protein kinase C zinc-binding repeat homology <K21>

F:151-264/Domain: protein kinase C C2 region homology <K22>

F:349-614/Domain: protein kinase homology <KIN>

F:357-365/Region: protein kinase ATP-binding motif

Query Match 75.5%; Score 37; DB 2; Length 697;

Best Local Similarity 66.7%; Pred. No. 47;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9

Db 548 MLAGQPPFD 556

RESULT 39

S69657

hypothetical protein YDR490c - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002

C:Accession: S69657

R:Dietrich, F.S.

Submitted to the EMBL Data Library, August 1995

A:Description: The sequence of S. cerevisiae cosmid 9410, 8035, 8166, and 9787.

A:Reference number: S69554

A:Accession: S69657

A:Molecule type: DNA

A:Residues: 1-766 <DIE>

A:Cross-references: EMBL:U33050; NID:927726; PIDN:AAB64917.1; PID:927745; MIPS:YDR

C:Genetics:

A:Gene: SGD:PKH1

A:Cross-references: SGD:S0002898

A:Map position: 4R

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho

C:Keywords: ATP

F:123-391/Domain: protein kinase homology <KIN>

F:131-139/Region: protein kinase ATP-binding motif

Query Match 75.5%; Score 37; DB 2; Length 766;

Best Local Similarity 66.7%; Pred. No. 52;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9

Db 330 MLAGKPPFK 338

RESULT 40

T15903

protein kinase C homolog - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jun-2000

C:Accession: T15903

R:Fulton, B.

Submitted to the EMBL Data Library, June 1995

A:Description: The sequence of C. elegans cosmid E01H11.

A:Reference number: Z18426

A:Accession: T15903

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-861 <FUL>

A:Cross-references: EMBL:U29376; NID:9868170; PID:9868172; PIDN:AAA68710.1

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP.kin.11
 A:Accession: 79/1; 102/2; 136/1; 163/3; 244/1; 297/3; 377/3; 484/3; 552/3; 623/1; 669/3; 6
 C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kin
 F:104-153/Domain: protein kinase C zinc-binding repeat homology <KZN1>
 F:169-218/Domain: protein kinase C zinc-binding repeat homology <KZN2>
 Query Match 75.5%; Score 37; DB 2; Length 86;
 Best Loca: Similarity 66.7%; Pred. NC: 58;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy : MLLGRPF 9
 Db : 605 MLAGQPF 613

Search completed: November 14, 2003, 13:28:50
 Job time : 10.8 secs

Result No.	Query score	Query		Length	DB	ID	Description
		Match	%				
1	49	100.0	682	1	SNK_MOUSE	P53351	mus musculus
2	49	100.0	682	1	SNK_RAT	Q91012	rattus norv
3	49	100.0	685	1	SNK_HUMAN	Q91973	homo sapien
4	40	81.6	282	1	STKD_MOUSE	C68445	mus musculus
5	40	81.6	603	1	PLK1_HUMAN	P53350	homo sapien
6	40	81.6	603	1	PLK1_MOUSE	Q67832	mus musculus
7	40	81.6	603	1	PLK1_RAT	Q62673	rattus norv
8	39	79.6	576	1	POLO_DROME	P52104	drosophila
9	39	79.6	679	1	KPC1_HUMAN	P53130	drosophila
10	39	79.6	690	1	PKNB_BIFLAG	C696P9	bifidobacte
11	38	77.6	156	1	STKC_PIG	Q63X00	mus scrofa
12	38	77.6	344	1	STKC_HUMAN	Q66G34	homo sapien
13	38	77.6	403	1	STR6_HUMAN	Q14965	homo sapien
14	38	77.6	407	1	STR6_XENLA	Q91820	xenopus lae
15	38	77.6	408	1	STG1_XENLA	Q91819	xenopus lae
16	38	77.6	634	1	KPC3_GROVE	P13678	drosophila
17	38	77.6	649	1	PLK1_CAEEL	P14331	caenorhabdi
18	38	77.6	660	1	PKM1_COREP	C65115	corynebacte
19	39	77.6	683	1	PLD1_SCHPO	C65528	schistosacc
20	39	77.6	705	1	CDG5_YEAST	F32562	saccharomyc
21	39	77.6	707	1	KPC2_CAEEL	P14885	caenorhabdi
22	38	77.6	737	1	KPC2_RABIT	P10830	oryctolagus
23	38	77.6	736	1	KPC2_HUMAN	Q02156	homo sapien
24	38	77.6	737	1	KPC2_MOUSE	P16054	mus musculus
25	38	77.6	737	1	KPC2_RAT	P09216	rattus norv
26	38	77.6	743	1	KPC2_APLICA	Q16975	aplysia cal
27	37	75.5	220	1	NHAB_PSECL	P27763	pseudomonas
28	37	75.5	380	1	PKM5_MYXXA	P54737	myxococcus
29	37	75.5	632	1	PLK2_CAEEL	Q96217	caenorhabdi
30	37	75.5	649	1	KPC1_APLICA	Q16974	aplysia cal
31	37	75.5	658	1	KPC1_DLYPE	Q25179	lytechinus
32	37	75.5	672	1	KPCA_BOVIN	P34409	bos taurus
33	37	75.5	672	1	KPCA_HUMAN	P17252	homo sapien

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FT BINDING 108 108 ATP (BY SIMILARITY).
FT ACT_SITE 202 202 BY SIMILARITY.
FT DOMAIN 507 570 POLO BOX 1.
FT DOMAIN 603 674 POLO BOX 2.
SQ SEQUENCE 682 AA: 7781 MW: 586DEABPD720HA9D CRC64:
Query Match 100.0%; Score 49; DB 1; Length 682;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPE 9
Db 270 MLLGRPPE 278

RESULT 2
SNK RAT STANDARD; PRT; 682 AA.
AC Q9R12; 060679; Q96CV7; Q9UE61;
DT 16-OCT-2001 (Rel. 40, Created;
DT 16-OCT-2001 (Rel. 40, Last sequence update;
DT 16-OCT-2001 (Rel. 40, Last annotation update;
DE Serine/threonine-protein kinase SNK (EC 2.7.1.1) (Serum inducible
DE kinase).
GN SNK
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9745276; PubMed=10531297;
RA Kauselmann G., Weiler M., Wulff P., Jessberger S., Konietzko U.,
RA Seifried C., Staab U., Breiter-Hahn J., Streibhardt K., Kuhl D.;
RA "The polo-like protein kinases Pnk and Snk associate with a Ca(2+)-and
RA integrin-binding protein and are regulated dynamically with synaptic
RA plasticity."
RL EWOC J. 38:528-539(1999).
CC -!- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL
CC -!- TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS,
CC WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 2 POLO BOX DOMAINS.
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CC or send an email to license@ebi.ac.uk).
CC
CC EMBL: AF165533; AAF08366.1;
CC InterPro: IPR000959; POLO box.
CC InterPro: IPR033719; Prot_kinase.
CC InterPro: IPR002290; Ser_Thr_kinase.
CC Pfam: PF0069; pkinase; 1.
CC Pfam: PF00653; POLO box; 2.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00220; S_TKc; 1.
CC PROSITE: PS50078; POLO BOX; 2.
CC PROSITE: PS03107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS50311; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS03108; PROTEIN_KINASE_ST; 1.
CC Transferase: Serine/threonine-protein kinase; ATP-binding; Repeat.
FT DOMAIN 54 59 POLY-HIS.
FT DOMAIN 73 331 PROTEIN_KINASE.
FT RP_BIND 95 93 ATP (BY SIMILARITY).
FT BINDING 109 108 ATP (BY SIMILARITY).
FT ACT_SITE 202 202 BY SIMILARITY.
FT DOMAIN 507 570 POLO BOX 1.
FT DOMAIN 603 674 POLO BOX 2.
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SQ SEQUENCE 682 AA: 779:9 MW: 58C50DEBDE83D5F3 CRC64;
Query Match 100.0%; Score 49; DB 1; Length 682;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPE 9
Db 270 MLLGRPPE 278

RESULT 3
SNK HUMAN STANDARD; PRT; 685 AA.
AC Q9NTY3; 060679; Q96CV7; Q9UE61;
DT 16-OCT-2001 (Rel. 40, Created;
DT 28-FEB-2003 (Rel. 41, Last sequence update;
DT 15-SEP-2003 (Rel. 42, Last annotation update;
DE Serine/threonine-protein kinase SNK (EC 2.7.1.1) (Serum inducible
DE kinase).
GN SNK
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ouyang B., Dai W.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Anderson K.M., Nerurkar S.S., Hansbury M.J., Fornwald J., Scott G.,
RA Bouzyk M., Mui P., Imbruglia G.S., Carlson K., Marshall L.A.,
RA Roshak A.K.;
RA "Identification and characterization of human serum-inducible kinase
RA (SNK), a novel member of the polo-kinase family of cell cycle
RA regulators: potential implication for regulation of vascular smooth
RA muscle proliferation."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=2238257; PubMed=1247932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wörley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 110-408 FROM N.A.
RA Fidler C., Boultwood J., Wang Jabs E., Wainscoat J.S.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL
CC -!- TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS,
CC WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
```

```
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AF059617; AAC14573.1;
DR EMBL: AF223574; AAF62897.1;
DR EMBL: U85755; AAC00575.1;
DR EMBL: H0013879; AAH13879.1;
DR MIN: 607023;
DR InterPro: IPR000959; POLO_box;
DR InterPro: IPR000719; Prot_kinase;
DR InterPro: IPR002290; Ser_thr_pkinase;
DR Pfam: PF00069; pkinase; 1;
DR Pfam: PF00659; POLO_box; 2;
DR ProDom: PD030001; Prot_kinase; 1;
DR SMART: SM00220; S_TKC; 1;
DR ProSITE: PS00078; POLO_BOX; 2;
DR ProSITE: PS00107; PROTEIN_KINASE_ATP; 1;
DR ProSITE: PS00011; PROTEIN_KINASE_DOM; 1;
DR ProSITE: PS00108; PROTEIN_KINASE_ST; 1;
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
FT DOMAIN 57 64 POLY-HIS.
FT DOMAIN 82 334 PROTEIN_KINASE.
FT NP_BIND 88 96 ATP (BY SIMILARITY).
FT BINDING 111 111 ATP (BY SIMILARITY).
FT ACT_SITE 205 205 BY SIMILARITY.
FT DOMAIN 510 573 POLC_BOX_1.
FT DOMAIN 606 677 POLC_BOX_2.
FT CONFLICT 28 28 A -> G (IN REF. 1).
SQ SEQUENCE 685 AA; 78236 MW; 642956FEF383CB13 CRC64;

Query Match 100.0%; Score 49; DB 1; Length 685;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
.. 273 MLGRRPPE 281

RESULT 4
STKD_MOUSE STANDARD; PRT; 282 AA.
AC 088445; Q9JLC2;
DT 28-FEB-2003 (Rel. 4); Created;
DT 28-FEB-2003 (Rel. 4); Last sequence update;
DT 15-SEP-2003 (Rel. 42); Last annotation update;
DE Serine/threonine protein kinase 13 (EC 2.7.1.37) (Aurora/Ipl1/Eg2
DE protein 1) (Aurora-C).
GN STK13 OR AIE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BAJB/C;
RA MEDLINE=99025616; PubMed=9809744;
RA Tserg T.C., Chen S.H., Hsu Y.P., Tang T.K.;
RA "Protein kinase profile of sperm and eggs: cloning and
RA characterization of two novel testis-specific protein kinases (AIE1,
RA AIE2) related to yeast and fly chromosome segregation regulators.";
RA DNA Cell Biol. 17:823-833(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129;
RA MEDLINE=25551164; PubMed=11098217;
```

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RA Hu H.M., Chuang C.K., Lee M.J., Tseng T.C., Tang T.K.;
RT "Genomic organization, expression, and chromosome localization of a
RT third aurora-related kinase gene, Aie1.";
RL DNA Cell Biol. 19:679-688(2000).
CC -!- FUNCTION: May play a part in organizing microtubules in relation
CC to the function of the centrosome/spindle pole during mitosis.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to spindle pole from anaphase to
CC cytokinesis (by similarity).
CC -!- TISSUE SPECIFICITY: Expressed only in testis.
CC -!- DEVELOPMENTAL STAGE: Expressed on day 14 dpc in prepubertal
CC testis, expression reached its plateau on day 21 dpc and remained
CC at a high level in adult.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AF054620; AAC25954.1;
DR EMBL: AF195272; AAF25838.1;
DR HSSP: Q63450; 1A06.
DR MGD: MGI:132119; Stk13.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR01245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1;
DR PRINTS: PR00169; TYRKINASE.
DR ProDom: PD000031; Prot_kinase; 1;
DR SMART: SM00220; S_TKC; 1;
DR ProSITE: PS00107; PROTEIN_KINASE_ATP; 1;
DR ProSITE: PS00108; PROTEIN_KINASE_ST; 1;
DR ProSITE: PS00011; PROTEIN_KINASE_DOM; 1;
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 16 266 PROTEIN_KINASE.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT CONFLICT 74 74 R -> P (IN REF. 2).
SQ SEQUENCE 282 AA; 32907 MW; 7C88AEC4984B7883 CRC64;

Query Match 91.6%; Score 40; DB 1; Length 282;
Best Local Similarity 66.7%; Pred. No. 2.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DB 205 LLVGKPPPE 213
.. :||: |||

RESULT 5
PLK1_HUMAN STANDARD; PRT; 603 AA.
ID PLK1_HUMAN
AC P53350;
DT 01-OCT-1996 (Rel. 34); Created;
DT 01-OCT-1996 (Rel. 34); Last sequence update;
DT 15-SEP-2003 (Rel. 42); Last annotation update;
DE Serine/threonine-protein kinase PLK (EC 2.7.1.-) (PLK-1) (Serine-
DE threonine protein kinase 13) (STPK13).
GN PLK OR PLK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RA MEDLINE=94289293; PubMed=8018557;
```

RA Hamanaka R., Maloid S., Smith M.R., O'Connell C.D., Longo D.L.,
 RA Ferris D.K.;
 RA "Cloning and characterization of human and murine homologues of the
 RA Drosophila polo serine-threonine kinase";
 RL Cell Growth Differ. 5:249-257(1994).
 RN (2).
 RP SEQUENCE FROM N.A. PubMed=7902533;
 RX MEDLINE=94067140; PubMed=7902533;
 RA Lake R.C., Jelinek W.R.;
 RA "Cell cycle- and terminal differentiation-associated regulation of
 RT the mouse mRNA encoding a conserved mitotic protein kinase";
 RI Mol. Cell. Biol. 13:7793-7801(1993).
 RN (3).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95051109; PubMed=7962193;
 RA Goldstein R.M., Schultz S.J., Bartek J., Ziemiecki A., Ried T.,
 RA Nigg E.A.;
 RA "Cell cycle analysis and chromosomal localization of human Plk1, a
 RT putative homologue of the mitotic kinases Drosophila polo and
 RT Saccharomyces cerevisiae Cdc5";
 RL J. Cell Sci. 107:1509-1517(1994).
 RN (4).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94173904; PubMed=8127874;
 RA Holtrich J., Wolf G., Braeckinger A., Karn T., Boehme B.,
 RA Rueschen-Wagmann H., Streibhardt K.;
 RA "Induction and down-regulation of Plk1, a human serine/threonine
 RT kinase expressed in proliferating cells and tumors";
 RI Proc. Natl. Acad. Sci. U.S.A. 91:1736-1740(1994).
 RN (5).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22389257; PubMed=12477932;
 RA Klausner R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ciachenko L., Marusina K., Farret A., Rubin G.M., Hong L.,
 RA Stepleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay S.J., Hulyk S.W.,
 RA Villalon D.K., Murry D.M., Sodergren E.C., Lu X., Gibbs S.A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Baifard G.G.,
 RA Bialesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Skallus D.E.,
 RA Scherch A., Schein J.E., Jones S.M., Marita M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 CC human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16895-16903(2002).
 CC (1). FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
 CC DURING G1 OR S PHASE.
 CC (2). SUBCELLULAR LOCATION: Nuclear.
 CC (3). TISSUE SPECIFICITY: PLACENTA AND COLON.
 CC (4). DEVELOPMENTAL STAGE: ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
 CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
 CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
 CC DURING S PHASE.
 CC (5). INDUCTION: BY GROWTH-STIMULATING AGENTS.
 CC (6). SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC COCS/POLO SUBFAMILY.
 CC (7). SIMILARITY: Contains 2 POLO box domains.
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 CC -----
 DR EMBL; U01038; AAA56634.1; -
 DR EMBL; L19559; AAA36659.1; -
 DR EMBL; X73458; CAA51837.1; -
 DR EMBL; X75932; CAA53536.1; -
 DR EMBL; BC002369; AAH02369.1; -
 DR EMBL; BC003002; AAH03002.1; -
 DR EMBL; BC014846; AAH14846.1; -
 DR PIR; S34130; S34130.
 DR Genew; HGNC:9077; PLK.
 DR GK; P53350; -
 DR MIM; 602098; -
 DR GO; GO:0004674; F:protein:serine/threonine kinase activity; TAS.
 DR GO; GO:0007067; P:mitosis; TAS.
 DR GO; GO:0007048; P:oncogenesis; TAS.
 DR GO; GO:0000074; P:regulation of cell cycle; TAS.
 DR InterPro; IPR000959; POLC box.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00659; POLO box; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS50078; POLO BOX; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
 KW Nuclear protein.
 FT DOMAIN 53 305 PROTEIN KINASE.
 FT NP_BIND 59 67 ATP (BY SIMILARITY).
 FT BINDING 82 82 ATP (BY SIMILARITY).
 FT ACT_SITE 176 176 BY SIMILARITY.
 FT DOMAIN 417 480 POLO BOX 1.
 FT DOMAIN 515 584 POLO BOX 2.
 FT CONFLICT 2 2 S -> T (IN REF. 1).
 FT CONFLICT 11 11 A -> P (IN REF. 1).
 FT CONFLICT 58 58 F -> L (IN REF. 1).
 FT CONFLICT 60 60 G -> S (IN REF. 1).
 FT CONFLICT 73 73 A -> V (IN REF. 2).
 FT CONFLICT 141 141 L -> P (IN REF. 4).
 FT CONFLICT 227 227 G -> E (IN REF. 4).
 FT CONFLICT 301 301 N -> G (IN REF. 2).
 FT CONFLICT 495 495 A -> G (IN REF. 2).
 FT CONFLICT 501 501 E -> Q (IN REF. 2).
 SQ SEQUENCE 603 AA; 68254 MW; 178C2F13C10E8206 CRC64;
 Query Match 81.6%; Score 40; DB 1; Length 603;
 ID Best Local Similarity 66.7%; Pred. No. 4.7;
 Matches 6; Conservative 3; Mismatches 0; Gaps 0;
 Qy 1 MLLGRPPPE 9
 Db 244 LLVGKPPPE 252
 RESULT 6
 ID PLK1_MOUSE STANDARD; PRT; 603 AA.
 AC Q07832;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine/threonine-protein kinase PLK (EC 2.7.1.-) (PLK-1) (serine-
 DE threonine protein kinase 13) (StpK13).
 GN PLK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of *Drosophila melanogaster*."
Science 287:2185-2195(2000).
CC -!- FUNCTION: MAY PLAY A ROLE IN REGULATING BOTH NUCLEAR AND
CC CYTOPLASMIC ASPECTS OF THE MITOTIC CYCLE.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: LARVAL DISCS, BRAIN AND TESTIS.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.

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CC or send an email to license@sib-sb.ch).

CC EMBL; X63361; CAA44963.1; .
CC EMBL; AE003514; AAF49036.1; .
CC PIR; S22127; S22127.
CC HSSP; Q63450; IAG6.
CC Flybase; FBgn0003124; polo.
CC GO; GO:0005813; C:centrosome; IDA.
CC GO; GO:0005819; C:spindle; IDA.
CC GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
CC GO; GO:0007140; P:male meiosis; IMP.
CC GO; GO:0007067; P:mitosis; IMP.
CC InterPro; IPR000959; POLO_box.
CC InterPro; IPR000719; prot_kinase.
CC InterPro; IPR002293; Ser_thr_kinase.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00659; POLO_box; 2.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SMC0220; S_TKC; 1.
CC PROSITE; PS00078; POLO_BOX; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC Transfaser; Serine/threonine-protein kinase; ATP-binding; Repeat.
KW DOMAIN 25 277 PROTEIN KINASE.
FT NP_BIND 31 39 ATP (BY SIMILARITY).
FT BINDING 54 54 ATP (BY SIMILARITY).
FT ACT_SITE 148 148 BY SIMILARITY.
FT DOMAIN 398 461 POLO_BOX_1.
FT DOMAIN 496 564 POLO_BOX_2.
FT CONFLICT 187 187 P -> A (IN REF. 1).
SQ SEQUENCE 576 AA; 66973 MW; 5022B9AC0E88FAD CRC64;

Query Match 79.6%; Score 39; DB 1; Length 576;
Best Local Similarity 66.7%; Pred. No. 6.9;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MELGRPFPE 9
Db 216 LLVGQPPFE 224
:::|::|::|

RESULT 9
KPC1_DROME STANDARD; PRT; 679 AA.
ID AC P05130; Q9V7V6; Q9V7V7;
DT 13-AUG-1987 (Rel. 05, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C, brain isozyme (EC 2.7.1.-) (PKC) (dPKC53E(BR)).
GN PKC53E OR KPC1 OR CG6622.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydrozoa; Drosophilidae; Drosophila.
OX NCBI: TaxID=7227;

Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of *Drosophila melanogaster*."
Science 287:2185-2195(2000).
CC -!- FUNCTION: MAY PLAY A ROLE IN REGULATING BOTH NUCLEAR AND
CC CYTOPLASMIC ASPECTS OF THE MITOTIC CYCLE.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: LARVAL DISCS, BRAIN AND TESTIS.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.

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CC or send an email to license@sib-sb.ch).

CC EMBL; X63361; CAA44963.1; .
CC EMBL; AE003514; AAF49036.1; .
CC PIR; S22127; S22127.
CC HSSP; Q63450; IAG6.
CC Flybase; FBgn0003124; polo.
CC GO; GO:0005813; C:centrosome; IDA.
CC GO; GO:0005819; C:spindle; IDA.
CC GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
CC GO; GO:0007140; P:male meiosis; IMP.
CC GO; GO:0007067; P:mitosis; IMP.
CC InterPro; IPR000959; POLO_box.
CC InterPro; IPR000719; prot_kinase.
CC InterPro; IPR02293; Ser_thr_kinase.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00659; POLO_box; 2.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SMC0220; S_TKC; 1.
CC PROSITE; PS00078; POLO_BOX; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC Transfaser; Serine/threonine-protein kinase; ATP-binding; Repeat.
KW DOMAIN 25 277 PROTEIN KINASE.
FT NP_BIND 31 39 ATP (BY SIMILARITY).
FT BINDING 54 54 ATP (BY SIMILARITY).
FT ACT_SITE 148 148 BY SIMILARITY.
FT DOMAIN 398 461 POLO_BOX_1.
FT DOMAIN 496 564 POLO_BOX_2.
FT CONFLICT 187 187 P -> A (IN REF. 1).
SQ SEQUENCE 576 AA; 66973 MW; 5022B9AC0E88FAD CRC64;

Query Match 79.6%; Score 39; DB 1; Length 576;
Best Local Similarity 66.7%; Pred. No. 6.9;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MELGRPFPE 9
Db 216 LLVGQPFPE 224
:::|::|::|

RESULT 9
KPC1_DROME STANDARD; PRT; 679 AA.
ID AC P05130; Q9V7V6; Q9V7V7;
DT 13-AUG-1987 (Rel. 05, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C, brain isozyme (EC 2.7.1.-) (PKC) (dPKC53E(BR)).
GN PKC53E OR KPC1 OR CG6622.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI: TaxID=7227;

```

RM PP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC SRA'N=Carton-S. and Oregon-R.
RX MEDLINE=87228499; PubMed=3107983;
RA Rosenzhal A., Rhee L., Yadegari R., Paro R., Ullrich A., Goeddel D.V.;
RT "Structure and nucleotide sequence of a Drosophila melanogaster
RL protein kinase C gene.";
RMBC C. 6:433-441(1987);
RN [2]
RP SEQUENCE FROM N.A.
RC SRA'N=Berkeley;
RX MEDLINE=20-96036; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amandides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazer R.G., Champe M., Efeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.-G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Plankenhorn C., Baldwin D.,
RA Bailew R.V., Basu A., Bakendale C., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Borshakov S.,
RA Barkova D., Borchan M.R., Buck C., Stockstein P., Brothier F.,
RA Chertis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
RA de Pazlos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Durkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Godek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman C.J., Hernandez J.R., Hock C.,
RA Hostin D., Houston K.A., Howland T.W., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshref A.,
RA Mount S.M., Voy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacich J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pellard C., Puri V., Reese M.G.,
RA Reibert K., Remington K., Saunders R.B.C., Scheeler F., Shen H.,
RA Shue B.C., Sider-Klimos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weirick G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao C., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RC Sequence 287:2185-2195(2003);
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC SRA'N=Berkeley; TISSUE=Ovary;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,
RA Charpe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R.A., Gonzalez M., Guarin H., Krommiller B., Li P.W., Liao G.,
RA Miranda A., Murgali C.J., Nunoo J., Pacich J.M., Paragas V., Park S.,
RA Patel S., Phouenavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
RA Celisner S.E.;
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RC -1- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC IsoId=P05130-1; Sequence=Displayed;
CC Name=Long;
CC IsoId=P05130-2; Sequence=VSP_004743;
CC Name=Short;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: HEAD NEURAL TISSUE.
CC -1- MISCELLANEOUS: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-
CC DEPENDENT, SERINE- AND THREONINE-SPECIFIC ENZYME.

```

Query Match

Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 6; Conservative 3; Mismatches 0; Gaps 0;

QY 1 MLGRRPPE 9
|||
DB 542 MLVGQPPED 550

RESULT 10
PKNE_BIFLO STANDARD; PRT; 690 AA.
AC Q836P9;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable serine/threonine-protein kinase pknB (EC 2.7.1.37).
GN PKNB OR R00589.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteriales; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium;
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC 2705;
RX MEDLINE=22294377; PubMed=1387267;
RA Schell M.A., Karimanzou M., Snel B., Vlianova D., Berger B.,
RA Press G., Zwielen M.-C., Desiere F., Bork P., Delley M.,
RA Pittmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract";
RI Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -|- SIMILARITY: CONTAINS 4 PASTA DOMAINS.
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).

EMBL; AEC14680; BAN24413.1;
DR InterPro; IPR005543; PASTA;
DR InterPro; IPR000719; Prot_Kinase;
DR InterPro; IPR002290; Ser_Thr_Kinase;
DR Pfam; PF00069; pkinase;
DR Pfam; PF03793; PASTA_2;
DR Pfam; PF00069; pkinase; 1;
DR ProDom; PD00069; Prot_Kinase; 1;
DR SMART; SM00740; PASTA; 4;
DR SMART; SM00220; S_TKc; 1;
DR SMART; SM00219; TYKc; 1;
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1;
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1;
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1;
KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW ATP binding; Repeat; Complete proteome;
FT DOMAIN 14 285 PROTEIN KINASE.
FT DOMAIN 399 467 PASTA 1;
FT DOMAIN 468 536 PASTA 2;
FT DOMAIN 539 601 PASTA 3;
FT DOMAIN 602 666 PASTA 4;
FT DOMAIN 667 689 GLY-RICH;
FT NP_BIND 22 28 ATP (BY SIMILARITY);
FT BINDING 43 43 ATP (BY SIMILARITY);
FT ACT_SITE 146 146 BY SIMILARITY;
SQ SEQUENCE 690 AA; 7223 MW; 6A49EABCE5D92D CRC64;

Query Match 79.6%; Score 39; DB 1; Length 690.
Best Local Similarity 87.5%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPE 8
|||
DB 217 MLTGRPPE 224

RESULT 11
STKC_PIG STANDARD; PRT; 156 AA.
AC Q9NOX0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase 12 (EC 2.7.1.37) (Aurora-B;
DE fragment);
GN STK12.
OS Sus scrofa (pig);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus;
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=2223238; PubMed=12270437;
RA Braun F., Hosseini S.W., Lorf T., Laabs S., Ringe B.;
RT "Differential gene expression during intestinal ischemia-reperfusion
RT injury";
RI Transplant. Proc. 34:2301-2302(2002).
CC -|- FUNCTION: Maybe directly involved in regulating the cleavage of
CC polar spindle microtubules and is a key regulator for the onset of
CC cytokinesis during mitosis (By similarity).
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -|- SUBCELLULAR LOCATION: Localized to the midzone of central spindle
CC in late anaphase and concentrated into the midbody in telophase
CC and cytokinesis. Colocalized with gamma tubulin in the mid-body
CC (By similarity).
CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.

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or send an email to license@sib-sib.ch).

EMBL; AF243364; AAP61735.1;
DR InterPro; IPR002052; N6_Mase;
DR InterPro; IPR000719; Prot_Kinase;
DR InterPro; IPR002290; Ser_Thr_Kinase;
DR Pfam; PF001245; Tyr_pkinase;
DR Pfam; PF00069; pkinase; 1;
DR PRINTS; PR00109; TYRKINASE;
DR ProDom; PD000001; Prot_Kinase; 1;
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1;
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1;
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding.
FT NON_TER 1 1
FT DOMAIN <1> 156 PROTEIN KINASE.
FT ACT_SITE 51 51 BY SIMILARITY.
FT NON_TER 156 156
SQ SEQUENCE 156 AA; 17867 MW; CD23040EDB633FCE CRC64;

Query Match 77.6%; Score 38; DB 1; Length 156;
Best Local Similarity 66.7%; Pred. No. 2.8;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
|||
DB 117 LLVGNPPE 125

RESULT 12

STXN_HUMAN STANDARD; PRT; 344 AA.
AC Q96G04; O14630; G60446; Q95083; Q96G05; Q9JQ46;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase 12 (EC 2.7.1.37) (Aurora- and Ipl1-
DE like midbody-associated protein 1) (AIM-1) (Aurora/PL1-related kinase
DE 2) (Aurora-related kinase 2) (STK-1) (Aurora-B).
GN STK12 OR AIM1 OR ARK2 OR AIK2.
OS Homo sapiens (Human)
OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
OC Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=98183439; PubMed=9514916;
RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
RT "cDNA cloning, expression, subcellular localization, and chromosomal
RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)
RT 1 and 2".
RL Biochem. Biophys. Res. Commun. 244:285-292(1998).
RN 2;
RP SEQUENCE FROM N.A.
RX MEDLINE=99025855; PubMed=9803983;
RA Tatsuka M., Katayama H., Ota T., Tanaka T., Odashima S., Suzuki F.,
RA Terada Y.;
RT "Multinuclearity and increased ploidy caused by overexpression of the
RT aurora- and Ipl1-like midbody-associated protein mitotic kinase in
RT human cancer cells".
RL Cancer Res. 58:4511-4516(1998).
PN 3;
RP SEQUENCE FROM N.A.
PC TISSUE=Liver, and Spleen;
RX MEDLINE=99077743; PubMed=9858806;
RA Kimura M., Matsuda Y., Yoshida T., Suta N., Okano Y.;
RT "Identification and characterization of STK12/AIK2: a human gene
RT related to aurora of Drosophila and yeast Ipl1".
RL Cytogenet. Cell Genet. 82:147-152(1998).
RN 4;
RP SEQUENCE FROM N.A.
RX MEDLINE=21364697; PubMed=1471245;
RA Prigent C., Gill R., Trower M., Sansseau P.;
RT "In silico cloning of a new protein kinase, AIK2, related to
RT Drosophila aurora using the new tool: EST Blast".
RL In Silico Biol. 1:123-128(1999).
PN 5;
RP SEQUENCE FROM N.A.
RA Zhang C., Yu L., Bi A.;
RT "Cloning of a novel human gene homologous to mouse STK 1".
RL Submitted (JUL-1997) to the EMBL/GenBank/CCRG databases.
PN 6;
RP SEQUENCE FROM N.A.
PC TISSUE=Lung, Lymph, and Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Xie S., Wang J., Hsieh F.,
RA Diachenko J., Marusina K., Farrer A.A., Rubin G.M., Horg L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Tsien R.B., Toshiyuki S., Carrincci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.C., Abramson R.D., Mullahey S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gurakar P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 7;
RP REVIEW
RX MEDLINE=21306577; PubMed=11413462;
RA Nigg B.A.;
RT "Mitotic kinases as regulators of cell division and its checkpoints".
RL Nat. Rev. Mol. Cell Biol. 2:21-32(2001).
CC 1- FUNCTION: May be directly involved in regulating the cleavage of
CC polar spindle microtubules and is a key regulator for the onset of
CC cytokinesis during mitosis.
CC 1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC 1- SUBCELLULAR LOCATION: Localized to the midzone of central spindle
CC in late anaphase and concentrated into the midbody in telophase
CC and cytokinesis. Colocalized with gamma tubulin in the mid-body.
CC 1- TISSUE SPECIFICITY: High level expression seen in the thymus. It
CC is also expressed in the spleen, lung, testis, colon, placenta and
CC fetal liver. Expressed during S and G2/M phase and expression is
CC upregulated in cancer cells during M phase.
CC 1- DISEASE: Disruptive regulation of expression is a possible
CC mechanism of the perturbation of chromosome integrity in cancer
CC cells through its dominant-negative effect on cytokinesis.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC
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CC
CC EMBL; AF008552; AAC12709.1; -
CC EMBL; AB011450; BAA32136.1; -
CC EMBL; AB011446; BAA82709.1; -
CC EMBL; AF004022; AAB65786.1; -
CC EMBL; AF015254; AAC98891.1; -
CC EMBL; BC000442; AAH00442.1; -
CC EMBL; BC009751; AAH09751.1; -
CC EMBL; BC013300; AAH13300.1; -
CC HSSP; Q63450; 1A06.
CC Genew; HGNC:11390; STK12.
CC GIK; Q96G04; -
CC MIM; 604970; -
CC InterPro; IPR002052; N6_Mtase.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC SMART; SM00219; TyrKc; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 77 327
FT PROTEIN KINASE.
FT NP_BIND 83 91
FT BINDING 106 106 ATP (BY SIMILARITY).
FT ACT_SITE 200 200 BY SIMILARITY.
FT CONFLICT 14 15 RQ -> DK (IN REF. 5).
FT CONFLICT 70 70 R -> RR (IN REF. 6; AAH13300).
FT CONFLICT 161 161 E -> M (IN REF. 4 AND 5).
FT CONFLICT 167 169 QAS -> HKT (IN REF. 4).
FT CONFLICT 179 179 T -> TVRR (IN REF. 4).
FT CONFLICT 180 180 I -> VRV (IN REF. 5).
FT CONFLICT 226 226 P -> T (IN REF. 3).
FT CONFLICT 249 250 MH -> ID (IN REF. 3).
FT CONFLICT 271 271 MISSING (IN REF. 3).
FT CONFLICT 298 298 T -> M (IN REF. 6; AAH09751/AAH13300).

SQ SEQUENCE 344 AA; 39280 MW; 8325E3EF5A1FB170 CRC64;
 Query Match 77.6%; Score 38; DB 1; Length 344;
 Best Local Similarity 66.7%; Pred. No. 6.3;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VLLGRPPPE 9
 :|||:
 DB 266 LLVGNPPPE 274
 :|||:
 RESULT 13
 STK6 HUMAN STANDARD: PRT: 403 AA.
 AC Q14955; Q60445; Q75873; Q9BDQ6; Q9UPG5;
 DT 28-FEB-2003 (Rel. 41; Last sequence update)
 DE Serine/threonine kinase 6 (EC 2.7.1.37) (Serine/threonine kinase 15)
 DE (Aurora-A) (Breast-tumor-amplified kinase 1) (Aurora-related kinase 1) (BARK1)
 DE (Aurora-A) (Breast-tumor-amplified kinase 1) (Aurora-related kinase 1) (BARK1)
 GN STK6 CR STK15 CR AIK CR ARK1 CR AUKA OR BTKA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Hmo.
 CX NCBI_TaxID:9606;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC TISSUE:Brain;
 RX MEDLINE=97298083; PubMed=9553231;
 RA Kimura M., Kotani S., Hattori T., Sumi N., Yeshioka T., Todokoto K.,
 RA Okano Y.;
 RT "Cell cycle-dependent expression and spindle pole localization of a
 RT novel human protein kinase, Aik, related to Aurora of Drosophila and
 RT Yeast (p11)."
 RL C. Biol. Chem. 272:13766-13771(1997).
 RN 12;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98183439; PubMed=9514916;
 RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
 RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
 RT "cDNA cloning, expression, subcellular localization, and chromosomal
 RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)
 RT 1 and 2.";
 RL 1 and 2;
 RA Biochem. Biophys. Res. Commun. 244:285-292(1998).
 RN 13;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98442657; PubMed=9771714;
 RA Zhou H., Kuang J., Zhong L., Kuo W.L., Gray C.W., Sahin A.,
 RA Brinkley B.R., Sen S.;
 RT "Tumour amplified kinase STK15/BTKA induces centrosome amplification,
 RT aneuploidy and transformation.";
 RL Nat. Genet. 20:189-193(1998).
 RN 14;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones X., Stavrides G., Almeida J.P., Babbage A.K., Aggleley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Bead C.M., Beare D.M.,
 RA Beasley C.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck C., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corry N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grahn D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leivaalao M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McMay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.M., Ramey H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Williams J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN 16;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cervix, Colon, Kidney, and Muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Jodan T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN 17;
 RP CELL-CYCLE REGULATION.
 RX MEDLINE=21895866; PubMed=11790771;
 RA Tanaka M., Ueda A., Kanamori H., Ideguchi H., Yang J., Kitajima S.,
 RA Ishigatsubo Y.;
 RT "Cell-cycle-dependent regulation of human aurora A transcription is
 RT mediated by periodic repression of E4f1.";
 RL J. Biol. Chem. 277:10719-10726(2002).
 RN 18;
 RP REVIEW.
 RX MEDLINE=21306577; PubMed=11413462;
 RA Nigg E.A.;
 RT "Mitotic kinases as regulators of cell division and its checkpoints.";
 RL Nat. Rev. Mol. Cell Biol. 2:21-32(2001).
 CC 1- FUNCTION: May play a role in cell cycle regulation during anaphase
 CC and/or telophase, in relation to the function of the
 CC centrosome/spindle pole region during chromosome segregation.
 CC Maybe involved in microtubule formation and/or stabilization. May
 CC play a key role during tumor development and progression.
 CC 1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC 1- SUBCELLULAR LOCATION: Localizes on centrosomes in interphase cells
 CC and at each spindle pole in mitosis.
 CC 1- TISSUE SPECIFICITY: Highly expressed in testis and weakly in
 CC colon, ovarian, prostate, neuroblastoma, breast and cervical
 CC cancer cell lines. Expression is cell-cycle regulated, low in
 CC G1/S, accumulates during G2/M, and decreases rapidly after.
 CC 1- PTM: Phosphorylated
 CC 1- DISEASE: Defects in STK6 are responsible for numerical centrosome
 CC aberrations including aneuploidy.
 CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC AURORA SUBFAMILY.
 CC 1- CAUTION: Ref.1 sequence differs from that shown due to frameshifts

Serine/threonine protein kinase Eg2 (EC 2.7.1.37) (pB92) (p456g265).

DE Serine/threonine protein kinase Eg2 (EC 2.7.1.37) (pB92) (p456g265).
GN
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
OX [1]
RN
RP
SEQUENCE FROM N.A.
RC
TISSUE=Egg;
RX MEDLINE=98122855; PubMed=9454730;
RA Roghi C., Giet R., Ubekov R., Morin N., Chartrain I., Le Guellec R.,
RA Couturier A., Doree M., Philippe M., Prigent C.,
RA "The Xenopus protein kinase p32 associates with the centrosome in a
RT cell cycle-dependent manner, binds to the spindle microtubules and is
RT involved in bipolar mitotic spindle assembly.";
RL J. Cell Sci. 111:557-572(1998).
CC
CC -!- FUNCTION: Associates with the centrosome in a cell-cycle dependent
CC manner and invades the microtubules at the poles of the spindle
CC during mitosis suggesting that it may be involved in the correct
CC formation of bipolar mitotic spindles.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis
CC especially from prophase through anaphase. Partially colocalised
CC with gamma tubulin in the centrosome, from S to M phase.
CC -!- TISSUE SPECIFICITY: Highly expressed in ovary and testis.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- AURORA SUBFAMILY.
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CC
DR EMBL; Z17207; CAAT78915.1; -
DR PIR; S52243; S52243.
DR HSPSP; P24941; 1AQ1.
DR InterPro; IPR007119; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pk_kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS0108; PROTEIN_KINASE_ST; 1.
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 140 390 PROTEIN KINASE.
FT NP_BIND 146 154 ATP (BY SIMILARITY).
FT BINDING 169 169 ATP (BY SIMILARITY).
FT ACT_SITE 263 263 BY SIMILARITY.
FT SEQUENCE 407 AA; 46372 MW; DE1628A2C6D11277 CRC64;
SQ
Query Match 77.6%; Score 38; DB 1; Length 407;
Best Local Similarity 75.0%; Pred. No. 7.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

QY      2  LLORPFFE  9
      |:|:|:|
DB      330  LVGKPPFE 337

RESULT 15
ST6L_XENLA
ID-ST6L_XENLA  STANDARD;  PRT;  408  AA.
AC  Q91819;
DT  28-FEB-2003  (Rel. 41, Created)
DT  28-FEB-2003  (Rel. 41, Last sequence update)
DT  28-FEB-2003  (Rel. 41, Last annotation update)

```

DE Serine/threonine protein kinase Bg2-like (EC 2.7.1.37) [p46XLEq22].
 CC Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 CC Xenopodinae; Xenopus.
 CC NCBI: TaxID=8355;
 CC [1]; TaxID=8355;
 RN
 RP
 RP SEQUENCE FROM N.A.
 RC
 RC ISSUES: Egg.
 RA Rogni C., Le Guellec R., Paris C., Couturier A., Philippe M.
 RT "Eg2, selected by differential screening encodes a new Xenopus protein
 RT kinase family".
 RC Submitted (Oct-1992) to the EMBL/GenBank/DBJ databases.
 CC
 CC CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC
 CC SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis
 CC especially from prophase through anaphase. Partially colocalised
 CC with gamma tubulin in the centrosome, from S to M phase (by
 CC similarity).
 CC
 CC PTM: Phosphorylated (by similarity).
 CC
 CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC AURORA SUBFAMILY.
 CC
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 CC
 CC EMBL: Z17206; CAA78914.1; ALT_INIT.
 CC HSSP: P24941; IAG1.
 CC InterPro: IPR003719; Prot_Kinase.
 CC InterPro: IPR002290; Ser_Thr_kinase.
 CC Pfam: PF00369; pkinase; 1.
 CC ProDom: PD000031; Prot_Kinase; 1.
 CC SMART: SMC0220; S_TKc; 1.
 CC SMART: SMC0219; Tyr_Kc; 1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00111; PROTEIN_KINASE_DCM; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC Cell cycle; Transferrase; Serine/threonine-protein kinase; ATP binding;
 KW Phosphorylation.
 FT DOMAIN 146 390 PROTEIN KINASE.
 FT NP_BIND 146 154 ATP (BY SIMILARITY).
 FT BINDING 146 169 ATP (BY SIMILARITY).
 FT ACT_SITE 263 263 BY SIMILARITY.
 SQ SEQUENCE 406 AA, 46461 MW, 9756A63C7157AEE5 QRCE4.
 Query Match 77.6%; Score 18, DB 1; Length 408;
 Best Local Similarity 75.0%; Pred. No. 7.5;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LLGRPPFE 9
 Db 33C LVGRPPFE 337
 RESULT 16
 KPC3 DROME
 ID KPC3 DROME STANDARD; PRT; 534 AA.
 AC 213678; Q9VAA06.
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 GN Protein kinase C (EC 2.7.1.1) (PKC) (GPKC98F).
 GN PKC98E OS PKC3 OR CG1954
 OS Drosophila melanogaster (fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Reoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI: TaxID=7227;
 RN [1].

RP
 RX SEQUENCE FROM N.A.
 RX MEDLINE=89249302; PubMed=2720775;
 RA Schaeffer E., Smith D., Mardon G., Quinn W., Zuker C.;
 RT "Isolation and characterization of two new Drosophila protein kinase
 RT C genes, including one specifically expressed in photoreceptor
 RT cells".
 RL Cell 57:403-412(1989).
 RN [2]
 RP
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andreva-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadeu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Hartis M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li C., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,
 RA Shue B.C., Siden-Kiamos S., Simpson M., Skupski M.P., Smith T.,
 RA Spier E.C., Stadling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster".
 RL Science 287:2185-2195(2000).
 CC
 CC -1- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
 CC
 CC -1- MISCELLANEOUS: THIS IS A CALCIUM-ACTIVATED,
 CC PHOSPHOLIPID-DEPENDENT, SERINE- AND THREONINE-SPECIFIC ENZYME.
 CC
 CC -1- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
 CC BINDING DOMAINS.
 CC
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC
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 CC
 CC EMBL: J04848; AAA28818.1;
 CC EMBL: AE003768; AAF56846.1; ALT_INIT.
 CC PIR: P32392; B32392.
 CC HSSP: P28867; IPTQ.
 CC FlyBase: FBgc001033; PKC98E.
 CC InterPro: IPR002219; DAG_PE-bind.
 CC DR

InterPro: IPR003361; Pkinase_C.
 InterPro: IPR000719; Prot_kinase.
 InterPro: IPR002290; Ser_thr_kinase.
 Pfam: PF00130; DAG_PE-bind_2.
 Pfam: PF00269; pkinase_1.
 Pfam: PF00433; pkinase_C_1.
 PRNTS: PD00038; DAGPEDOMAIN.
 ProDom: PD000021; Prot_Kinase; 1.
 SMART: SM0109; C1_2.
 SMART: SM0133; S-TK_X; 1.
 SVART: SY00220; STKG; 1.
 PROSITE: PS02479; DAG_PE_BIND_DOM_1; 2.
 PROSITE: PS0381; DAG_PE_BIND_DOM_2; 2.
 PROSITE: PS0107; PROTEIN KINASE ATP; 1.
 PROSITE: PS0011; PROTEIN KINASE DOM; 1.
 PROSITE: PS0108; PROTEIN KINASE ST; 1.
 Calcium-binding; Repeat; ATP-binding; Transferase;
 Serine/threonine-protein kinase; Multigene family; Zinc;
 Phorbol-ester binding.
 DCMAIN: 72 121 PHORBOL-ESTER AND DAG BINDING 1.
 FT DCMAIN 147 196 PHORBOL-ESTER AND DAG BINDING 2.
 FT DCMAIN 303 560 PROTEIN KINASE.
 FT NP_BIND 309 317 ATP [BY SIMILARITY].
 FT BINDING 332 332 ATP [BY SIMILARITY].
 FT ACT_SITE 427 427 BY SIMILARITY.
 SO SEQUENCE 634 AA; 71156 MW; 3AE3AD6B7A276BA CRC64;

Query Match 77.6%; Score 38; DB 1; Length 634;
 Best Local Similarity 66.7%; Pred.No.12;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 3;

QY 1 MLAGRPFE 9
 LAGRPFE
 PL 495 MLAGRPFE 503

RESULT 1:
 ID PKI_CABEL STANDARD; PAT; 649 AA.
 DT P4331; Q61662; O76763; A7
 DT 01-FEB-1994 (rel. 28, Created)
 DT 28-FEB-2003 (rel. 41, Last sequence update)
 DT 28-FEB-2003 (rel. 41, Last annotation update)
 DE Serine/threonine-protein kinase plx; EC 2.7.11.1 (Polo like
 Kinase-1).
 GN PLK1 OR PLCL OR CL4B9.4.
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;
 CC Rhabditidae; Pelodierinae; Caenorhabditis.
 CC NCBI_TaxID:6219;
 RN 1.
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RX MEDLINE=99304501; PubMed=10376213;
 RA Guyard B., Wang Y., Dai W.;
 RT "Caenorhabditis elegans contains structural homologs of human prk and
 plx".
 RL DNA Seq. 10:109-113(1999).
 RN 2.
 RP SEQUENCE FROM N.A. (ISOFORM A), FUNCTION, AND SUBCELLULAR LOCATION.
 RX STRAIN=Bristol N2;
 RX MEDLINE=20190108; PubMed=1060571;
 RA Chase D., Serafinas C., Ashcroft N., Kosinski M., Longo D.,
 RA Ferris D.K., Golden A.;
 RT "The polo-like kinase PLX-1 is required for nuclear envelope breakdown
 and the completion of meiosis in Caenorhabditis elegans".
 RL Genesis 26:26-41(2000).
 RN 3.
 RP SEQUENCE FROM N.A.
 RX STRAIN=Bristol N2;
 RX MEDLINE=94150718; PubMed=7963398;
 RA Wilson R., Ainscough R., Anderson K., Bayres C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kiraten J., Laister N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons S., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 RA Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans";
 RL Nature 368:32-38(1994).
 RN 4.
 RP REVISIONS, AND ALTERNATIVE SPLICING.
 RL Waterston R.;
 CC Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC FUNCTION: Required for oocyte nuclear envelope breakdown before
 entry of oocyte into spermatheca. In mitotic cells, plays a role
 in spindle organization and centrosome maturation. In meiotic
 cells, required for spindle dynamics and probably for spindle
 attachment to the chromosomes. Zygotic role in the development of
 the germline and nerve cord.
 CC SUBCELLULAR LOCATION: In mitosis, remains associated with
 centrosomes entering prophase through to anaphase. During
 metaphase, found at the centrosomes of the metaphase plate. In
 meiosis, detected at centrosomes after pronuclear meeting in post-
 meiotic 1-cell embryos. Associated with chromatin during
 chromosome segregation of anaphase and in the region between the
 dividing chromosomes. Cytoplasmic in mature, unfertilized oocytes.
 CC ALTERNATIVE PROCUCES:
 CC Event-Alternative splicing: Named isoforms=2;
 CC Name=b;
 CC IsoId=P34331-1; Sequence=Displayed;
 CC Name=a;
 CC IsoId=P34331-2; Sequence=VSP_004928;
 CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDC5/POLO SUBFAMILY.
 CC SIMILARITY: Contains 2 POLO box domains.

KW ATP-binding; Serine/threonine-protein kinase; Transferase; Repeat;
 KW Nuclear protein; Alternative splicing.
 FT DOMAIN 38 290
 FT NP BINDING 45 52
 FT BINDING 67 67
 FT ACT SITE 162 162
 FT DOMAIN 420 485
 FT DOMAIN 520 589
 FT VARSPLIT 93 89
 SQ SEQUENCE 649 AA; 73633 MW; 54C949F140D7A43B CRC64;

Query Match 77.6%; Score 15; DB 1; Length 643;
 Best Local Similarity 66.7%; Pred. No. 12;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPFE 9
 DB 229 LFGQPFPE 237

RESULT 19
 PKN1 COREF
 AC 08P3J5; STANDARD; PRT; 660 AA.
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Probable serine/threonine protein kinase CE0033 (NC 2.7.1.37).
 GN CE0033
 OS Corynebacterium efficiens.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
 CX NCBI_TaxID=152794;
 RN 1;
 RP SEQUENCE FROM N.A.
 SC STRAIN=YS 314 / AJ 12310 / DSM 44549 / JCM 11159;
 RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
 RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
 RA Usuda Y., Sugimoto S.;
 RT "The entire genomic sequence of Corynebacterium efficiens YS 314.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DSJ databases.
 CC 1. CATALYTIC ACTIVITY: ATP -> a protein - ADP + a phosphate.
 CC 2. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC 3. SIMILARITY: Contains 3 PASTA domains.
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 CC EMBL: APC05214; PAC16843.1;
 DR InterPro: IPR003543; PASTA
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF03793; PASTA; 3.
 DR Pfam: PF00569; kinase; 1.
 DR ProDom: PD000003; Prot_kinase; 1.
 DR SMART: SM00740; PASTA; 3.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TyrKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW Hypothetical protein; Transferase; Serine/threonine protein kinase;
 KW ATP-binding; Repeat; Complete proteome.
 FT DOMAIN 9 278
 FT DOMAIN 377 443
 FT DOMAIN 444 512
 FT DOMAIN 512 512

FT DOMAIN 513 577
 FT NP BIND 15 23
 FT BINDING 38 38
 FT ACT SITE 136 136
 SQ SEQUENCE 660 AA; 69646 MW; D33D797EB02D4B1 CRC64;

Query Match 77.6%; Score 38; DB 1; Length 660;
 Best Local Similarity 66.7%; Pred. No. 12;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPFE 9
 DB 207 LVTGRPFE 215

RESULT 19
 PLO1 SCHPO
 ID PLO1 SCHPO STANDARD; PRT; 683 AA.
 AC P50528;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Serine/threonine-protein kinase p101 (EC 2.7.1.37).
 GN PLO1 OR SPAC23C11.16.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes.
 CX NCBI_TaxID=4896;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=95262899; PubMed=7744248;
 RA Okura H., Hagan I.M., Glover D.M.;
 RT "The conserved Schizosaccharomyces pombe kinase p101, required to
 RT form a bipolar spindle, the actin ring, and septum, can drive septum
 RT formation in G1 and G2 cells.";
 RL Genes Dev. 9:1059-1073(1995).
 RN 2;
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=1059360;
 RA Wood V., Gwilliam R., Rastandrea M.A., Lyne M., Lyne R., Stewart A.,
 RA Scuro J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsis K.,
 RA Jares K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Glynnprez B.,
 RA Welter J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs W., Fritze C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Bartell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC 1. FUNCTION: REQUIRED TO FORM A BIPOLAR SPINDLE, THE ACTIN RING AND
 CC SEPTUM. FUNCTIONS UPSTREAM OF THE WHOLE SEPTUM FORMATION PATHWAY,
 CC INCLUDING ACTIN RING FORMATION (REGULATED BY LATE SEPTATION GENES)
 CC AND SEPTAL MATERIAL DEPOSITION (REGULATED BY EARLY SEPTATION
 CC GENES). BEHAVES AS A "SEPTUM-PROMOTING FACTOR", AND COULD ALSO BE

CC INVOLVED IN INDUCING OTHER LATE EVENTS OF CELL DIVISION.

CC - CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC CDC5/POLO SUBFAMILY.

CC - SIMILARITY: Contains 2 POLO box domains.

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CC EMBL; X85758; CAA59766.1; .

CC EMBL; Z98559; CAB1167.1; .

CC PIR; T38254; T38254.

CC HSSP; Q63450; 1A06.

CC GeneDB Spombe; SPAC23C1.16; .

CC InterPro; IPR000959; POLO_box.

CC InterPro; IPR000719; Prot_kinase.

CC Pfam; PF00069; pkinase; 1.

CC ProDom; PD000001; Prot_kinase; 1.

CC SMART; SMC0220; S_TKC; 1.

CC PROSITE; PS00078; POLO_BOX; 2.

CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

CC Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.

CC DOMAIN 41 296 PROTEIN_KINASE.

CC NP_BIND 47 55 ATP (BY SIMILARITY).

CC BINDING 69 69 ATP (BY SIMILARITY).

CC ACT_SITE 163 163 BY SIMILARITY.

CC DOMAIN 500 567 POLO_BOX 1.

CC DOMAIN 624 670 POLO_BOX 2.

CC SEQUENCE 683 AA; 77301 MW; F1CD0EF9B31917 CRC64;

Query Match 77.6%; Score 38; DB 1; Length 683;

Best Local Similarity 55.6%; Pred. No. 13;

Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9

DR 233 LLGKRPPEQ 241

RESULT 20

CDC5_YEAST

AC CDC5_YEAST STANDARD; PRT; 705 AA.

AC P32562;

DI 01-OCT-1993 (Rel. 27, Created)

DI 01-OCT-1993 (Rel. 27, Last sequence update)

DI 15-SEP-2003 (Rel. 42, Last annotation update)

DE Cell cycle protein kinase CDC5/MSD2 (EC 2.7.1.37);

GN CDC5 OR PAX2 OR MSD2 OR YMR001C OR YMR270.03C.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3364A;

RC MEDLINE=93109479; PubMed=8321244;

RA Kitada K., Sugino A., Johnston L.H., Johnson A.L.;

RT "A multicopy suppressor gene of the Saccharomyces cerevisiae G1 cell

RT cycle mutant gene dbf4 encodes a protein kinase and is identified as

RT CDC5.";

RJ Mol. Cell. Biol. 13:4445-4457(1993).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=S288C / AB972;

RX PubMed=9169872;

RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,

RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,

RA Jagels K., Lyle G., Moule S., Odell C., Pearson D., Rajandream M.A.,

RA Rice P., Skelton J., Walsh S., Whitehead S., Bartell B.G.;

RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome

RT XIII.";

RL Nature 387:90-93(1997).

RN [3]

RP PHOSPHORYLATION OF SCCL.

RX PubMed=11371343;

RA Alexandru G., Uhlmann F., Mechtler K., Poupard M.-A., Nasmith K.;

RT "Phosphorylation of the cohesin subunit Sccl by Polo/Cdc5 kinase

RT regulates sister chromatid separation in yeast.";

RL Cell 105:459-472(2001).

CC - CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC CDC5/POLO SUBFAMILY.

CC - SIMILARITY: Contains 2 POLO box domains.

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CC or send an email to license@isb-sib.ch).

CC EMBL; M84220; AAA02576.1; .

CC EMBL; Z48613; CAA88516.1; .

CC PIR; A48144; A48144.

CC HSSP; Q63450; 1A06.

CC SGD; S0004603; CDC5.

CC GO; GO:0005634; C:nucleus; IDA.

CC GO; GO:0006261; P:DNA dependent DNA replication; IDA.

CC GO; GO:0006468; P:protein amino acid phosphorylation; IDA.

CC InterPro; IPR000959; POLO_box.

CC InterPro; IPR000719; Prot_kinase.

CC InterPro; IPR002290; Ser_thr_kinase.

CC Pfam; PF00069; pkinase; 1.

CC Pfam; PF00659; POLO_box; 2.

CC PRINTS; PR00109; TYRKINASE.

CC ProDom; PD000001; Prot_kinase; 1.

CC SMART; SMC0220; S_TKC; 1.

CC PROSITE; PS00078; POLO_BOX; 2.

CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

CC Cell cycle; Cell division; Serine/threonine-protein kinase;

CC Transferase; ATP-binding; Repeat.

CC DOMAIN 82 337 PROTEIN_KINASE.

CC NP_BIND 88 96 ATP (BY SIMILARITY).

CC BINDING 110 110 ATP (BY SIMILARITY).

CC ACT_SITE 204 204 BY SIMILARITY.

CC DOMAIN 520 587 POLO_BOX 1.

CC DOMAIN 619 692 POLO_BOX 2.

CC SEQUENCE 705 AA; 81030 MW; B5A25F1BBEAA3DC CRC64;

Query Match 77.6%; Score 38; DB 1; Length 705;

Best Local Similarity 55.6%; Pred. No. 13;

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9

DR 274 LLGKRPPEQ 282

RESULT 21

KPC2_CAEEL

ID KPC2_CAEEL STANDARD; PRT; 707 AA.

AC P34885; 1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 CC 15 JUL-1999 (Rel. 38, Last annotation update)
 DE Protein Kinase C-like 2 (EC 2.7.1.1) (PKC1B)
 UN K1N-13 OR PKC1B
 CS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditioidea;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 CX K1B; TaxID=6239;
 PY 1;
 PE SEQUENCE FROM N.A.
 RC STRAIN=BT1501; N2;
 RX MEDLINE=94179145; PubMed=8132661;
 RA Land M., Islas-Trejo A., Freedman J.H., Rubin C.S.;
 RT "Structure and expression of a novel, neuronal protein kinase C
 (PKC1B) from Caenorhabditis elegans. PKC1B is expressed selectively
 RT in neurons that receive, transmit, and process environmental
 RT signals."
 RJ C. Biol. Chem. 269:9234-9244 (1994).
 CC 1- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
 CC 2- SUBCELLULAR LOCATION: ASSOCIATED WITH MEMBRANES AND THE
 CC CYTOSKELETON.
 CC T-ISSUE SPECIFICITY: EXPRESSED SELECTIVELY IN NEURONS THAT RECEIVE.
 CC TRANSMIT AND PROCESS ENVIRONMENTAL SIGNALS.
 CC 3- SIMILARITY: Contains 2 zinc-dependent phorbol ester and DAG
 CC binding domains.
 CC 4- SIMILARITY: Contains 1 C2 domain.
 CC 5- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC
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 CC
 CC EMBL: U00381; AAA18259.1;
 CC EMBL: U00365; AAA17996.1;
 CC EMBL: A53530; A53530.
 CC HSSP: P28867; IPTQ.
 CC InterPro: IPR000008; C2.
 CC InterPro: IPR002219; DAG_PE-bind.
 CC InterPro: IPR000961; PKinase_C.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR002290; Ser_thr_kinase.
 CC Pfam: PF00168; C2; 1.
 CC Pfam: PF00130; DAG_PE-bind; 2.
 CC Pfam: PF00069; pkinaase; 1.
 CC Pfam: PF00433; pkinaase_C; 1.
 CC PRINTS: PR00068; DAGPEDOMAIN.
 CC ProDom: PD000001; Prot_kinase; 1.
 CC SMART: SM00239; C2; 1.
 CC SMART: SM00133; S_TK_X; 1.
 CC SMART: SM00220; S_TK; 1.
 CC PROSITE: PS50004; C2_DOMAIN_2; 1.
 CC PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
 CC PROSITE: PS00381; DAG_PE_BIND_DOM_2; 2.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC Transferase; Serine/threonine-protein kinase, ATP-binding; Zinc;
 KW Phorbol-ester binding; Repeat; Membrane; Cytoskeleton.
 FT DOMAIN 1 98
 FT DOMAIN 171 221 PHORBOL-ESTER AND DAG BINDING 1;
 FT DOMAIN 249 298 PHORBOL-ESTER AND DAG BINDING 2;
 FT DOMAIN 378 638 PROTEIN KINASE
 FT NP_BIND 384 392 ATP (BY SIMILARITY).

FT BINDING 407 407 ATP (BY SIMILARITY).
 FT ACT_SITE 502 502 BY SIMILARITY.
 SQ SEQUENCE 707 AA; 80122 MW; 3DC72C8A7A7BA64 CRC64;
 Query Match 77.6%; Score 38; DB 1; Length 707;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLGRRPPE 9
 Db 570 MMAGQPPPE 578
 RESULT 22
 KPCE RABIT STANDARD; PRT: 736 AA.
 ID KPCE RABIT
 AC PIC830;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Protein kinase C, epsilon type (EC 2.7.1.1) (nPKC-epsilon).
 GN PKCCE.
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 CC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88233367; PubMed=3370672;
 RA Ohno S., Akita Y., Konno Y., Imajoh S., Suzuki K.;
 RT "A novel phorbol ester receptor/protein kinase, nPKC, distantly
 RL Cell 53:731-741 (1988).
 CC 1- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
 CC SERINE- AND THREONINE-SPECIFIC ENZYME.
 CC 2- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
 CC 3- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC 4- SIMILARITY: Contains 1 C2 domain.
 CC 5- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC
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 CC
 CC EMBL: M20014; AAA31426.1;
 CC HSSP: P28867; IPTQ.
 CC InterPro: IPR000008; C2.
 CC InterPro: IPR002219; DAG_PE-bind.
 CC InterPro: IPR000961; PKinase_C.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR002290; Ser_thr_kinase.
 CC Pfam: PF00168; C2; 1.
 CC Pfam: PF00130; DAG_PE-bind; 2.
 CC Pfam: PF00069; pkinaase; 1.
 CC Pfam: PF00433; pkinaase_C; 1.
 CC PRINTS: PR00008; DAGPEDOMAIN.
 CC ProDom: PD000001; Prot_kinase; 1.
 CC SMART: SM00109; C1; 2_kinase; 1.
 CC SMART: SM00239; C2; 1.
 CC SMART: SM00133; S_TK_X; 1.
 CC SMART: SM00220; S_TK; 1.
 CC PROSITE: PS50004; C2_DOMAIN_2; 1.
 CC PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
 CC PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

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ER PROSITE: PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00128; PROTEIN_KINASE_SF; 1.
KW Repeat; ATP-binding; Transferase; Phosphorylation;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT DOMAIN 1 99 C2 DOMAIN.
FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 407 667 PROTEIN KINASE.
FT NP_BIND 423 421 ATP (BY SIMILARITY).
FT BINDING 436 436 ATP (BY SIMILARITY).
FT ACT_SITE 531 531 BY SIMILARITY.
FT MOD_RES 702 702 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 709 709 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 736 AA; 83515 MW; 26124FE59E95EB CRC64;

Query Match 77.6%; Score 38; DB 1; Length 736;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
Db 599 MMAGQPPPE 607

RESULT 23
KPCE_HUMAN STANDARD; PRT; 737 AA.
ID KPCE_HUMAN STANDARD; PRT; 737 AA.
AC Q02156; Q9U981;
DT 01-JUL-1993 (Rel. 26, Created);
DT 01-JUL-1993 (Rel. 26, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Protein kinase C, epsilon type (EC 2.7.1.1-) (npkc-epsilon).
GN PKCE OR PKCE.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RV MEDLINE=93033118; PubMed=1382605;
RA Batta P., Strickland M.B., Holmes W., Loomis C.R., Gallas L.M.,
RA Burns D.G.;
RT "Sequence and expression of human protein kinase C-epsilon.";
RL Biochim. Biophys. Acta 1132:154-160(1992);
RN [2]_TaxID=9606;
RP SEQUENCE OF 1-116 FROM N.A.
RA Waterston R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC 1-1- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC 1-1- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC 1-1- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC 1-1- SIMILARITY: Contains 1 C2 domain.
CC 1-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.

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EMBL: X65293; CAA46388.1;
DB EMBL: U51244; AAC38855.1;
DB PIR: S28942; S28942.
DB HSP: F48867; IPTQ.
DB Genes: HGNC:9401; PKCE.
DB MIM: 176975;

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DR GO: GO:0005624; C:membrane fraction; TAS.
DR GO: GO:0004697; F:protein kinase C activity; TAS.
DR GO: GO:0004871; F:signal transducer activity; TAS.
DR GO: GO:0006917; P:induction of apoptosis; TAS.
DR GO: GO:0006468; P:protein amino acid phosphorylation; TAS.
DR InterPro: IPR000308; C2.
DR InterPro: IPR002219; DAG PE-bind.
DR InterPro: IPR000961; PKinase C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00130; DAG PE-bind; 2.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00433; pkinase C; 1.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SM00239; C2; 1.
DR SMART: SM00133; S-TK X; 1.
DR SMART: SM00220; S-TKC; 1.
DR PROSITE: PS00004; C2 DOMAIN 2; 1.
DR PROSITE: PS00479; DAG PE BIND DOM 1; 2.
DR PROSITE: PS00081; DAG PE BIND DOM 2; 2.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_SF; 1.
KW Repeat; ATP-binding; Transferase; Phosphorylation;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT DOMAIN 1 99 C2 DOMAIN.
FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 408 668 PROTEIN KINASE.
FT NP_BIND 414 422 ATP (BY SIMILARITY).
FT BINDING 437 437 ATP (BY SIMILARITY).
FT ACT_SITE 532 532 BY SIMILARITY.
FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 710 710 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 737 AA; 83673 MW; 85032D0A091A1F7F CRC64;

Query Match 77.6%; Score 38; DB 1; Length 737;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
Db 603 MMAGQPPPE 608

RESULT 24
KPCE_MOUSE STANDARD; PRT; 737 AA.
ID KPCE_MOUSE STANDARD; PRT; 737 AA.
AC P16054;
DT 01-APR-1990 (Rel. 14, Created);
DT 01-APR-1990 (Rel. 14, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Protein kinase C, epsilon type (EC 2.7.1.1-) (npkc-epsilon).
GN PKCE OR PKCE OR PKCEA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RV MEDLINE=89137541; PubMed=2917656;
RA Schaap D., Parker P.J., Bristol A., Kriz R., Knopf J.;
RT "Unique substrate specificity and regulatory properties of
RT PKC-epsilon: a rationale for diversity.";
RL FEBS Lett. 243:351-357(1989);
RN [2]
RP SEQUENCE FROM N.A.
RV TISSUE=Brain;
RX MEDLINE=98127436; PubMed=9467942;
RA Wang Q.J., Acs P., Goodnight J., Blumberg P.M., Mischak H.,

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RA Mushinski, J.F.;
 RE "The catalytic domain of PKC-epsilon, in reciprocal PKC-delta and -
 RT epsilon chimeras, is responsible for conferring tumorigenicity to
 RT NIH3T3 cells, whereas both regulatory and catalytic domains of
 RT PKC-epsilon contribute to in vitro transformation.";
 R1. Oncogene 16:53-60(1998).
 R2.
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Wheeler D.L.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/CCDB databases.
 CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
 CC SERINE- AND THREONINE-SPECIFIC ENZYME.
 CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
 CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC -!- SIMILARITY: Contains 1 C2 domain.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC
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 DR EYBL; AF028009; BAB84189.1;
 DR EMBL; AF325507; BAG53692.1;
 DR PIR; S02270; KIMSCF.
 DR HSSP; P28867; IPTQ.
 DR MGI; MGI:97599; PKCK.
 DR GO; GO:0004699; F-calciun independent protein kinase C activity; IDA.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00130; DAG_PE-bind; 2.
 DR Pfam; PF00065; pkinase; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR PRINTS; PR00008; DAGPECDMAIN.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR ProSITE; PS00047; DAG_PE_BIND_DOM_1; 2.
 DR ProSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
 DR ProSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR ProSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR ProSITE; PS00138; PROTEIN_KINASE_ST; 1.
 KW Repeat; ATP-binding; Transferase; Phosphorylation;
 KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
 FT DOMAIN 1 99 C2 DOMAIN
 FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 408 668 PROTEIN KINASE
 FT NP_BIND 414 422 ATP (BY SIMILARITY).
 FT BINDING 437 437 ATP (BY SIMILARITY).
 FT ACT_SITE 532 532 BY SIMILARITY.
 FT MCD_RES 703 703 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MCD_RES 710 710 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 SQ SEQUENCE 737 AA; 83560 MW; 7AE888CC1C99F57 CRC64;

Query March 77.6% Score 38; DS 1; Length 737;
 Best local similarity 66.7% Pred. No. 14;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 DB 600 MWAGQPPPE 608
 RESULT 25
 KPCE_RAT
 ID KPCE_RAT STANDARD; PRT; 737 AA.
 AC P09216;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE PROTEIN kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
 GN PKCE OR KPCE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=88198270; PubMed=2834397;
 RA Ouo Y., Fujii T., Ogita K., Kikkawa U., Igatashi K., Nishizuka Y.;
 RT "The structure, expression, and properties of additional members of
 RT the protein kinase C family.";
 RL J. Biol. Chem. 263:6927-6932(1988).
 RN [2]
 RP SEQUENCE OF 135-297 FROM N.A.
 RX MEDLINE=88083621; PubMed=3691811;
 RA Ouo Y., Fujii T., Ogita K., Kikkawa U., Igatashi K., Nishizuka Y.;
 RT "Identification of three additional members of rat protein kinase C
 RT family: delta-, epsilon- and zeta-subspecies.";
 RL FEBS Lett. 226:125-128(1987).
 CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
 CC SERINE- AND THREONINE-SPECIFIC ENZYME.
 CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
 CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC -!- SIMILARITY: Contains 1 C2 domain.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC
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 CC
 DR EMBL; M18331; AAA41872.1;
 DR PIR; B28163; KIRTCF.
 DR PDB; 1GMI; 25-OCT-01.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00130; DAG_PE-bind; 2.
 DR Pfam; PF00065; pkinase; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR PRINTS; PR00008; DAGPECDMAIN.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00109; C1; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR ProSITE; PS00047; DAG_PE_BIND_DOM_1; 2.
 DR ProSITE; PS00081; DAG_PE_BIND_DOM_2; 2.

DR PROSITE; PS00081; DAG PE BIND DOM 2; 2;
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1;
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1;
 DR PROSITE; PS00118; PROTEIN KINASE ST; 1;
 KW Repeat; ATP-binding; Transferase; Phosphorylation;
 KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
 FT 1D-structure.
 FT DOMAIN 1 99 C2 DOMAIN
 FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1;
 FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2;
 FT DOMAIN 408 668 PROTEIN KINASE.
 FT NP BIND 414 422 ATP (BY SIMILARITY);
 FT BINDING 437 437 ATP (BY SIMILARITY);
 FT ACT SITE 532 532 BY SIMILARITY
 FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-); (POTENTIAL);
 FT MOD_RES 720 720 PHOSPHORYLATION (AUTO-); (POTENTIAL);
 SQ SEQUENCE 737 AA; 83478 MW; 6AD5999EFDD2659F CRC64;
 Query Match 77.6%; Score 38; DB 1; Length 737;
 Best local Similarity 66.7%; Pred. No. 14;
 Matches 6; Conservative 2; X-matches 1; Indels 0; Gaps 0;
 QY 1 MLLGRPPFE 9
 UG 600 MVAGQPPFE 608
 RESULT 24
 KP22_APLCA
 ID KP22_APLCA STANDARD; PRT: 743 AA.
 AC Q16975;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Calcium-independent protein kinase C (EC 2.7.11-); (APC II);
 GN PRKC2.
 OS Aplysia californica [California sea hare].
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidae;
 OC Aplysioidea; Aplysiidae; Aplysia.
 OX NCBI_TaxID:6550;
 RN [1]_SEQUENCE FROM N.A.
 RX MEDLINE=9332620; PubMed=1859917;
 RA Kruger A.E., Sossin W.S., Sacktor T.C., Baird P.L., Baumann S.,
 RA Schwartz J.H.;
 RT "Cloning and characterization of Ca²⁺-dependent and Ca²⁺-
 RT independent PKCs expressed in Aplysia sensory cells";
 RJ J. Neurosci. 11:2303-2313(1991).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=93394877; PubMed=8449941;
 RA Sossin W.S., Diaz-Arastia R., Schwartz J.H.;
 RT "Characterization of two isoforms of protein kinase C in the nervous
 RT system of Aplysia californica";
 RJ J. Biol. Chem. 268:5763-5768(1993).
 RN [3]
 RP DOMAIN C2.
 RX MEDLINE=93348616; PubMed=8346555;
 RA Sossin W.S., Schwartz J.H.;
 RT "Ca(2+)-independent protein kinase Cs contain an amino-terminal domain
 RT similar to the C2 consensus sequence";
 RJ Trends Biochem. Sci. 18:207-208(1993).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=9668085; PubMed=9668085;
 RA Pepio A.M., Fan X., Sossin W.S.;
 RT "The role of C2 domains in Ca²⁺-activated and Ca²⁺-independent protein
 RT kinase Cs in Aplysia";
 RJ J. Biol. Chem. 273:19040-19048(1998).
 RN [5]
 RP BRATUM.
 RA Pepio A.M., Fan X., Sossin W.S.;

RL J. Biol. Chem. 273:22856-22856(1998).
 [6]
 RN CHARACTERIZATION.
 RX MEDLINE=98138438; PubMed=9477951;
 RA Pepio A.M., Sossin W.S.;
 RT "The C2 domain of the Ca(2+)-independent protein kinase C Apl II
 RT inhibits phorbol ester binding to the C1 domain in a phosphatidic
 RT acid-sensitive manner";
 RJ Biochemistry 37:1256-1263(1998).
 RL Biochemistry 37:1256-1263(1998).
 CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
 CC SERINE- AND THREONINE-SPECIFIC ENZYME.
 CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
 CC SIMILARITY).
 CC -!- ENZYME REGULATION: REQUIRES HIGH LEVELS OF PHOSPHATIDYL SERINE TO
 CC BE ACTIVATED. THE PRESENCE OF THE C2 DOMAIN LOWERS THE AFFINITY OF
 CC PROTEIN KINASE C ACTIVATORS FOR THE C1 DOMAINS AND THIS INHIBITION
 CC CAN BE REMOVED BY PHOSPHATIDYL SERINE. PHOSPHATIDIC ACID, HOWEVER,
 CC IS MUCH MORE POTENT THAN PHOSPHATIDYL SERINE IN REDUCING C2 DOMAIN-
 CC MEDIATED INHIBITION, SUGGESTING THAT PHOSPHATIDYL SERINE IN REDUCING C2 DOMAIN-
 CC REQUIRED COFACTOR FOR THE ACTIVATION OF APL II.
 CC -!- SUBCELLULAR LOCATION: Membrane-associated.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN NERVOUS TISSUES, OVOTESTIS AND
 CC GUT.
 CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC -!- SIMILARITY: Contains 1 C2 domain.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; M94884; AAA27771.1; .
 DR HSSP; P28867; IPTQ.
 DR InterPro; IPR000308; C2.
 DR InterPro; IPR002219; DAG_PE_BIND.
 DR InterPro; IPR000961; PKinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00130; DAG_PE_BIND; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase_C; 1.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00189; C1; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS00499; C2_DOMAIN_1; FALSE NEG.
 DR PROSITE; PS50004; C2_DOMAIN_2; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
 DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Transferase; Serine/threonine-protein kinase;
 KW Phorbol-ester binding; Zinc; Repeat.
 FT DOMAIN 1 108 C2 DOMAIN.
 FT DOMAIN 177 226 PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 248 297 PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 403 663 PROTEIN KINASE.
 FT NP_BIND 409 417 ATP (BY SIMILARITY).
 FT BINDING 432 432 ATP (BY SIMILARITY).
 FT ACT_SITE 527 527 BY SIMILARITY
 SQ SEQUENCE 743 AA; 84413 MW; 4C982C563CA2B659 CRC64;

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Query Match      77.6%; Score 38; DB 1; Length 743;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 595 MMAGQPPFE 603

RESULT 27
NHAB_PSECL
ID NHAB_PSECL STANDARD; PRT; 220 AA.
AC P27763;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrile hydratase subunit beta (EC 4.2.1.84) (Nitrilase) (NHase).
GN NTHB.
OS Pseudomonas chlororaphis (Pseudomonas aureofaciens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
CX NCBI_TaxID=333;
RN P1;
RP SEQUENCE FROM N.A.
RX MEDLINE=91193202; PubMed=2013568;
RA Nishiyama M., Horinouchi S., Kobayashi M., Nagasawa T., Ya-ada H.,
RA Sefu T.;
RT "Cloning and characterization of genes responsible for metabolism of
RT nitrile compounds from Pseudomonas chlororaphis B23";
RA J. Bacteriol. 173:2465-2472(1991).
CC : FUNCTION: NHASE CATALYZES THE HYDRATION OF VARIOUS NITRILE
CC COMPOUNDS TO THE CORRESPONDING AMIDES. INDUSTRIAL PRODUCTION OF
CC ACRYLAMIDE IS NOW BEING DEVELOPED USING SOME OF THESE ENZYMES.
CC : CATALYTIC ACTIVITY: An aliphatic amide = a nitrile + H(2)O.
CC : SUBUNIT: Heterodimer of an alpha and a beta chain.
CC : SIMILARITY: BELONGS TO THE NITRILE HYDRATASE SUBUNIT BETA FAMILY.
CC
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CC or send an e-mail to license@isb-sib.ch).
CC
CC EMBL; D90216; BAA14246.1;
CC F18; B42725; B42725.
CC H5SP; F33449; 2AHJ.
CC InterPro; IPR003168; NHase_beta.
CC Pfam; PF02211; NHase_beta; 1.
CC Lyase.
CC
CC QUERY MATCH 75.5%; Score 37; DB 1; Length 220;
CC Best Local Similarity 75.0%; Pred. No. 6.2;
CC Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLGRPPFE 9
DB 118 LLGRPPFE 125

RESULT 28
PKN5 MYXXA
ID PKN5 MYXXA STANDARD; PRT; 360 AA.
AC P54737;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase pkn5 (EC 2.7.1.37).
DE Serine/threonine-protein kinase pkn5 (EC 2.7.1.37).
GN PKN5.

Query Match      75.5%; Score 37; DB 1; Length 380;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 314 LLGRPPFE 322

RESULT 29
PLK2 CAEEL
ID PLK2 CAEEL STANDARD; PRT; 632 AA.
AC Q9N2L7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase plk-2 (EC 2.7.1.-) (Polo-like
DE kinase-2).
GN PLK-2 OR Y71F9B.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
CX NCBI_TaxID=6239;
RN P1;
RP SEQUENCE FROM N.A.

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OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cystobacterineae; Myxococcaceae; Myxococcus.
CX NCBI_TaxID=34;
RN P1;
RP SEQUENCE FROM N.A.
RX STRAIN=DZF1;
RX MEDLINE=96310380; PubMed=8733241;
RA Zhang W., Inouye M., Inouye S.;
RT "Reciprocal regulation of the differentiation of Myxococcus xanthus
RT by Pkn5 and Pkn6, eukaryotic-like Ser/Thr protein kinases.";
RL Mol. Microbiol. 20:435-447(1996).
CC : FUNCTION: Pkn5 and pkn6 may have reciprocal roles in growth and
CC development. Pkn5 may be a kinase that negatively regulates
CC development.
CC : CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC : SUBCELLULAR LOCATION: Cytoplasmic.
CC : DEVELOPMENTAL STAGE: Expressed constitutively throughout the life
CC cycle, with slight increases at an early stage of development.
CC : PTM: Autophosphorylated at serine residues.
CC : SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC
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CC
CC EMBL; U40656; AAB40049.1;
CC PIR; S70964; S70964.
CC PhosSite; P54737;
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
CC Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 9 378 PROTEIN KINASE.
FT NP_BIND 15 23 ATP (BY SIMILARITY).
FT BINDING 38 38 ATP (BY SIMILARITY).
FT ACT_SITE 244 244 BY SIMILARITY.
FT ACT_SITE 380 AA; 41924 MW; DCJADFB24420C1F1 CRC64;
SQ SEQUENCE 380 AA; 75.5%; Score 37; DB 1; Length 380;
Query Match      75.5%; Score 37; DB 1; Length 380;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 314 LLGRPPFE 322

RESULT 29
PLK2 CAEEL
ID PLK2 CAEEL STANDARD; PRT; 632 AA.
AC Q9N2L7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase plk-2 (EC 2.7.1.-) (Polo-like
DE kinase-2).
GN PLK-2 OR Y71F9B.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
CX NCBI_TaxID=6239;
RN P1;
RP SEQUENCE FROM N.A.

```

RX MEDLINE=20541295; PubMed=11092748;
 RA Chase D., Golden A., Heidecker G., Ferris D.K.;
 RT "Caenorhabditis elegans contains a third polo-like kinase gene.";
 RL DNA Seq. 11:327-334(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN: Bristol N.2.
 RA Bradshaw-Cordum H., Scott K., Graves T.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May be required for cell division and may have a role
 CC during G1 or S phase (By similarity).
 CC ! SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDC5/POLC SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 POLC box domains.
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 CC
 DR EMBL; ACC2420; AAF36014.1;
 DR FMSJ; AF194964; AAF28314.1;
 DR HSSP; C63450; LA06.
 DR WormRef; Y71F9B.7; CE22877.
 DR GO; GO:0005634; Cytoplasm; NAS.
 DR GO; GO:0005524; F-ATP binding activity; ISS.
 DR GO; GO:0034674; F-ATP binding activity; ISS.
 DR GO; GO:0037049; P-actin; cycle; NAS.
 DR GO; GO:0034668; P-protein actin acid phosphorylation; ISS.
 DR InterPro; IPR000959; POLC box.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PDC00001; POLC box; 2.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS00078; POLC BOX; 2.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00158; PROTEIN KINASE ST; 1.
 KW ATP-binding; Serine/threonine-protein kinase; Transferrin; Repeat;
 KW Nuclear protein.
 FT DOMAIN 36 297 PROTEIN KINASE
 FT NP_BIND 43 50 ATP (By SIMILARITY)
 FT BINDING 65 65 ATP (By SIMILARITY)
 FT ACT_SITE 159 159 BY SIMILARITY
 FT DOMAIN 412 476 POLC BOX 1
 FT DOMAIN 511 580 POLC BOX 2
 SQ SEQUENCE 632 AA: 72071 MW: 1825586C15ABED9 CRG64;
 Query Match: 75.5%; Score 37; DS 1; Length 632;
 Res. Local Similarity 66.7%; Pred. No. 18;
 Yatches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 3;
 QY 1 NLLGRPPPE 9
 Db 226 LLLFGHPPE 234
 RESULT 30
 KPC1_APLCA STANDARD; PRT; 649 AA.
 ID KPC1_APLCA
 AC Q16974;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Calcium-dependent protein kinase C (EC 2.7.1.-) (APL 1).
 GN PRKC.
 GN Aplysia californica (California sea hare).

CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 CC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidae;
 CC Aplysioidea; Aplysiidae; Aplysia.
 OX NCBI_TaxID=6500;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91332620; PubMed=1869917;
 RA Kruger K.E., Sossin W.S., Sacktor T.C., Bergold P.J., Beushausen S.,
 RA Schwartz J.H.;
 RT "Cloning and characterization of Ca(2+)-dependent and Ca(2+)-
 RT independent PKCs expressed in Aplysia sensory cells.";
 RL J. Neurosci. 11:2303-2313(1991).
 RN [2]
 RP CHARACTERIZATION
 RX MEDLINE=91194877; PubMed=8449941;
 RA Sossin W.S., Diaz-Arreola R., Schwartz J.H.;
 RT "Characterization of two isoforms of protein kinase C in the nervous
 RT system of Aplysia californica.";
 RL J. Biol. Chem. 268:5763-5768(1993).
 RN [3]
 RP CHARACTERIZATION
 RX MEDLINE=98334636; PubMed=9668085;
 RA Pepio A.M., Fan X., Sossin W.S.;
 RT "The role of C2 domains in Ca2+-activated and Ca2+-independent protein
 RT kinase Cs in Aplysia.";
 RL J. Biol. Chem. 273:19040-19048(1998).
 RN [4]
 RP ERRATUM
 RA Pepio A.M., Fan X., Sossin W.S.;
 RL J. Biol. Chem. 273:22856-22856(1998).
 CC -!- FUNCTION: THIS IS CALCIUM-DEPENDENT, PHOSPHOLIPID-DEPENDENT,
 CC SERINE- AND THREONINE-SPECIFIC ENZYME. ACTIVATION OF PKC BY
 CC SEROTONIN RESULTS IN PRESYNAPTIC FACILITATION OF DEPRESSED
 CC SENSORY-TO-MOTOR NEURON SYNAPSES, WHICH IS THOUGHT TO UNDERLIE
 CC BEHAVIORAL DISHABITUATION.
 CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
 CC SIMILARITY).
 CC -!- ENZYME REGULATION: ACTIVATED BY PHOSPHATIDYL SERINE.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC; TRANSLOCATED TO NEURONAL
 CC MEMBRANES.
 CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC -!- SIMILARITY: Contains 1 C2 domain.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
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 CC
 DR EMBL; M94883; AAA27770.2;
 DR HSSP; P05697; ITEN.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR002219; DAG_PS-bind.
 DR InterPro; IPR000961; Pkinase C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00130; DAG_PS-bind; 2.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00433; pkinase C; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR ProDom; PDC00001; Prot_kinase; 1.
 DR SMART; SM00109; C1; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00133; S_TK_X; 1.


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DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00168; C2_1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; Pkinase_1.
DR Pfam; PF00433; Pkinase_C; 1.
DR PRINTS; PRO0360; C2DOMAIN.
DR PRINTS; PRO0008; DAGPEDOMAIN.
DR PRINTS; PRO0109; TYRKINASE.
DR ProDom; PDC00001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S-TK_X; 1.
DR SMART; SM00220; S-TK; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00137; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00108; Serine/threonine-protein kinase;
KW ATP-binding; Transferase; Serine/threonine-protein kinase;
FT PHORBOL-ester binding; Zinc; Repeat.
FT DOMAIN 28 77 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 93 142 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 164 251 C2 DOMAIN
FT DOMAIN 325 583 PROTEIN KINASE
FT NP_BIND 331 339 ATP (BY SIMILARITY).
FT BINDING 354 354 ATP (BY SIMILARITY).
FT ACT_SITE 449 449 BY SIMILARITY.
SQ SEQUENCE 658 AA; 74871 MW; 74B5A27A49C835A2 CRC64;

Query Match 75.5%; Score 37; DB 1; Length 658;
Best Local Similarity 66.7%; Pred.No. 19; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches

QY 1 MLLGRPPE 9
|||:||||
DB 517 MLAGQPPFD 525

RESULT 32
KPCA_BOVIN STANDARD; PRT; 672 AA.
ID KPCA_BOVIN
AC P044C9;
DT 13-AUG-1987 (Rel. C5, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
DE PRKCA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId:9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=86289425; PubMed=3755547;
RA Parker P.J., Coussens L., Totty N., Rhee L., Young S., Chen E.,
RA Stabel S., Waterfield M.D., Ullrich A.;
RT "The complete primary structure of protein kinase C -- the major
RT phorbol ester receptor.";
RL Science 233:853-859(1986).
RN [2]
RP REVIEW.
RX MEDLINE=88318921; PubMed=3045562;
RA Nishizuka Y.;
RT "The molecular heterogeneity of protein kinase C and its implications
RT for cellular regulation.";
RL Nature 334:661-665(1988).

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DR ProDom; PR000000; Prot_kinase; 1.
DR SMART; SM00139; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S TK X; 1.
DR SMART; SM00120; S TK; 1.
DR PROSITE; PS00499; C2 DOMAIN 1; 1.
DR PROSITE; PS00499; C2 DOMAIN 2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM 1; 2.
DR PROSITE; PS00479; DAG_PE_BIND_DOM 2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT VARIANT 106 106 I -> V (IN MUTANT FORM UV25).
FT VARIANT 111 111 S -> G (IN MUTANT FORM UV25).
FT VARIANT 240 240 L -> Q (IN MUTANT FORM UV25).
FT VARIANT 339 339 F -> L (IN MUTANT FORM UV25).
FT VARIANT 147 147 D -> V (IN REF. 2).
FT CONFLICT 218 218 N -> T (IN REF. 2).
FT CONFLICT 277 278 AH -> LL (IN REF. 2).
FT CONFLICT 313 313 V -> A (IN REF. 2).
FT CONFLICT 467 467 N -> D (IN REF. 2).
FT CONFLICT 472 472 N -> D (IN REF. 2).
FT CONFLICT 576 576 Q -> H (IN REF. 2).
SQ SEQUENCE 672 AA; 76764 MW; 8758D050388C12FA CDS64;

Query Match 75.5%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPE 9
DR 531 MLLGRPPE 539

RESULT 34
KC KPCA MOUSE STANDARD; PRT; 672 AA.
AC P23444;
DT 01 FEB 1991; Rel. 17; Created;
DT 01 FEB 1991; Rel. 17; Last sequence update;
DT 15-SEP-2003; Rel. 42; Last annotation update;
DE Protein kinase C, alpha type (EC 2.7.11.37) (PKC-alpha) (PKC-A).
GN PKCA OR PKCA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata;
OC Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232737; PubMed=2469625;
RA Rose John S.; Dietrich A.; Marks F.;
RT 'Molecular cloning of mouse protein kinase C (PKC) cDNA from Swiss
RT 3T3 fibroblasts.';
RL Nature 342:465-471(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=RA/B/C; TISSUE=Brain;
RX MEDLINE=90098082; PubMed=2601719;
RA Meguidish T.; Yazurek N.;
RT 'A mutant protein kinase C that can transform fibroblasts.';
RL Nature 342:807-811(1989).
RN [3]
RP INTERACTION WITH PRKCAP.
RX MEDLINE=95146534; PubMed=7844141;
RA Standinger J.; Zhou J.; Burgess R.; Ellledge S.J.; Olson E.N.;
RT 'Pick1: A perinuclear binding protein and substrate for protein kinase
RT C isolated by the yeast two-hybrid system.';
RL J. Cell Biol. 128:263-271(1995).
CC 1. FUNCTION: This is a calcium-activated, phospholipid-dependent,
CC serine- and threonine-specific enzyme, which in turn
CC 1. FUNCTION: PKC is activated by diacylglycerol which in turn

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phosphorylates a range of cellular proteins. PKC also serves as
the receptor for phorbol esters, a class of tumor promoters.
CC 1. CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC 1. SUBUNIT: Interacts with PRKCAP.
CC 1. DISEASE: Expression of the mutant form UV25 causes malignant
transformation of cells.
CC 1. SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
binding domains.
CC 1. SIMILARITY: Contains 1 C2 domain.
CC 1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
CC
EMBL; M25811; AAA39934.1; ALT_SEQ.
EMBL; X52685; CAA36908.1; .
EMBL; X52684; CAA36907.1; .
PIR; S07104; KIMSCA.
HSSP; P04410; 1A25.
MGD; MGI:97595; Pkca.
GO; GO:0004698; F:calcium dependent protein kinase C activity; IDA.
InterPro; IPR000008; C2.
InterPro; IPR002219; DAG_PE-bind.
InterPro; IPR000961; Pkinase_C.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR002230; Ser_thr_kinase.
Pfam; PF00168; C2; 1.
Pfam; PF00130; DAG_PE_bind; 2.
Pfam; PF00669; pkinase; 1.
Pfam; PF0433; pkinase_C; 1.
PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S TK X; 1.
DR SMART; SM00220; S TK; 1.
DR PROSITE; PS00499; C2 DOMAIN 1; 1.
DR PROSITE; PS00499; C2 DOMAIN 2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM 1; 2.
DR PROSITE; PS00479; DAG_PE_BIND_DOM 2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT VARIANT 106 106 I -> V (IN MUTANT FORM UV25).
FT VARIANT 111 111 S -> G (IN MUTANT FORM UV25).
FT VARIANT 240 240 L -> Q (IN MUTANT FORM UV25).
FT VARIANT 339 339 F -> L (IN MUTANT FORM UV25).
FT VARIANT 147 147 D -> V (IN REF. 2).
FT CONFLICT 218 218 N -> T (IN REF. 2).
FT CONFLICT 277 278 AH -> LL (IN REF. 2).
FT CONFLICT 313 313 V -> A (IN REF. 2).
FT CONFLICT 467 467 N -> D (IN REF. 2).
FT CONFLICT 472 472 N -> D (IN REF. 2).
FT CONFLICT 576 576 Q -> H (IN REF. 2).

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SQ SEQUENCE 672 AA; 76852 MW; 394B48C952BB6D50 CRC64;
Query Match 75.5%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DQ 531 MLAGQPPFD 539

RESULT 35
KPCA_RAT
ID KPCA_RAT STANDARD; PRT; 672 AA.
AC P1C102;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
GN PRKCA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87115893; PubMed=3838073;
RA Ohno S., Kawasaki H., Imajoh S., Suzuki K., Inagaki M., Yokokura H.,
RA Sakoh T., Hidaka H.;
RT "Issue-specific expression of three distinct types of rabbit protein
RT kinase C";
RL Nature 325:161-166(1997).
RN 12;
RP REVIEW.
RX MEDLINE=89318921; PubMed=3045562;
RA Nishizuka Y.;
RT "The molecular heterogeneity of protein kinase C and its implications
RL Nature 334:661-665(1988).
CC 1- FUNCTION: This is a calcium-activated, phospholipid dependent,
CC serine- and threonine-specific enzyme.
CC 2- FUNCTION: PKC is activated by diacylglycerol which in turn
CC phosphorylates a range of cellular proteins. PKC also serves as
CC the receptor for phorbol esters, a class of tumor promoters.
CC 3- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated
CC protein.
CC 4- SUBUNIT: Interacts with PRKCAP (By similarity).
CC 5- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC 6- SIMILARITY: Contains 1 C2 domain.
CC 7- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EYBL; X04796; CAA28493.1; -.
CC PIR; C26037; KIRBC.
CC HSP; P04410; 1A25.
CC InterPro: IPR000008; C2.
CC InterPro: IPR002219; DAG_PE-bind.
CC InterPro: IPR000961; Pkinase_C.
CC InterPro: IPR003719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam; PFC0168; C2; 1.
CC Pfam; PFC0130; DAG_PE-bind; 2.
CC Pfam; PFC0369; pkinase; 1.
CC Pfam; PFC0433; pkinase_C; 1.

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DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR PRODOM: PD000001; Prot_Kinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SM00239; C2; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00499; C2_DOMAIN_1; 1.
DR PROSITE: PS00004; C2_DOMAIN_2; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 638 639 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 672 AA; 76782 MW; 3D311367D3577A77 CRC64;

Query Match 75.5%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DQ 531 MLAGQPPFD 539

RESULT 16
KPCA_RAT
ID KPCA_RAT STANDARD; PRT; 672 AA.
AC P05696;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
GN PRKCA OR PKCA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OC NCBI_TaxID=10116;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88262515; PubMed=3387228;
RA Ono Y., Fujii T., Igarashi K., Kikkawa U., Ogita K., Nishizuka Y.;
RT "Nucleotide sequences of cDNAs for alpha and gamma subspecies of rat
RT brain protein kinase C";
RL Nucleic Acids Res. 16:5199-5200(1988).
RN 12;
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88030055; PubMed=3666147;
RA Kikkawa U., Ogita K., Ono Y., Asaoka Y., Shearman M.S., Fujii T.,
RA Ase K., Sekiguchi K., Igarashi K., Nishizuka Y.;
RT "The common structure and activities of four subspecies of rat brain
RT protein kinase C family";
RL FEBS Lett. 223:212-216(1987).
RN 13;
RP REVIEW.
RX MEDLINE=88318921; PubMed=3045562;
RA Nishizuka Y.;
RT "The molecular heterogeneity of protein kinase C and its implications
RT for cellular regulation.";

```

RL Nature 334:661-665(1988).
 CC -|- FUNCTION: This is a calcium-activated, phospholipid-dependent,
 CC serine- and threonine-specific enzyme.
 CC -|- FUNCTION: PKC is activated by diacylglycerol which in turn
 CC phosphorylates a range of cellular proteins. PKC also serves as
 CC the receptor for phorbol esters, a class of tumor promoters.
 CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated protein.
 CC -|- SUBUNIT: Interacts with PRKCBP (By similarity).
 CC -|- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC -|- SIMILARITY: Contains 1 C2 domain.
 CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X27286; GenBank: U02666.1; .
 CC PIR: S22248; KIRC
 CC PRO: 1051; 26-JAN-00.
 CC InterPro: IPR000008; C2.
 CC InterPro: IPR002219; DAG_PE-bind.
 CC InterPro: IPR000961; PKinase C.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR002290; Ser_thr_kinase.
 CC Pfam: PF00168; C2; 1.
 CC Pfam: PF00130; DAG_PE-bind; 2.
 CC Pfam: PF00369; PKinase; 1.
 CC Pfam: PF00433; PKinase C; 1.
 CC PRINTS: PR00360; C2DOMAIN.
 CC PRINTS: PR00008; DAGPEDOMAIN.
 CC ProDom: PD000001; Prot_kinase; 1.
 CC SMART: SM00109; C1; 2.
 CC SMART: SM00133; S_TK_X; 1.
 CC SMART: SM00220; S_TK; 1.
 CC PROSITE: PS00499; C2_DOMAIN_1; 1.
 CC PROSITE: PS00004; C2_DOMAIN_2; 1.
 CC PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
 CC PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC
 CC Query Match 75.5%; Score 37; DB 1; Length 672;
 CC Best Local Similarity 66.7%; Pred. No. 20;
 CC Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 1 W.LGRPPE 9
 CC
 CC Dt 531 MEAGQPPD 539
 CC
 CC RESULT 37
 CC KPCC_BOVIN

ID KPCC_BOVIN STANDARD; PRT; 682 AA.
 AC P05128;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Protein kinase C, gamma type (EC 2.7.1.37) (PKC-gamma) (Fragment).
 GN PKCCG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86289426; PubMed=3755548;
 RA Coussens L., Parker P.J., Rhee L., Yang-Feng T.L., Chen E.,
 RA Waterfield M.D., Francke U., Ullrich A.;
 RT "Multiple, distinct forms of bovine and human protein kinase C
 RT suggest diversity in cellular signaling pathways.";
 RL Science 233:859-866(1986).
 RN [2]
 RP REVIEW.
 RX MEDLINE=88318921; PubMed=3045562;
 RA Nishizuka Y.;
 RT "The molecular heterogeneity of protein kinase C and its implications
 RT for cellular regulation.";
 RL Nature 334:661-665(1988).
 CC -|- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
 CC SERINE- AND THREONINE-SPECIFIC ENZYME.
 CC -|- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
 CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated protein.
 CC -|- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC -|- SIMILARITY: Contains 1 C2 domain.
 CC -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC
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 CC
 CC EMBL: M33976; AAA30704.1; .
 CC PIR: C24664; KIBOGC.
 CC HSP: P05697; LTEN.
 CC InterPro: IPR000008; C2.
 CC InterPro: IPR002219; DAG_PE-bind.
 CC InterPro: IPR000961; PKinase C.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR002290; Ser_thr_kinase.
 CC InterPro: IPR001245; Tyr_kinase.
 CC Pfam: PF00168; C2; 1.
 CC Pfam: PF00130; DAG_PE-bind; 2.
 CC Pfam: PF00369; PKinase; 1.
 CC Pfam: PF00433; PKinase C; 1.
 CC PRINTS: PR00360; C2DOMAIN.
 CC PRINTS: PR00008; DAGPEDOMAIN.
 CC PRINTS: PR00109; TYRKINASE.
 CC ProDom: PD000001; Prot_kinase; 1.
 CC SMART: SM00109; C1; 2.
 CC SMART: SM00133; S_TK_X; 1.
 CC SMART: SM00220; S_TK; 1.
 CC PROSITE: PS00499; C2_DOMAIN_1; 1.
 CC PROSITE: PS00004; C2_DOMAIN_2; 1.
 CC PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
 CC PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

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DR PROSITE: PS00108; PROTEIN KINASE DOM: 1.
DR PROSITE: PS00108; PROTEIN_KINASE_SF: 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phospho-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 1 1 70 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 21 1 70 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 86 135 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 155 245 C2 DOMAIN.
FT DOMAIN 336 599 PROTEIN KINASE.
FT NP BIND 342 350 ATP (BY SIMILARITY).
FT BINDING 365 365 ATP (BY SIMILARITY).
FT ACT SITE 465 465 BY SIMILARITY.
FT XCD_RES 633 633 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MCD_RES 640 640 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 682 AA: 77156 MW: 2039221188C711C CRC64;

Query Match 75.5%; Score 37; DB 1; Length 692;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGGRPPPE 9
|||
DB 533 MLGGRPPPE 54;

RESULT 38
KPCG HUMAN STANDARD; PRT: 697 AA.
AC P5529;
DT 13-AUG-1987 (Rel. 05, Created)
DT 21-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, gamma type (EC 2.7.1.37) (PKC-gamma).
GN PRKCG OR PKCG.
OS Homo sapiens (Human).
CC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RF SEQUENCE FROM N.A.
RA Cui W.C., Yu J., Chu Y.Y., Wang J., Zheng L.H., Zhou G.J., Zhao S.Y.;
RL Submitted (FEB-2001) to the EMBL/GenBank/CDDB databases.
RN [2]
RP SEQUENCE OF 1-318 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=86289426; PubMed=3755548;
RA Cussens I., Parker P.J., Rhee L., Yang-Peng T., Chen E.,
RA Waterford M.D., Francke U., Ulrich A.;
RT "Multiple, distinct forms of bovine and human protein kinase C
RT suggest diversity in cellular signaling pathways.";
RJ Science 233:859-866(1986).
RN [3]
RP SEQUENCE OF 162-697 FROM N.A.
RC TISSUE=Hippocampus;
RX MEDLINE=9337332; PubMed=8375336;
RA Kochs G., Meyer D., Hug H., Marre O., Sarrre C.F.;
RT "Activation and substrate specificity of the human protein kinase C
RT alpha and zeta isoenzymes.";
RJ Eur. J. Biochem. 216:597-606(1993).
RN [4]
RP VARIANTS CYS-141; GLN-415; ASP-523 AND SER-659.
RX MEDLINE=98213587; PubMed=9545390;
RA Al-Maghrabi Y., Vithana E.N., Inglehearn C.F., Moore T., Bird A.C.,
RA Bhattacharya S.S.;
RT "Segregation of a PRKCG mutation in two RPL1 families.";
RJ Am. J. Hum. Genet. 62:1248-1252(1998).
RN [5]
RE SHOWS THAT THE VARIANTS ARE NOT A CAUSE OF RPL1.
RX MEDLINE=99375047; PubMed=10441600;
RA Dwyja T.P., McEvoy J., McGeer T.L., Betson E.L.;
RT "No mutations in the coding region of the PRKCG gene in three families
RT with retinitis pigmentosa linked to the RPL1 locus on chromosome

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RT 19q.";
RL Am. J. Hum. Genet. 65:926-928(1999).
CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC-S ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS. A CLASS OF TUMOR PROMOTERS.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -!- DATABASE: NAME-Mutations of the PRKCG gene;
CC NOTE:Retina International's Scientific Newsletter;
CC WWW="http://www.retina-international.com/sci-news/prkcgmut.htm".
-----
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CC or send an email to license@isb-sib.ch).
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DR EMBL: AF345987; AAK13533.1;
DR EMBL: M13977; AAG60102.1; ALT_TERM.
DR EMBL: Z15114; CAA78820.1; -.
DR PIR: D24664; D24664.
DR HSSP: P05697; 1TBN.
DR GENE: HGNC:9402; PRKCG.
DR MIX: 176980; -.
DR GO: GO:0004697; F:protein kinase C activity; TAS.
DR GO: GO:0006468; P:protein amino acid phosphorylation; TAS.
DR InterPro: IPR000008; C2.
DR InterPro: IPR002219; DAG_PE-bind.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00130; DAG_PE-bind; 2.
DR Pfam: PF00069; Pkinase; 1.
DR Pfam: PF00433; Pkinase_C; 1.
DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR PRODOM: PD003001; Prot_kinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SM00239; C2; 1.
DR SMART: SM00133; S-TK_X; 1.
DR SMART: SM00220; S-TK; 1.
DR PROSITE: PS00499; C2 DOMAIN 1; 1.
DR PROSITE: PS50004; C2 DOMAIN 2; 1.
DR PROSITE: PS00479; DAG PE BIND DOM 1; 2.
DR PROSITE: PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PS00107; PROTEIN KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation; Polymorphism
FT DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 170 260 C2 DOMAIN.
FT DOMAIN 351 614 PROTEIN KINASE.
FT NP BIND 357 365 ATP (BY SIMILARITY).
FT BINDING 380 380 ATP (BY SIMILARITY).
FT ACT_SITE 480 480 BY SIMILARITY.
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT VARIANT 14; 141 R -> C.
/FTid=VAR_008755.

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FT VARIANT 415 415 H -> Q
FT VARIANT 523 523 A -> D
FT VARIANT 659 659 R -> S
FT VARIANT 659 659 /FTID=VAR_008756
SQ SEQUENCE 697 AA: 78447 MW: 35911 B55EP73041 CRC64:
75.5% Score 37; DB 1; Length 697;
Query Match
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YLLGRPPFE 9
| | | | |
Db 548 MLAGQPPFD 556

RESULT 39
KPCG MOUSE
ID_KPCG_MOUSE STANDARD; PR7: 697 AA.
AC P05697;
DT 01-NOV-1998 (Rel. 09, Created)
DI C1-NOV-1988 (Rel. 09, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, gamma type (EC 2.7.1.37) (PKC-gamma).
GN PKCG OR PKGC OR PRKCC OR PKCC.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10290, 10116;
EN [1]
PP SEQUENCE FROM N.A.
FC SPECIES=rat; TISSUE=Brain;
FX MEDLINE=86262515; PubMed=3387228;
FA Cuo Y., Fujii T., Igarashi K., Kikkawa U., Ogita K., Nishizuka Y.;
FT "Nucleotide sequences of cDNAs for alpha and gamma subtypes of rat
brain protein kinase C";
RU Nucleic Acids Res. 16:5199-5200(1988);
PN [2]
PP SEQUENCE FROM N.A.
FC SPECIES=rat;
FX MEDLINE=86272097; PubMed=3755375;
FA Koopf C.L., Lee M.H., Sultzman L.A., Kriz R.W., Loomis C.R.,
RA Hewick R.M., Bell R.M.;
RT "Cloning and expression of multiple protein kinase C cDNAs";
RL Cell 46:491-502(1986);
RN [3]
PP SEQUENCE OF 1-56 FROM N.A.
FC SPECIES=rat;
FX MEDLINE=91060619; PubMed=2246272;
RA Chen X.H., Widen S.G., Wilson C.L., Huang K.P.;
RT "Characterization of the 5'-flanking region of the rat protein kinase
C gamma gene";
RL J. Biol. Chem. 265:19961-19965(1990);
RN [4]
PP SEQUENCE FROM N.A.
FC SPECIES=Mouse; TISSUE=Brain;
FX MEDLINE=93154595; PubMed=8428669;
RA Bowers B.J., Farham C.L., Sikelä J.M., Webster J.V.;
RT "Isolation and sequence of a mouse brain cDNA coding for protein
kinase C-gamma isoform";
RL Gene 123:263-265(1993);
RN [5]
PP SEQUENCE FROM N.A.
FC SPECIES=Mouse; STRAIN=BAJB/c; TISSUE=Brain;
RA Tseng C.P., Verma A.;
RT Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
RN [6]
PP STRUCTURE BY NMR OF 91-172.
FC SPECIES=rat;
FX MEDLINE=97419134; PubMed=9271531;
XA X.R.X., Pawelczyk T., Xia T.-H., Brown S.C.;

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RT "NMR structure of a protein kinase C-gamma phorbol-binding domain and
study of protein-lipid micelle interactions.";
RL Biochemistry 36:10709-10717(1997);
CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
-----
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DR EMBL; X07287; CAA30267.1; -
DR EMBL; M13707; AAA41874.1; -
DR EMBL; M55417; AAA41873.1; -
DR EMBL; X67129; CAA47608.1; -
DR EMBL; L28035; AAA39939.1; -
DR PIR; A05105; KIRTCG.
DR PIR; JN0548; JN0548.
DR PDB; 1TBN; 29-APR-98.
DR PDB; 1TBO; 29-APR-98.
DR MGD; MGI:97597; Prkcc.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002230; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00038; DAGPEDOMAIN.
DR PRINTS; PR00169; TYRKINASE.
DR ProDom; PD000002; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation; 3D-structure.
FT DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 170 260 C2 DOMAIN.
FT DOMAIN 351 614 PROTEIN KINASE.
FT NP_BIND 357 365 ATP (BY SIMILARITY).
FT BINDING 380 380 ATP (BY SIMILARITY).
FT ACT_SITE 480 480 BY SIMILARITY.
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT STRAND 103 105
FT STRAND 113 113
FT STRAND 120 120

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FT TURN 123 124
FT STRAND 129 131
FT TURN 132 134
FT STRAND 137 138
FT TURN 140 145
SQ SEQUENCE 697 AA; 78357 MW; E6E2F7A3B930A2FF CRC64;

Query Match: 75.5%; Score 37; DB 1; Length 697;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DB 548 MLGQPPFD 556

RESULT 40
KPCG RABBIT STANDARD; PRT; 697 AA.
AC P:0829;
DT 01-JUL-1989 (Rel. 11, Created);
DD 01-JUL-1989 (Rel. 11, Last sequence update);
DE 28 FEB-2003 (Rel. 41, Last annotation update);
CE Protein Kinase C, gamma type (EC 2.7.11.37); (PKC-gamma) (PKC-delta);
GN PKCG.
CS Oryctolagus cuniculus (Rabbit);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI:TaxID=9986;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=88241036; PubMed=2837282;
RA Ono S., Kawasaki H., Konno Y., Inagaki M., Hidaka H., Suzuki K.;
RT "A fourth type of rabbit protein kinase C";
RD Biochemistry 27:2083-2087(1988);
SQ : FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
SERINE AND THREONINE-SPECIFIC ENZYME.
CC : FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS. A CLASS OF TUMOR PROMOTERS.
CC : CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated
CC : SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC : : SIMILARITY: Contains 1 C2 domain.
CC : : SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC
CC EMBL: N:9338; AAA11449.1;
CC EFN: A28208; KIRRCG.
CC HSSP: P05697; ITBN.
CC
CC InterPro: IPR000088; C2.
CC InterPro: IPR022119; DAG_PE-bind.
CC InterPro: IPR000961; Kinase C.
CC InterPro: IPR000719; Prot kinase.
CC InterPro: IPR002290; Ser Thr kinase.
CC InterPro: IPR001245; Tyr_kinase.
CC Pfam: PF00168; C2; 1.
CC Pfam: PF00130; DAG_PE-bind; 2.
CC Pfam: PF00069; pkinase; 1.
CC Pfam: PF00433; pkinase; C; 1.
CC PRINTS: PR00360; C2DOMAIN.
CC PRINTS: PR00008; DAGPEDOMAIN.
CC PRINTS: PR00104; TYRKINASE.
CC ProDom: PD000001; Prot kinase; 1.
CC SMART: SMC0109; C1; 2.

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DR SMART; SMC0239; C2; 1.
DR SMART; SMC0133; S-TKC; 1.
DR SMART; SMC0220; S-TKC; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PSS0004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 170 260 C2 DOMAIN.
FT DOMAIN 352 614 PROTEIN KINASE.
FT NP_BIND 357 365 ATP (BY SIMILARITY).
FT BINDING 380 380 ATP (BY SIMILARITY).
FT ACT_SITE 480 480 BY SIMILARITY.
FT MCD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MCD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 697 AA; 78371 MW; 925D2221F78E5BF CRC64;

Query Match: 75.5%; Score 37; DB 1; Length 697;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DB 548 MLGQPPFD 556

```

Search completed: November 14, 2003, 13:25:57
Job time : 6.68571 secs

GenCore version 5.1.6
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OM protein - protein search, using sw mode:

Run on: November 14, 2003, 13:18:40 : Search time 27 Seconds

Without alignments:
86.018 Million cell updates/sec

Title: US-09-736-076-15
Perfect score: 49
Sequence: 1 MLLGRPPFE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SP-REMBL 23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacterioph:
17: sp_archaea:

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	316	Q9BDK4	Q9BDK4 sus scrofa
2	49	100.0	372	Q8N7M6	Q8N7M6 homo sapien
3	49	100.0	666	Q90XS4	Q90XS4 xenopus lae
4	49	100.0	682	Q8K226	Q8K226 mus musculus
5	43	87.8	673	Q62567	Q62567 suberites d
6	43	87.8	677	Q96997	Q96997 geodia cydo
7	43	87.8	769	Q97143	Q97143 drosophila
8	42	85.7	456	Q8MYF1	Q8MYF1 dictyosteli
9	41	83.7	324	Q9CVR6	Q9CVR6 mus musculus
10	41	83.7	568	Q8MXG6	Q8MXG6 caenorhabdi
11	41	83.7	749	Q8MXG7	Q8MXG7 caenorhabdi
12	41	83.7	780	Q76360	Q76360 caenorhabdi
13	41	83.7	925	Q8R015	Q8R015 mus musculus
14	41	83.7	925	Q64702	Q64702 mus musculus
15	41	83.7	970	Q96Q95	Q96Q95 homo sapien
16	41	83.7	970	Q00444	Q00444 homo sapien

17	41	83.7	970	4	Q8IYF0	Q8IYF0 homo sapien
18	40	81.6	526	6	Q8BDP8	Q8BDP8 sus scrofa
19	40	81.6	582	5	Q9GRB7	Q9GRB7 hemicentrot
20	40	81.6	598	13	P70032	P70032 xenopus lae
21	40	81.6	623	5	Q8IU35	Q8IU35 asterina pe
22	39	79.6	235	5	Q9GP07	Q9GP07 leishmania
23	39	79.6	358	5	Q03872	Q03872 leishmania
24	39	79.6	690	16	Q8G6P9	Q8G6P9 bifidobacte
25	39	79.6	1337	2	Q9KJN7	Q9KJN7 myxococcus
26	38	77.6	80	13	Q91891	Q91891 xenopus lae
27	38	77.6	240	11	Q63432	Q63432 rattus norv
28	38	77.6	305	5	Q01427	Q01427 caenorhabdi
29	38	77.6	332	16	Q9AJZ9	Q9AJZ9 streptomyce
30	38	77.6	554	5	Q95778	Q95778 drosophila
31	38	77.6	660	16	Q8FUI5	Q8FUI5 corynebacte
32	38	77.6	661	5	Q01669	Q01669 hydra atten
33	38	77.6	707	5	Q20953	Q20953 caenorhabdi
34	38	77.6	754	5	Q8MXB6	Q8MXB6 limulus poi
35	38	77.6	769	10	Q9LLJ1	Q9LLJ1 chlamydomon
36	37	75.5	178	16	Q8CR93	Q8CR93 staphylococ
37	37	75.5	301	8	Q950L6	Q950L6 rhizophyidiu
38	37	75.5	484	11	Q9LY16	Q9LY16 mus musculu
39	37	75.5	622	4	Q9H9T2	Q9H9T2 homo sapien
40	37	75.5	670	5	Q01715	Q01715 hydra atten
41	37	75.5	670	13	Q8JFZ9	Q8JFZ9 figu rubrip
42	37	75.5	674	5	Q01716	Q01716 hydra atten
43	37	75.5	675	3	P87248	P87248 collettotric
44	37	75.5	680	5	P90980	P90980 caenorhabdi
45	37	75.5	680	5	Q8MQ88	Q8MQ88 caenorhabdi

ALIGNMENTS

RESULT 1

Q9BDK4 PRELIMINARY; PRT: 316 AA.
ID Q9BDK4
AC Q9BDK4
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Serum-inducible Kinase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_taxonomy:9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Anger M., Kues W.A., Klima J., Motlik J., Carnwath J.W., Niemann H.;
RT "Porcine serum-inducible Kinase";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF348424; AAK27154.1; -
DR InterPro; IPR000959; POLO box.
DR InterPro; IPR00719; Prot_Kinase.
DR Pfam; PF00069; pkinase; 1
DR Pfam; PF00659; POLO box; 1
DR ProDom; P000001; Prot_kinase; 1.
DR PROSITE; PS00078; POLO_BOX; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
FT NON_TER 1
FT NON_TER 316
SQ SEQUENCE 316 AA; 35330 MW; F63BBE4A2691D62F CRC64;

Query Match 100.0%; Score 49; DB 6; Length 316;

Best Local Similarity 100.0%; Pred.No. 0.24;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9

Db 25 MLLGRPPFE 33

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RESULT 2
ID Q8NTM6 PRELIMINARY; PRT; 372 AA.
AC Q8NTM6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ40844.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Trachea;
RA Suzuki C., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shichata N.,
RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
RA Matsumura Y., Moriya S., Chiba E., Momiyama H., Onogawa S.,
RA Kaeriyama S., Satoh N., Matsunawa H., Takarashi E., Kataoka R.,
RA Kuga N., Karoda A., Satoh I., Kamata K., Takami S., Terashima Y.,
RA Watanabe M., Sugiyama T., Irie K., Otsuki T., Sato H., Ota T.,
RA Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K.,
RA Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y.,
RA Sekine M., Kikuchi H., Kanda K., Wagatsura M., Murakawa K.,
RA Kasehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuno Y., Nagai K., Isogai T.;
RT "NDO human cDNA sequencing project.";
SC Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK098163; BAC05247.1;
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR022290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Transferase.
SQ SEQUENCE 372 AA; 42632 MW; 7E3C3BF65C20AC09 CRC64;

Query Match 100.0%; Score 49; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DB 264 MLGRRPPE 274

RESULT 3
ID Q90XS4 PRELIMINARY; PRT; 666 AA.
AC Q90XS4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Polo-like kinase 2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN 1;
RP SEQUENCE FROM N.A.
RC MEDLINE=21481843; PubMed=1159129;
RA Duncan P.I., Poller N., Niehrs C., Nigg E.A.;
RT "Cloning and Characterization of P1x2 and P1x3, Two Additional Polo-
RL Exp. Cell Res. 270:78-87(2001).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

Query Match 100.0%; Score 49; DB 11; Length 682;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DB 270 MLGRRPPE 278

RESULT 5
ID O62567 PRELIMINARY; PRT; 673 AA.
AC O62567;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)

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DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DI 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serine/threonine protein kinase.
OS Suberites demuncula (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
CC Hadromerida; Suberitidae; Suberites.
CX NCBI_TaxID=55567;
RN [1]
RP SEQUENCE FROM N.A.
RA Mueller W.E.G.;
RL Submitted (APR-1997) to the EMBL/GenBank/CDRJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=36394689; PubMed=8798342;
RA Kruse M., Gamlin V., Cerkovic H., Pancer Z., Mueller I.M.,
RA Mueller W.E.G.;
RI "Molecular evolution of the Metazoan protein kinase C multigene
RT family".
RL J. Mol. Evol. 43:374-383(1996).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL; Y13099; CAATJ553.1; -.
DR HSSP; P28867; IPTQ.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPECDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00304; C2_DOMAIN_2; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00361; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 673 AA; 77344 MW; 86D24E554977C253 CRC64;

Query Match 87.8%; Score 43; DB 5; Length 673;
Best Local Similarity 77.8%; Pred. No. 7;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DB 535 MLVGRPPFD 543

RESULT 6
O96997 ID C36997 PRELIMINARY; PRT; 677 AA.
AC O96997;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein kinase C.
GN PKC2.
OS Geodia cydonium (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
CC Asipheoidea; Geodiidae; Geodia.
CX NCBI_TaxID=6047;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99147839; PubMed=10023072;
RA Seack J., Kruse M., Mueller I.M., Mueller W.E.G.;
RI "Promoter and exon-intron structure of the protein kinase C gene from
RT the marine sponge Geodia cydonium: Evolutionary considerations and
RT promoter activity".
RL Biochim. Biophys. Acta 1444:241-253(1999).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL; Y17882; CAA76911.1; -.
DR HSSP; P28867; IPTQ.
DR InterPro; IPR000008; C2.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPECDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00304; C2_DOMAIN_2; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00361; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 677 AA; 76787 MW; 8D0025C8183DBA33 CRC64;

Query Match 87.8%; Score 43; DB 5; Length 677;
Best Local Similarity 77.8%; Pred. No. 7;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DB 539 MLVGRPPFD 547

RESULT 7
O97143 ID O97143 PRELIMINARY; PRT; 769 AA.
AC O97143;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SAK protein.
GN SAK OR CG7186.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
CX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazei R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abvil J.F., Agbayan A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Sasu A., Baxendale J., Bayraktaroglu T., Beasley E.M.,
 RA Beson R.Y., Betos P.V., Bertram B.P., Bhandari D., Boishakoy S.,
 RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Butts K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 RA de Pablo E., DeJcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup J.E., Downes M., Dugan-Roca S., Etkov A.C., Dunn P.,
 RA Durkin K., Evangelista C., Ferraz C., Fertner S., Fleischmann W.,
 RA Foster C., Gabriella A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Gladek A., Gong F., Gorrell C.H., Gu Z., Guan P., Harris M.,
 RA Harris M.L., Harvey D., Heznan T.C., Hernandez J.P., Hock C.,
 RA Hostin D., Houston K.A., Howard T.C., Wei M.H., Beggs C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison C.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp C., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li C., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshira N.V., Mobarry C., Morris J.Y., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.Y., Nelson D.L.,
 RA Nelson E.R., Nelson K.A., Nixon K., Nusskern D.R., Pacifici J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Sher H.,
 RA Shue B.C., Stien-Kiamos I., Simpson M., Skipski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tecor C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach C.,
 RA Williams S.M., Woodage T., Wocley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.F., Zaveri J.S., Zhan M., Zhao G., Zhao C., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.G.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of Drosophila melanogaster,"
 RA Science 287:2185-2195(2000).
 RA [2]
 RP SEQUENCE FROM N.A.
 RA Hudson C.W., Dennis J.W.,
 RA Submitted (NCV-1398) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A003594; AAF51737.1;
 DR EMBL: AF156952; AAC19607.1;
 DR HSP: F03518; PHK.
 DR Flybase: F590026371; SAK.
 DR InterPro: IPR000959; POLO_box.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR02290; Ser_thr_kinase.
 DR InterPro: IPR02245; Tyr_kinase.
 DR Pfam: PF0069; pkinase.
 DR TrkRS: P00034; TYRKINASE.
 DR ProDom: PD00001; Prot_kinase.
 DR SMART: SM0022; S_TKc; 1.
 DR PROSITE: PS0078; POLO_BOX; 1.
 DR PROSITE: PS0107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS0109; PROTEIN_KINASE_TYR; 1.
 KW ATP binding; Kinase; Transferase.
 SQ SEQUENCE 769 AA; 85886 MW; F05B56CA5D94AA4 CRC64;

Query Match 87.8%; Score 43; DB 5; Length 769;
 Best Local Similarity 77.8%; Pred. No. 7.9;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY : MLGRRPPE 9

Db 236 LIVGRPPE 214

RESULT 8

QWYF1 ID QWYF1 PRELIMINARY; PRT; 456 AA.

AC QWYF1

DT 01-SEP-2002 (TrEMBLrel. 22, Created)

DT 01-SEP-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE RAC family serine/threonine kinase homolog.

OS Dictyostelium discoideum (Slime mold).

OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
 RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
 RA Lungal B., Cox E., Quail X.A., Platzer M., Rosenthal A., Noegel A.A.,
 RA "Sequence and Analysis of Chromosome 2 of Dictyostelium,"
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC117081; AAM43765.1;
 DR InterPro: IPR000961; pkinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR02290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF0069; pkinase; 1.
 DR Pfam: PF00433; pkinase_C; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD00001; Prot_kinase; 1.
 DR SMART: SM0022; S_TKc; 1.
 DR SMART: SM0033; S_TKc; 1.
 DR SMART: SMC0219; TyKc; 1.
 DR PROSITE: PS0107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS0109; PROTEIN_KINASE_TYR; 1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 456 AA; 51154 MW; EB8749EC64C89309 CRC64;

Query Match 85.7%; Score 42; DB 5; Length 456;

Best Local Similarity 66.7%; Pred. No. 7.4;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLGRRPPE 9

Db 319 MM:GKPPPE 327

RESULT 9

Q9CVR6 ID Q9CVR6 PRELIMINARY; PRT; 324 AA.

AC Q9CVR6

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Serine/threonine kinase 18 (fragment).

GN Strk18

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Testis;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,

RA Kadoka K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai X., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,

RA Hayaehizaki Y.,

RT "Functional annotation of a full-length mouse cDNA collection.";

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R1 Nature 499:685-690(2001).
R2 EXBL: AK006827; BAB24759.1; -.
R3 HSSP; Q03534; IB18.
R4 MGD; MG1101783; SK18.
R5 InterPro: IPR000719; Prot_kinase.
R6 InterPro: IPR002290; Ser_thr_kinase.
R7 InterPro: IPR001245; Tyr_kinase.
R8 Pfam; PF00069; Pkinase_1.
R9 PRINTS; PR00109; TYRKINASE.
R10 DR PRODOM; P000001; Prot_kinase; 1.
R11 DR SMART; SM00220; S_TKc; 1.
R12 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
R13 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
R14 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
R15 KW ATP-binding; Transferase.
R16 FT NON-TER 324 324
R17 SQ SEQUENCE 324 AA; 36568 MW; C4247065DFB198CC CRC64;

Query Match 83.7%; Score 41; DB 1; Length 324;
Best Local Similarity 66.7%; Pred. No. 8.3;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DB 204 LMLGRPPFQ 212

RESULT 10
Q8MXG6 Q8MXG6 PRELIMINARY; PRT; 568 AA.
AC Q8MXG6
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE EGL-4 protein (corresponding sequence F55A8.2d).
GN F55A8.2 OR EGL-4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Langston Y., Wohldmann P., Duckels G.;
RT "The sequence of C. elegans cosmid F55A8."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Waterston R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067612; AAM98011.1; -.
DR WormPep; F55A8.2d; CE31542.
DR InterPro; IPR002373; CAMP_kin.
DR InterPro; IPR002374; cGMP_kin.
DR InterPro; IPR000595; cNMP_binding.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00027; cNMP_binding; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00027; pkinase_C; 1.
DR PRINTS; PR00103; CAMPKINASE.
DR ProDom; P000001; Prot_kinase; 1.
DR SMART; SM00100; cNMP; 2.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TK_X; 1.

Query Match 83.7%; Score 41; DB 5; Length 568;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DB 448 LMLGRPPFQ 456

RESULT 11
Q8MXG7 Q8MXG7 PRELIMINARY; PRT; 749 AA.
AC Q8MXG7
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE EGL-4 protein (corresponding sequence F55A8.2c).
GN F55A8.2 OR EGL-4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Langston Y., Wohldmann P., Duckels G.;
RT "The sequence of C. elegans cosmid F55A8."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Waterston R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067612; AAM98010.1; -.
DR WormPep; F55A8.2c; CE31541.
DR InterPro; IPR002373; CAMP_kin.
DR InterPro; IPR002374; cGMP_kin.
DR InterPro; IPR000595; cNMP_binding.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00027; cNMP_binding; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00027; pkinase_C; 1.
DR PRINTS; PR00103; CAMPKINASE.
DR ProDom; P000001; Prot_kinase; 1.
DR SMART; SM00100; cNMP; 2.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TK_X; 1.

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DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00888; CNMP_BINDING_1; 2.
DR PROSITE: PS00889; CNMP_BINDING_2; 2.
DR PROSITE: PS00442; CNMP_BINDING_3; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; transferase.
SQ SEQUENCE 749 AA; 84497 MW; ADE0B9F5F54D93C6 CRC64;

Query Match 83.7%; Score 41; DB 5; Length 749;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 629 LMLGRPPFQ 637

RESULT 12
ID Q76360 PRELIMINARY; PRT; 780 AA.
AC Q76360.
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 86.7 kDa protein F55A8.2 in chromosome IV.
GN F55A8.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
CC Rhabditidae; Peloderinae; Caenorhabditis.
CX NCBI_TaxID:6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Langston Y.; Wohldmann P.; Duckels G.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterson R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; MAY BE
PRODUCED BY ALTERNATIVE SPLICING.
CC -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DE EMBL; AF067612; AAD36954.1; --
DR EMBL; AF067612; AAD36953.1; --
DR FSSP; PS5132; 1APM.
DR WormPep; F55A8.2a; CE19897.
DR WormPep; F55A8.2b; CE19898.
DR InterPro; IPR002374; CNMP_kin.
DR InterPro; IPR000595; CNMP_binding.
DR InterPro; IPR000961; Kinase_C.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00327; CNMP_binding_2.
DR Pfam; PF00669; Kinase; 1.
DR Pfam; PF00433; Kinase_C; 1.
DR PRINTS; PR00104; CGMPKINASE.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00100; CNMP; 2.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; 2.
DR PROSITE; PS00889; CNMP_BINDING_2; 2.
DR PROSITE; PS00442; CNMP_BINDING_3; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Hypothetical protein; ATP-binding; Alternative splicing; Kinase;
SR Serine/threonine-protein kinase; Transferase.
FT VARSPIC 1 52 MSSGRPSGGGGGGGASGAGGAGGAGGGGG;RGFTSKL
FT RRPSPQPNQNG -> MKQPPRIY (IN ISOFORM B).

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SQ SEQUENCE 780 AA; 86741 MW; 55E036AF50626DD2 CRC64;

Query Match 83.7%; Score 41; DB 5; Length 780;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 660 LMLGRPPFQ 668

RESULT 13
ID Q8R015 PRELIMINARY; PRT; 925 AA.
AC Q8R015.
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 103.9 kDa protein.
GN STK18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026785; AAH26785.1; --
DR MGD; MGI:101783; Stk18.
DR InterPro; IPR000959; POLO_box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00078; POLO_BOX; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Hypothetical protein; ATP-binding; Transferase.
SQ SEQUENCE 925 AA; 10386; MW; 844AF8C9AAC54C1 CRC64;

Query Match 83.7%; Score 41; DB 11; Length 925;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 204 LMLGRPPFD 212

RESULT 14
ID Q64702 PRELIMINARY; PRT; 925 AA.
AC Q64702.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SMK/PLK-AKIN kinase (Protein kinase SMK/PLK-AKIN) (EC 2.7.1.-).
GN STK18 OR SAK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2; TISSUE=Lymphoma;
RX MEDLINE=94294387; PubMed=8022793;
RA Fode C.; Morio B.; Yousefi S.; Heffernan M.; Dennis J.W.;
RT "Sak, a murine protein-serine/threonine kinase that is related to the
RT Drosophila polo kinase and involved in cell proliferation.";

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RL Proc. Natl. Acad. Sci. U.S.A. 91:6388-6392(1994).
CC 1- ALTERNATIVE PRODUCTS; 2 ISOFORMS; SAK-A (SHOWN HERE) AND SAK-B;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
DR EMBL: L29479; AAC37648.1; -.
DR HSSP: Q0C534; 1B18.
DR MGC: MGI:101783; STK18.
DR InterPro: IPR000959; POLO_box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00078; POLO_BOX; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Alternative splicing; Serine/threonine-protein kinase;
KW Transferase.
FT VARSPLOC 417 464 SSNHRCLGKTPFPFAQDTQFMETVQWFGNLQVNAHLGETN
FT EHVIVSP -> RISPTRSNVNVTSUNTKCPVVKLLKDR
FT MTEQYKCNLLNLEKDFR (IN ISOFORM SAK-B).
FT MISSING (IN ISOFORM SAK-B).
SQ SEQUENCE 925 AA; 103685 MW; D868A76BB7343E8; CRC64.

Query Match 83.7%; Score 41; DB 11; Length 925;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DE 204 LLIGRPPE 212

RESULT 15
Q96Q95 PRELIMINARY; PRT; 970 AA.
AC Q96Q95
DT 01-DEC-2001 (TrEMBLrel. 19, Created;
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE SAK.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Karn T., Holtrich U., Wolf G., Hock B., Streibhardt K.,
RA Ruebsaenen-Waigmann H.;
RT *Human SAK related to the PLK/polo family of cell cycle kinases shows
RT high mRNA expression in testis.*;
RL Oncol. Rep. 4:505-510(1997).
DR EMBL: Y13115; CAA73575.1; -.
DR HSSP: Q63450; 1A06.
DR Genew: HGNC:11397; STK18.
DR InterPro: IPR000959; POLO_box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00078; POLO_BOX; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 970 AA; 108955 MW; 552535615F95E8DF CRC64;

Query Match 83.7%; Score 41; DB 4; Length 970;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DE 204 LLIGRPPE 212

RESULT 17
Q81YFO PRELIMINARY; PRT; 970 AA.
AC Q81YFO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created);
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Similar to serine/threonine protein kinase.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
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RL Proc. Natl. Acad. Sci. U.S.A. 91:6388-6392(1994).
CC 1- ALTERNATIVE PRODUCTS; 2 ISOFORMS; SAK-A (SHOWN HERE) AND SAK-B;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
DR EMBL: L29479; AAC37648.1; -.
DR HSSP: Q0C534; 1B18.
DR MGC: MGI:101783; STK18.
DR InterPro: IPR000959; POLO_box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00078; POLO_BOX; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Alternative splicing; Serine/threonine-protein kinase;
KW Transferase.
FT VARSPLOC 417 464 SSNHRCLGKTPFPFAQDTQFMETVQWFGNLQVNAHLGETN
FT EHVIVSP -> RISPTRSNVNVTSUNTKCPVVKLLKDR
FT MTEQYKCNLLNLEKDFR (IN ISOFORM SAK-B).
FT MISSING (IN ISOFORM SAK-B).
SQ SEQUENCE 925 AA; 103685 MW; D868A76BB7343E8; CRC64.

Query Match 83.7%; Score 41; DB 11; Length 925;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DE 204 LLIGRPPE 212

RESULT 15
Q96Q95 PRELIMINARY; PRT; 970 AA.
AC Q96Q95
DT 01-DEC-2001 (TrEMBLrel. 19, Created;
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE SAK.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Karn T., Holtrich U., Wolf G., Hock B., Streibhardt K.,
RA Ruebsaenen-Waigmann H.;
RT *Human SAK related to the PLK/polo family of cell cycle kinases shows
RT high mRNA expression in testis.*;
RL Oncol. Rep. 4:505-510(1997).
DR EMBL: Y13115; CAA73575.1; -.
DR HSSP: Q63450; 1A06.
DR Genew: HGNC:11397; STK18.
DR InterPro: IPR000959; POLO_box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00078; POLO_BOX; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 970 AA; 108955 MW; 552535615F95E8DF CRC64;

Query Match 83.7%; Score 41; DB 4; Length 970;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DE 204 LLIGRPPE 212

RESULT 17
Q81YFO PRELIMINARY; PRT; 970 AA.
AC Q81YFO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created);
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Similar to serine/threonine protein kinase.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
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PL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 LR EMBL: BC36023; AAH36023.1; ...
 KW Kinase; Serine/threonine-protein kinase.
 SQ SEQUENCE 970 AA; 10897; MW: 405655ED983211A6 CRC64;

Query Match 83.7%; Score 41; DB 4; Length 970;
 Best Local Similarity 66.7%; Pred. No. 24;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLGRRPPE 9
 Db 204 LLVGRRPPE 212

RESULT 18
 Q9GRB7 PRELIMINARY; PRT; 526 AA.
 AC Q9B0P8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created;
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Polo like protein kinase (Fragment);
 OS Sus scrofa (Pig);
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN NCBI_TaxID=9823;
 RP SEQUENCE FROM N.A.
 RA Anger M., Kues W.A., Klima J., Mielenz M., Motlik J., Carnwath J.W.,
 RA Niemann H.;
 RT "Expression Of Polo-like Kinase In Cell Cycle Synchronized Fc10ine
 RT Fetal Fibroblasts";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF139021; AAK28550.1; ...
 DR HSSP; Q63450; 1A06.
 CR InterPro: IPR000959; POLO box.
 CR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00659; pkinase; 1.
 DR Pfam: PF00659; POLO box; 2.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 UR PROSITE; PS00078; POLO BOX; 2.
 UR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 UR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 UR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON_TER 1 1
 FT NON_TER 526 526
 SQ SEQUENCE 526 AA; 60399 MW; 1AFA1E5E0982CEB3 CRC64;

Query Match 81.6%; Score 40; DB 6; Length 526;
 Best Local Similarity 66.7%; Pred. No. 21;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLGRRPPE 9
 Db 199 LLVGRRPPE 207

RESULT 19
 Q9GRB7 PRELIMINARY; PRT; 582 AA.
 AC Q9GRB7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created;
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Polo-like kinase.
 GN UPK.
 CC Hemiecentrotus puicherrimus (Sea urchin);
 CC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 CC Echinioidea; Euechinozoa; Echinacea; Echinoidea; Strongylocentrotidae;

OC Hemiecentrotus.
 OX NCBI_TaxID=7650;
 RN NCBI_TaxID=7650;
 RP SEQUENCE FROM N.A.
 RA Yonemura I., Fujimoto H., Mabuchi I.;
 RT "Cloning of sea urchin plk";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN NCBI_TaxID=7650;
 RP SEQUENCE FROM N.A.
 RA Yonemura I., Fujimoto H., Mabuchi I.;
 RT "Cloning of sea urchin polc-like kinase";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AB043897; BAB18588.1; ...
 DR InterPro: IPR001395; Aldo/ket_red.
 DR InterPro: IPR000959; POLO box.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00659; POLO box; 2.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 UR PROSITE; PS00063; ALDO-KETO REDUCTASE_3; 1.
 UR PROSITE; PS00078; POLO BOX; 2.
 UR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 UR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 UR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 582 AA; 66429 MW; A3774A0CAACFDE5D CRC64;

Query Match 81.6%; Score 40; DB 5; Length 582;
 Best Local Similarity 66.7%; Pred. No. 23;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLGRRPPE 9
 Db 218 LLVGRRPPE 226

RESULT 20
 P70032 PRELIMINARY; PRT; 598 AA.
 ID P70032;
 AC P70032;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Plx1.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 CC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN NCBI_TaxID=8355;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96355660; PubMed=8703070;
 RA Kumagai A., Dunphy W.G.;
 RT "Purification and molecular cloning of Plx1, a Cdc25-regulatory kinase
 RT from Xenopus egg extracts";
 RL Science 273:1377-1380(1996).
 CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: U58205; AAC60017.1; ...
 DR HSSP; O63450; 1A06.
 DR InterPro: IPR000959; POLO box.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00659; POLO box; 2.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 UR PROSITE; PS00078; POLO BOX; 2.
 UR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 UR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 UR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 598 AA; 68211 MW; 246795931P225E6 CRC64;

Query Match 81.6%; Score 40; DB 13; Length 598;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
:|||||
Db 235 LLVGRPPPE 243

RESULT 21

Q81U35 PRELIMINARY; PRT; 623 AA.
AC Q81U35;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Polo-like kinase.
GN PLK.
OS Asterina pectinifera (Starfish).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asterozoa; Valvatacea; Valvatida; Asterinidae; Asterina.
OX NCBI_TaxID=7594;
RN 1;
RF SEQUENCE FROM N.A.
RA Uchida T.O., Tachibana K., Kishimoto T.;
RT "Starfish Plk.";
RL Submitted (MAY-2002) to the EMBL/GenBank/CCDS databases.
RW EMBL; AB084465; EAC22692.1;
KW Kinase.
SQ SEQUENCE 623 AA; 70929 MW; CFC01900502E724A CRC64;

Query Match 81.6%; Score 40; DB 5; Length 623;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
:|||||
Db 220 LLVGRPPPE 228

RESULT 22

Q8G6P7 PRELIMINARY; PRT; 235 AA.
AC Q8G6P7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 23, Last annotation update)
DE Putative mitogen-activated protein kinase (Fragment).
GN MPK1.
OS Leishmania amazonensis.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5659;
RN 1;
RF SEQUENCE FROM N.A.
RA STRAIN=LV73;
RA Wiese M., Goerke I.;
RT "Homologues of LMPK, a mitogen-activated protein kinase from Leishmania mexicana, in different Leishmania species.";
RL Submitted (NOV-2000) to the EMBL/GenBank/CCDS databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ298021; CAG17612.1;
DR HSSP; P24941; IHCC;
DR 01-MAR-2003 (TrEMBLrel. 23, Created)
DR InterPro; IPR003527; MAP kin.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 235 235
SQ SEQUENCE 235 AA; 26791 MW; 7FEDF167C0FBD3B7 CRC64;

Query Match 79.6%; Score 39; DB 5; Length 235;
Best Local Similarity 88.9%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
:|||||
Db 192 MLLGRPLFE 200

RESULT 23

O00872 PRELIMINARY; PRT; 358 AA.
AC O00872;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MAP-kinase homologue.
GN LMPK.
OS Leishmania mexicana.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5665;
RN 1;
RF SEQUENCE FROM N.A.
RC STRAIN=MNYC/BZ/62/M379;
RX MEDLINE=98232507; PubMed=9564044;
RA Wiese M.;
RT "A mitogen-activated protein (MAP) kinase homologue of Leishmania mexicana is essential for parasite survival in the infected host.";
RL EMBL J. 17:2619-2628(1998).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; Z95887; CAB09307.1;
DR HSSP; Q00534; 1B18.
DR InterPro; IPR003527; MAP kin.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS01351; MAPK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 358 AA; 41151 MW; 7D2D43C6057D8D4F CRC64;

Query Match 79.6%; Score 39; DB 5; Length 358;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
:|||||
Db 212 MLLGRPLFE 220

RESULT 24

Q8G6P9 PRELIMINARY; PRT; 690 AA.
AC Q8G6P9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Probable serine/threonine-protein kinase PknB.
GN PKNB OR BL0589.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=26816;
RN 1;

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RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787;
RA Schell M.A., Kamirantzou M., Snel B., Vilianova D., Berger B.,
RA Pessi G., Zwaren M.-C., Desiere F., Bork P., Delley M.,
PA Fridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL: AE014680; AAN24413.1; -.
KW Kinase; Complete proteome.
SQ SEQUENCE 690 AA; 72243 MW; 6A419EA8CED5D92D CRC64;

Query Match 79.6%; Score 39; DB 16; Length 690;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLJGRPPF 8
|||
DB 217 MLTGRPPF 224

RESULT 25
Q9KJN7 PRELIMINARY; PRT; 1337 AA.
ID Q9KJN7;
AC Q9KJN7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created);
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
FE Putative serine/threonine protein kinase.
GN PRND2.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC Cytaobacteriaceae; Myxococcaceae; Myxotoccus
OX NCBI_TaxID:14;
RA Cho K.;
RW [1];
RP SEQUENCE FROM N.A.
RC STRAIN=D22;
RX MEDLINE=20032045; PubMed=10564511;
RA Cho K., Zusman D.R.;
RT "Sporulation timing in Myxococcus xanthus is controlled by the espAB
RT locus";
RL Mol. Microbiol. 34:714-725(1999).
RA Cho K., Zusman D.R.;
RP SEQUENCE FROM N.A.
RC STRAIN=D22;
RX Submitted (JUL-2000) to the EMBL/GenBank/CCPC databases.
DR EMBL: AF193841; AAF87932.1; -.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR001440; TPR.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF05515; TPR; 4.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00028; TPR; 3.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1337 AA; 144738 MW; 608658CA4C92439D CRC64;

Query Match 79.6%; Score 19; DB 2; Length 1337;
Best Local Similarity 87.5%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLJGRPPF 8
|||
DB 242 MLTGRPPF 249

RESULT 26
Q91891 PRELIMINARY; PRT; 60 AA.
ID Q91891;
AC Q91891;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);

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DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Hypothetical 9.4 kDa protein (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1];
RP SEQUENCE FROM N.A.
RA Bouvet P., Omilli F., ARLOT-BONNEVAIN Y., Legagneux V., Roghi C.,
RA Bassez T., OSBORNE H.;
RT "Deadenylation conferred by the 3' untranslated region of a
RT developmentally controlled mRNA in xenopus embryos is switched to
RT polyadenylation deletion of a short sequences element.";
RL Mol. Cell. Biol. 14:1893-1900(1995).
DR EMBL: Z24453; CAA80826.1; -.
DR InterPro: IPR000719; Prot_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; ATP-binding; Transferase.
FT NON_TER 1
SQ SEQUENCE 80 AA; 9388 MW; 8DFCEDBA14BE14FB CRC64;

Query Match 77.6%; Score 38; DB 13; Length 80;
Best Local Similarity 75.0%; Pred. No. 8;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPPF 9
|||
DB 3 LVGRPPPF 10

RESULT 27
G63432 PRELIMINARY; PRT; 240 AA.
ID G63432;
AC G63432;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Rat protein kinase C-family related (fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=8747193; PubMed=3469647;
RA Housley G.M., O'Brian C.A., Johnson M.D., Kirschmeier P.,
RA Weinstein I.B.;
RT "Isolation of cDNA clones encoding protein kinase C: Evidence for a
RT protein kinase C-related gene family.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:1065-1069(1987).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: M15523; AAA1877.1; -.
DR HSPS; Q63450; IAO6.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
FT NON_TER 240
SQ SEQUENCE 240 AA; 26848 MW; 289934FE257E4682 CRC64;

Query Match 77.6%; Score 38; DB 11; Length 240;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MLGRRPPE 9
|:|:|:|:|
204 MMAGQPPPE 212

RESULT 28
OC1427 PRELIMINARY; PRT; 305 AA.

AC 001427;
DT 01-JUL-1997 (TREMBlrel. 04, Created;
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update);
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update);
DE C. ELEGANS AJRORA/IPC1-related protein KINASE 2 (AIR-2) (GB:AF071207),
DE CONTAINS SIMILARITY TO PFAM domain PF0069 (PKINASE), SCORE=295.1,
DE E-VALUE=2.8E-85, N=1 (AIR-2) (PKINASE);
GN AIR-2.

OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:1202-1208 (1998).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Herkhaus J., Wohlmann P.;
RA "The sequence of C. elegans cosmid BC207.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3];
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Waterston R.;
RA Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [4];
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Waterston R.;
RA Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [5];
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Waterston R.;
RA Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [6];
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Waterston R.;
RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [7];
RP SEQUENCE FROM N.A.
RC STRAIN=N2 BRISTOL;
RX Schumacher J.M., Golden A., Dorovan P.J.;
RT "Air-2: An aurora/ipl1-related protein kinase associated with
RT chromosomes and midbody microtubules is required for polar body
RT extrusion and cytokinesis in C. elegans embryos.";
RL J. Cell Biol. 0:0-0 (1998).
CC -; SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U97196; AAC52459.2; -;
DR EMBL; AF071207; AAC70945.1; -;
DR HSSP; P24941; 1AQ1.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser/thr_kinase.
DR Pfam; PF00609; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMC0220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOF; 1.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 305 AA; 34749 MW; 1635EB60D2E14011 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 385;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPPE 9
|:|:|:|:|
220 LVGRPPPE 227

RESULT 29
Q9AJZ9 PRELIMINARY; PRT; 332 AA.

AC 09AJZ9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein SCO7729.
GN SCO7729 OR SC8D11.20.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX Saunders D.C., Harris D.;
RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RA Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3];
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96 (1996).
RN [4];
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147 (2002).
DR EMBL; AL939132; CAC22737.1; -;
DR InterPro; IPR003829; DUF209.
DR Pfam; PF02678; DUF209; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 332 AA; 35974 MW; 7E05869A9386B08D CRC64;

Query Match 77.6%; Score 38; DB 16; Length 332;
Best Local Similarity 77.8%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
|:|:|:|:|

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Db          262 ILGGPPPE 270

RESULT 40
ID Q95T78      PRELIMINARY;      PRT;      554 AA.
AC Q95T78;
DT 01-DEC-2001 (TRENBLrel. 19, Created;
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update;
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update;
DE GH13631p;
GN PKG98E CR CG-954;
OS Drosophila melanogaster (Fruit fly);
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Musco-orpha;
OC Ephydroidea; Drosophilidae; Drosophila.
CX NCB:_TaxID=7227;
RN [1];
RP SEQUENCE FROM N.A.

RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungali C.,
RA Nuccio J., Pacleb J., Paragas V., Park S., Phomavanong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celliker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AY066293; AAL25332.1;
DR Flybase: F53n000393; PKG98E;
DR InterPro: IPR002219; DAG_PE-bind;
DR InterPro: IPR000961; Pkinase C;
DR InterPro: IPR000719; Prot_kinase;
DR InterPro: IPR002290; Ser_thr_kinase;
DR Pfam: PF00130; DAG_PE-bind; 1;
DR Pfam: PF00069; Pkinase; 1;
DR Pfam: PF00433; Pkinase C; 1;
DR PRINTS: PR00008; DAGPEDOMAIN;
DR PRODOM: PD000031; Prot_kinase; 1;
DR SMART: SM00139; C1; 1;
DR SMART: SM00220; S-TKC; 1;
DR SMART: SM00133; S-TK X; 1;
DR PROSITE: PS00479; DAG_PE_BIND_DOM 1; 1;
DR PROSITE: PS00081; DAG_PE_BIND_DOM 2; 1;
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
DR PROSITE: PS00112; PROTEIN_KINASE_DOM; 1;
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1;
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 554 AA; 61598 MW; 100FAVU55NAD3E4 C6064;

Query Match 77.6%; Score 38; DB 5; Length 554;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 MLGGPPPE 9
Db 415 YMGQPPPE 423

RESULT 1;
ID Q8FJ15      PRELIMINARY;      PRT;      660 AA.
AC Q8FJ15;
DT 01-MAR-2003 (TRENBLrel. 23, Created;
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update;
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update;
DE Putative serine/threonine-protein kinase.
GN C8F013;
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
CX NCB:_TaxID=152794;
RN [1];
RP SEQUENCE FROM N.A.

RC STRAIN=Berkley;
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungali C.,
RA Nuccio J., Pacleb J., Paragas V., Park S., Phomavanong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celliker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AY066293; AAL25332.1;
DR Flybase: F53n000393; PKG98E;
DR InterPro: IPR002219; DAG_PE-bind;
DR InterPro: IPR000961; Pkinase C;
DR InterPro: IPR000719; Prot_kinase;
DR InterPro: IPR002290; Ser_thr_kinase;
DR Pfam: PF00130; DAG_PE-bind; 1;
DR Pfam: PF00069; Pkinase; 1;
DR Pfam: PF00433; Pkinase C; 1;
DR PRINTS: PR00008; DAGPEDOMAIN;
DR PRODOM: PD000031; Prot_kinase; 1;
DR SMART: SM00139; C1; 1;
DR SMART: SM00220; S-TKC; 1;
DR SMART: SM00133; S-TK X; 1;
DR PROSITE: PS00479; DAG_PE_BIND_DOM 1; 1;
DR PROSITE: PS00081; DAG_PE_BIND_DOM 2; 1;
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
DR PROSITE: PS00112; PROTEIN_KINASE_DOM; 1;
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1;
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 660 AA; 75054 MW; 3346B06EE4A2B2D5 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 661;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 MLGGPPPE 9
Db 207 LVTGRPPPE 215

RESULT 32
ID Q01669      PRELIMINARY;      PRT;      661 AA.
AC Q01669;
DT 01-JUL-1997 (TRENBLrel. 04, Created;
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update;
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update;
DE Protein Kinase C (fragment).
OS Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Anthomedusae;
OC Hydridae; Hydra.
CX NCB:_TaxID=6087;
RN [1];
RP SEQUENCE FROM N.A.

RC STRAIN=Zuerich;
RA Hassel M., Bridge D.M., Stover N.A., Kleinholz H., Steele R.E.;
RL Dev. Genes Evol. 207:502-514(1998);
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: Y12237; CAA72926.1;
DR HSSP: P05697; ITBN;
DR InterPro: IPR000088; C2;
DR InterPro: IPR002219; DAG_PE-bind;
DR InterPro: IPR000961; Pkinase C;
DR InterPro: IPR000719; Prot_kinase;
DR InterPro: IPR002290; Ser_thr_kinase;
DR Pfam: PF00168; C2; 1;
DR Pfam: PF00130; DAG_PE-bind; 2;
DR Pfam: PF00069; Pkinase; 1;
DR Pfam: PF00433; Pkinase C; 1;
DR PRINTS: PR00008; DAGPEDOMAIN;
DR PRODOM: PD000001; Prot_kinase; 1;
DR SMART: SM00109; C1; 2;
DR SMART: SM00239; C2; 1;
DR SMART: SM00220; S-TKC; 1;
DR SMART: SM00133; S-TK X; 1;
DR PROSITE: PS00004; C2_DOMAIN 2; 1;
DR PROSITE: PS00479; DAG_PE_BIND_DOM 1; 2;
DR PROSITE: PS00081; DAG_PE_BIND_DOM 2; 2;
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1;
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1;
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 661 661
SQ SEQUENCE 661 AA; 75054 MW; 3346B06EE4A2B2D5 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 661;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 MLGGPPPE 9
Db 207 LVTGRPPPE 215

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E6 561 MMAGQPPFE 569

RESULT 33

Q20953 PRELIMINARY; PRT; 707 AA.
AC Q20953;
DT C2-NOV-1996 (TREMBLrel. 01, Created;
01-DEC-2003 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE F57F5.5 protein.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP HARRIS B.R.;
RA Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2019(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA White S.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DE EMBL; Z75953; CAB00101.1;
DR EMBL; Z81497; CAB00101.2; JOINED.
DR EMBL; Z81497; CAC70080.1;
DR EMBL; Z75953; CAC70080.1; JOINED.
DR HSP; P28867; IPTQ.
DR Wormpep; F57F5.5; CE29092.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE_BIND.
DR InterPro; IPR000961; PKINASE_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE_BIND; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00219; TyRK; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; transferase.
SQ SEQUENCE 707 AA; 80151 MW; 08C13D1E7A911B49 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 707;
Best Local Similarity 66.7%; Pred. No. 66;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLGRPPFE 9

Db 570 MMAGQPPFE 578

RESULT 34

Q20953 PRELIMINARY; PRT; 707 AA.

AC Q20953;

DT C2-NOV-1996 (TREMBLrel. 01, Created;

01-DEC-2003 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE F57F5.5 protein.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Pelodierinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP HARRIS B.R.;

RA Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

RL [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for

investigating biology."

RL Science 282:2012-2019(1998).

RN [3]

RP SEQUENCE FROM N.A.

RA White S.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DE EMBL; Z75953; CAB00101.1;

DR EMBL; Z81497; CAB00101.2; JOINED.

DR EMBL; Z81497; CAC70080.1;

DR EMBL; Z75953; CAC70080.1; JOINED.

DR HSP; P28867; IPTQ.

DR Wormpep; F57F5.5; CE29092.

DR InterPro; IPR000008; C2.

DR InterPro; IPR002219; DAG_PE_BIND.

DR InterPro; IPR000961; PKINASE_C.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_kinase.

DR Pfam; PF00168; C2; 1.

DR Pfam; PF00130; DAG_PE_BIND; 2.

DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00433; pkinase; 1.

DR PRINTS; PR00008; DAGPEDOMAIN.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00109; C1; 2.

DR SMART; SM00239; C2; 1.

DR SMART; SM00133; S_TK_X; 1.

DR PROSITE; PS50004; C2_DOMAIN_2; 1.

DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.

DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW Hypothetical protein; ATP-binding; transferase.

SQ SEQUENCE 707 AA; 80151 MW; 08C13D1E7A911B49 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 707;

Best Local Similarity 66.7%; Pred. No. 66;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLGRPPFE 9

Db 570 MMAGQPPFE 578

RESULT 34

Q20953 PRELIMINARY; PRT; 707 AA.

AC Q20953;

DT C2-NOV-1996 (TREMBLrel. 01, Created;

01-DEC-2003 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE F57F5.5 protein.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Pelodierinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP HARRIS B.R.;

RA Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

RL [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for

investigating biology."

RL Science 282:2012-2019(1998).

RN [3]

RP SEQUENCE FROM N.A.

RA White S.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DE EMBL; Z75953; CAB00101.1;

DR EMBL; Z81497; CAB00101.2; JOINED.

DR EMBL; Z81497; CAC70080.1;

DR EMBL; Z75953; CAC70080.1; JOINED.

DR HSP; P28867; IPTQ.

DR Wormpep; F57F5.5; CE29092.

DR InterPro; IPR000008; C2.

DR InterPro; IPR002219; DAG_PE_BIND.

DR InterPro; IPR000961; PKINASE_C.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_kinase.

DR Pfam; PF00168; C2; 1.

DR Pfam; PF00130; DAG_PE_BIND; 2.

DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00433; pkinase; 1.

DR PRINTS; PR00008; DAGPEDOMAIN.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00109; C1; 2.

DR SMART; SM00239; C2; 1.

DR SMART; SM00133; S_TK_X; 1.

DR PROSITE; PS50004; C2_DOMAIN_2; 1.

DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.

DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW Hypothetical protein; ATP-binding; transferase.

SQ SEQUENCE 707 AA; 80151 MW; 08C13D1E7A911B49 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 707;

Best Local Similarity 66.7%; Pred. No. 66;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLGRPPFE 9

Db 570 MMAGQPPFE 578

RESULT 34

Q20953 PRELIMINARY; PRT; 707 AA.

AC Q20953;

DT C2-NOV-1996 (TREMBLrel. 01, Created;

01-DEC-2003 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE F57F5.5 protein.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Pelodierinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP HARRIS B.R.;

RA Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

RL [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for

investigating biology."

RL Science 282:2012-2019(1998).

RN [3]

RP SEQUENCE FROM N.A.

RA White S.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DE EMBL; Z75953; CAB00101.1;

DR EMBL; Z81497; CAB00101.2; JOINED.

DR EMBL; Z81497; CAC70080.1;

DR EMBL; Z75953; CAC70080.1; JOINED.

DR HSP; P28867; IPTQ.

DR Wormpep; F57F5.5; CE29092.

DR InterPro; IPR000008; C2.

DR InterPro; IPR002219; DAG_PE_BIND.

DR InterPro; IPR000961; PKINASE_C.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_kinase.

DR Pfam; PF00168; C2; 1.

DR Pfam; PF00130; DAG_PE_BIND; 2.

DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00433; pkinase; 1.

DR PRINTS; PR00008; DAGPEDOMAIN.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00109; C1; 2.

DR SMART; SM00239; C2; 1.

DR SMART; SM00133; S_TK_X; 1.

DR PROSITE; PS50004; C2_DOMAIN_2; 1.

DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.

DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW Hypothetical protein; ATP-binding; transferase.

SQ SEQUENCE 707 AA; 80151 MW; 08C13D1E7A911B49 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 707;

Best Local Similarity 66.7%; Pred. No. 66;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLGRPPFE 9

Db 570 MMAGQPPFE 578

RESULT 34

Q20953 PRELIMINARY; PRT; 707 AA.

AC Q20953;

DT C2-NOV-1996 (TREMBLrel. 01, Created;

01-DEC-2003 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE F57F5.5 protein.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Pelodierinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP HARRIS B.R.;

RA Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

RL [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99069613; PubMed=9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for

investigating biology."

RL Science 282:2012-2019(1998).

RN [3]

RP SEQUENCE FROM N.A.

RA White S.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DE EMBL; Z75953; CAB00101.1;

DR EMBL; Z81497; CAB00101.2; JOINED.

DR EMBL; Z81497; CAC70080.1;

DR EMBL; Z75953; CAC70080.1; JOINED.

DR HSP; P28867; IPTQ.

DR Wormpep; F57F5.5; CE29092.

DR InterPro; IPR000008; C2.

DR InterPro; IPR002219; DAG_PE_BIND.

DR InterPro; IPR000961; PKINASE_C.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_kinase.

DR Pfam; PF00168; C2; 1.

DR Pfam; PF00130; DAG_PE_BIND; 2.

DR Pfam; PF00069; pkinase; 1.

DR Pfam; PF00433; pkinase; 1.

DR PRINTS; PR00008; DAGPEDOMAIN.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00109; C1; 2.

DR SMART; SM00239; C2; 1.

DR SMART; SM00133; S_TK_X; 1.

DR PROSITE; PS50004; C2_DOMAIN_2; 1.

DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.

DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW Hypothetical protein; ATP-binding; transferase.

SQ SEQUENCE 707 AA; 80151 MW; 08C13D1E7A911B49 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 707;

Best Local Similarity 66.7%; Pred. No. 66;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLGRPPFE 9

Db 570 MMAGQPPFE 578

RESULT 34

Q20953 PRELIMINARY; PRT; 707 AA.

AC Q20953;

DT C2-NOV-1996 (TREMBLrel. 01, Created;

01-DEC-2003 (TREMBLrel. 19, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE F57F5.5 protein.

RT the flagella during gamete activation in Chlamydomonas.",
 RL J. Biol. Chem. 275:24106-24114(2000).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF199021; AAF97501.1; ..
 DR HSSP: C63450; 1AC6.
 DR InterPro: IPR002719; Prot_kinase.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR Pfam: PF00369; pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS5011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_SF; ..
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 769 AA; 80250 MW; D3G37FFCD42431C1 CRC64;
 Query Match 77.6%; Score 38; DB 10; Length 769;
 Best Local Similarity 55.6%; Pred. No. 72;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGRRPFF 9
 DB 241 LIVGRPPFD 249
 RESULT 36
 Q8CR93 PRELIMINARY; PRT; 178 AA.
 ID Q8CR93
 AC Q8CR93
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Conserved hypothetical protein.
 DE SF1984.
 OS Staphylococcus epidermidis.
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID:1228;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia C., Tu Y., Qin Z.,
 RA Chen Z., Wen Y.;
 RA Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 KD EMBL: A5016750; AAC05625.1; ..
 KW Hypothetical; protein; Complete Proteome.
 SQ SEQUENCE 178 AA; 20507 MW; F78C1D39DC4B7298 CRC64;
 Query Match 75.5%; Score 37; DB 16; Length 178;
 Best Local Similarity 85.7%; Pred. No. 27;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LLGRPPF 8
 DB 172 ILGRPPF 178
 RESULT 37
 Q950L6 PRELIMINARY; PRT; 301 AA.
 ID Q950L6
 AC Q950L6
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE NADH dehydrogenase subunit 1 (EC 1.6.5.3) (NADH ubiquinone
 DE oxidoreductase chain 1).
 DE NAD1.
 OS Rhizophidium sp. 136.
 CC Mitochondrion.
 CC Eukaryota; Fungi; Chytridiomycota; Chytridiales; Chytridiaceae;
 CC Rhizophidium.
 KW NCB: TaxID=60187;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=136;
 RA Forget L., Ustinova J., Wang Z., Huss V.A.R., Lang F.B.F.;
 RA "Hyatorphidium curvatum: a linear mitochondrial genome, tRNA editing,
 RT and an evolutionary link to lower fungi.",
 RL Mol. Biol. Evol. 0:0-0(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=136;
 RA Lang F.B.F.;
 RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
 CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
 DR EMBL: AF040366; AAK84292.1; ..
 DR InterPro: IPR001594; Resp_NADH_dh1.
 DR Pfam: PF00146; NADHdh; 1.
 KW NAD; Oxidoreductase; Transmembrane; Ubiquinone; Mitochondrion.
 SQ SEQUENCE 301 AA; 33286 MW; DD58195953EF41D5 CRC64;
 Query Match 75.5%; Score 37; DB 8; Length 301;
 Best Local Similarity 85.7%; Pred. No. 45;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LGRPPF 9
 DB 194 LGRPPFD 200
 RESULT 38
 Q91Y16 PRELIMINARY; PRT; 484 AA.
 ID Q91Y16
 AC Q91Y16
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical 55.9 kDa protein.
 DE GN A1649009.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC016629; AAH16629.1; ..
 DR MGD; MGI:2140950; A1649009
 DR InterPro: IPR001237; PAP_25A_core.
 DR InterPro: IPR002058; PAP_assoc.
 DR Pfam: PF03828; PAP_assoc; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 484 AA; 55933 MW; C60D799AASF14CB6 CRC64;
 Query Match 75.5%; Score 37; DB 11; Length 484;
 Best Local Similarity 85.7%; Pred. No. 71;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LLGRPPF 8
 DB 6 ILGRPPF 12
 RESULT 39
 Q9H9T2 PRELIMINARY; PRT; 622 AA.
 ID Q9H9T2
 AC Q9H9T2
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein FLJ12565.
 DE Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]

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RE  SEQUENCE FROM N.A.
RA  Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA  Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA  Wakisaka M., Hosokawa T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA  Takahashi M., Chiba Y., Ishida S., Murakawa K., Ota Y., Takiguchi S.,
RA  Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA  Yaezono J., Wakamatsu A., Nakamura Y., Nagakari K., Masuno Y.,
RA  Nakomiyu K., Iwayanagi T.
RI  "NEDO human cDNA sequencing project."
RL  Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL: AK22627; BAB14139.1; .
DR  InterPro: IPR001841; Znf_rir3.
DR  SMART: SM0184; RING_2.
DR  PROSITE: PS0089; ZF_RING_2; 1.
KW  Hypothetical protein.
SQ  SEQUENCE 622 AA; 70366 MW; B837A889163B88 CRC64;

      Query Match      75.5%; Score 37; DB 4; Length 622;
      Best Local Similarity 77.8%; Pred. No. 91;
      Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  1 MLLGRPPFE 9
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DE  37 LLLGRPPFE 45

RESULT 40
CO 001715 PRELIMINARY; PROT 670 AA.
AC 001715;
DT 01-JUL-1997 (TEMBLrel_04, Created)
DT 01-JUL-1997 (TEMBLrel_04, Last sequence update)
DT 01-MAR-2003 (TEMBLrel_23, Last annotation update)
DE Protein Kinase C.
GN PKC-Ca.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroidea; Anthomedusae;
OC Hydroidea; Hydra.
CX NCBI_TaxID=6257;
EN 1;
RF SEQUENCE FROM N.A.
RC STRAIN=Zuerich;
RX MEDLINE=98179224; Pubmed=9510544;
RA Hassel, M.;
RT Upregulation of a Hydra vulgaris ckr1 gene is tightly coupled to the
RT differentiation of head structures."
RL Dev. Genes Evol. 207:489-501(1998)
CC 1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -1 SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL: Y12858; CAA73363.1; .
DR HSPF: P05697; ITEN
DR InterPro: IPR000008; C2.
DR InterPro: IPR02219; DAG_PE-bind
DR InterPro: IPR000961; PKinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR02290; Ser_thr_kinase.
DR Pfam: PF00148; C2; 1.
DR Pfam: PF00130; DAG_PE-bind; 2.
DR Pfam: PF00069; kinase; 1.
DR Pfam: PF00433; kinase_C; 1.
DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR ProDom: PD00001; Prot_kinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SM00239; C2; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00133; S_TKc; 1.
DR PROSITE: PS00499; C2_DOMAIN_1; 1.
DR PROSITE: PS00004; C2_DOMAIN_2; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOW_1; 2.
DR PROSITE: PS00081; DAG_PE_BIND_DOW_2; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
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DR  PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW  ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ  SEQUENCE 670 AA; 76642 MW; EBFC370229065878 CRC64;

      Query Match      75.5%; Score 37; DB 5; Length 670;
      Best Local Similarity 66.7%; Pred. No. 97;
      Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  1 MLLGRPPFE 9
DE  |||||
DE  534 MLAGQPPPF 542

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Job time : 28 secs
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OM protein - protein search, using sw model

Run on: November 14, 2003, 12:54:54, Search time 30.5571 Seconds
without alignments:
41.15: Million cell updates/sec

Title: US-09-736-076-16

Perfect score: 44

Sequence: MLLGKPPF 8

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1981.DAT.*
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4: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1983.DAT.*
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6: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1988.DAT.*
10: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1990.DAT.*
12: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1991.DAT.*
13: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1992.DAT.*
14: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1993.DAT.*
15: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1994.DAT.*
16: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1995.DAT.*
17: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1996.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq-emb/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq-emb/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb/AA2001.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	8	AAW74160	HJ loop peptide J-
2	44	100.0	8	AAU98316	Polo kinase serine
3	44	100.0	9	AAW74161	HJ loop peptide J-
4	41	100.0	9	AAU98317	Polo kinase serine
5	41	93.2	9	AAW74159	HJ loop peptide J-
6	41	93.2	9	AAU98315	Polo kinase serine
7	41	93.2	10	AAW74213	HJ loop peptide K0
8	41	93.2	10	AAU98357	Polo kinase SNK se
9	41	93.2	11	AAW74163	HJ loop peptide J-

10	41	93.2	11	23	AAU98319	Polo kinase serine
11	41	93.2	469	22	AAU94717	Human protein sequ
12	41	93.2	469	22	AAG67426	Amino acid sequenc
13	41	93.2	685	20	AAU00915	Human serum induci
14	41	93.2	685	20	AAU88432	Disease associated
15	41	93.2	585	23	ABP61474	Human NF-kB activa
16	41	93.2	753	23	ABP41992	Human ovarian anti
17	39	88.6	304	21	AAG36347	Arabidopsis thalia
18	39	88.6	304	21	AAG37267	Arabidopsis thalia
19	39	88.6	305	21	AAG38660	Arabidopsis thalia
20	39	88.6	329	21	AAG36346	Arabidopsis thalia
21	39	88.6	329	21	AAG37266	Arabidopsis thalia
22	39	88.6	330	21	AAG38659	Arabidopsis thalia
23	39	88.6	465	21	AAG36345	Arabidopsis thalia
24	39	88.6	465	21	AAG37265	Arabidopsis thalia
25	39	88.6	466	21	AAG38658	Arabidopsis thalia
26	39	88.6	592	21	AAU93500	Amino acid sequenc
27	39	88.6	604	23	AAU74657	Yeast cycloin depen
28	39	88.6	766	21	AAU93498	Amino acid sequenc
29	38	86.4	8	20	AAW74211	HJ loop peptide K0
30	38	86.4	8	23	AAU98355	Polo kinase Plk se
31	38	86.4	20	20	AAW74173	HJ loop peptide PO
32	38	86.4	20	23	AAU98306	Peptide sequence o
33	38	86.4	329	21	AAU56690	Human prostate can
34	38	86.4	419	23	AAU83127	Novel secreted pro
35	38	86.4	528	23	ABP73734	Candida albicans e
36	38	86.4	531	23	AAU74656	Human lung tumour
37	38	86.4	603	16	AAW74620	Mammalian polo-like
38	38	86.4	603	23	AAU79306	Mouse polo-like ki
39	38	86.4	603	23	AAU79308	Mouse polo-like ki
40	38	86.4	603	23	AAU79309	Mouse polo-like ki
41	38	86.4	603	23	AAU79310	Mouse polo-like ki
42	38	86.4	603	23	AAU79311	Mouse polo-like ki
43	38	86.4	603	23	AAU79312	Mouse polo-like ki
44	38	86.4	603	23	AAU79313	Mouse polo-like ki
45	38	86.4	603	23	AAU79314	Mouse polo-like ki

ALIGNMENTS

RESULT 1
AAW74160
ID AAW74160 standard; peptide; 8 AA.
XX
AC AAW74160;

DT 05-MAY-1999 (first entry)

DE HJ loop peptide J-43.

XX

DE HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;

KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;

KW inflammatory disorder; central nervous system disease; septic shock;

KW Parkinson's disease; hypertension.

XX Synthetic.

XX

FT Key Location/Qualifiers

FT Modified-site 1 /note= "acetylated"

FT Modified-site 8 /note= "amidated"

FT

XX WO9853050-A2.

PN

XX

PD 26-NOV-1998.

XX

PF 20-MAY-1998; 98WG-US10319.

XX

PR 21-MAY-1997; 97US-0861338.

XX

PA (CHIL-) CHILDRENS MEDICAL CENT.

PA (YISS) YISSUM RES & DEV CO.
 XX Ben-Sasson SA;
 XX WP1: 1999-070142/36.
 XX
 XX New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders
 XX
 XX Claim 14: Fig 4: 70pp; English.
 XX
 XX This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.
 XX
 XX Sequence 8 AA:
 SQ
 Query Match 100.0%; Score 44; DB 20; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLLGKPPF 8
 Db : MLLGKPPF 8
 RESULT 2
 AAU98316
 ID AAU98316 standard; Peptide; 8 AA.
 AC AAU98316;
 XX
 XX 13-AUG-2002 (first entry)
 DE
 DE Polo kinase serine-threonine kinase HJ loop peptide J-43.
 XX
 XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
 KW modulating STK activity; polo kinase; J-43.
 XX
 XX Unidentified.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 8 /note= "C-terminal amide"
 FT
 XX
 XX US2002049301-A1.
 PN
 XX 25-APR-2002.
 PP
 PP 13-DEC-2002; 2000US-0736076.
 XY

PR 21-MAY-1997; 97US-0861338.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX Ben-Sasson SA;
 XX WP1: 2002-462787/49.
 XX
 XX New peptide from the HJ loop of serine-threonine kinase, useful for
 PT treating e.g. cancer and for producing diagnostic antibodies -
 XX
 XX Disclosure; Fig 4: 4pp; English.
 XX
 XX The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase
 CC serine-threonine kinase HJ loop peptide J-43. This sequence is one of
 CC the short peptides of the invention that selectively modulate the
 CC activity of STK.
 XX
 XX Sequence 8 AA:
 SQ
 Query Match 100.0%; Score 44; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLLGKPPF 8
 Db : MLLGKPPF 8
 RESULT 3
 AAU74161
 ID AAU74161 standard; peptide; 9 AA.
 AC AAU74161;
 XX
 XX 05-MAY-1999 (first entry)
 DT
 XX HJ loop peptide J-43.1.
 DE
 DE HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.
 XX
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "acetylated"
 FT Modified-site 9 /note= "amidated"
 FT
 XX
 XX MO9851050-A2.
 PN
 XX 26-NOV-1998.
 PD
 XX 20-MAY-1998; 98WO-US10319.
 PF
 XX 21-MAY-1997; 97US-0861338.
 PR
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA (YISS) YISSUM RES & DEV CO.
 XX Ben-Sasson SA;
 PI

```

XX WF1, 1989-070:42/36.
XX
XX New peptides for modulating serine/threonine Kinase activity -
PT comprise a sequence corresponding to the H3 loop of a
PT serine/threonine kinase, used for treating, e.g. cancers,
PT inflammatory disorders or autoimmune disorders
XX
XX Claim 14; Fig 4; 70pp: English.
XX
XX This sequence represents a peptide of the invention, and is a derivative
CC of the H3 loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, arteriosclerosis,
CC arterio-sclerosis, cardiac hypertrophy, ischaemia, reperfusion injury and
CC hypertension); immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the H3 loop of the STK
XX from which the peptide was derived.
XX SQ Sequence 9 AA;
Query Match: 100.0%; Score 44; DB 20; Length 9;
Best local Similarity 100.0%; Pred No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 MDLGGPPF 8
DB 1 MDLGGPPF 8
RESULT 4
ANU98117
IC ANU98117 standard; Peptide; 9 AA.
XX
AC ANU98117;
DT
DE 13-AUG-2002 (first entry)
XX
XX Polo kinase serine-threonine kinase H3 loop peptide 3-431.
KW H3 loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytotoxic; antidiabetic; trophic; neurological;
KW anti-inflammatory; immunosuppressive; cardiac; haemostatic;
KW modulating STK activity; polo kinase; 3-431.
XX
CS Unidentified.
CS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Modified site 1 /note= "N-terminal acetyl"
FT Modified site 9
FT Modified site 9 /note= "Benzyl ester of Glutamic acid, C-terminal amide"
XX
PN US2002C49301-A1.
XX
XX 25-APR-2002.
XX
XX 13-FEB-2000; ZOOUS-0736076.
XX
XX 21 MAY-1997; 9TUS-0861338.
XX
XX (CHILDREN'S MEDICAL CENT

```

DR WPI: 1999-070142/06.

XX New peptides for modulating serine/threonine kinase activity -

PT comprise a sequence corresponding to the HJ loop of a

PT serine/threonine kinase, used for treating, e.g. cancers,

PT inflammatory disorders or autoimmune disorders

XX

PS Claim 14; Fig 4; 70pp; English.

XX

CC This sequence represents a peptide of the invention, and is a derivative

CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be

CC used for the treatment of disorders caused by overactivity or

CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic

CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,

CC arteriosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury and

CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,

CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression

CC of organ transplant rejection, multiple sclerosis, inflammatory bowel

CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's

CC disease, stroke and trauma), septic shock, Parkinson's disease or

CC hypertension. The peptides can also be used to produce antibodies which

CC can be used to identify cells expressing the STK and to study the

CC intracellular distribution of the STK. In addition, the peptides can be

CC used to identify and quantitate ligands which bind the HJ loop of the STK

CC from which the peptide was derived.

XX

SQ Sequence 9 AA;

Query Match 93.2%; Score 41; DB 20; Length 9;

Best Local Similarity 87.5%; Pred. No. 9.3e-05;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MLLGRPPF 8

Db 1 MLLGRPPF 8

RESULT 6

AA099315

CC AA099315 standard; Peptide: 9 AA.

XX

AC AA099315;

DT 13-AUG 2002 (first entry)

XX

DE Polo kinase serine-threonine kinase HJ loop peptide J-42.

XX

KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;

KW central nervous system disorder; inflammatory disorder;

KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;

KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;

KW antiinflammatory; immunosuppressive; cardiac; haemostatic;

KW modulating STK activity; polo kinase; J-42.

XX

CS Unidentified.

OS Synthetic.

XX

PH Key Location/Qualifiers

FT Modified site 1 /note= "N-terminal acetyl"

FT Modified site 9 /note= "Benzyl ester of glutamic acid"

FT Modified site 9 /note= "C-terminal amide"

XX

PN US2002049301-A1.

XX

PD 25-APR 2002.

XX

PF 13 DEC 2000; 2000US-0736076.

XX

PR 21 MAY 1997; 97US-0861338.

XX

PA (CHIL-) CHILDRENS MEDICAL CENT.

XX Ben-Sasson SA;

XX WPI: 2002-462787/49.

XX

PT New peptide from the HJ loop of serine-threonine kinase, useful for

PT treating e.g. cancer and for producing diagnostic antibodies -

XX

PS Disclosure; Fig 4; 41pp; English.

XX

CC The present invention relates to new peptides derived from the HJ loop

CC of a serine/threonine kinase (STK). The peptides of the invention are

CC used to modulate STK activity, especially for treating cancer, diabetes,

CC obesity or a wide variety of central nervous system, inflammatory,

CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for

CC regulating lipid metabolism. The peptides are also used to generate

CC antibodies that bind specifically to the parent STK, used e.g. for

CC identifying STK-expressing cells and to study intracellular distribution

CC of STK, and to identify or quantify ligands that bind to the HJ loop.

CC The present amino acid sequence represents the polo kinase

CC serine-threonine kinase HJ loop peptide J-42. This sequence is one of

CC the short peptides of the invention that selectively modulate the

CC activity of STK.

XX

SQ Sequence 9 AA;

Query Match 93.2%; Score 41; DB 23; Length 9;

Best Local Similarity 87.5%; Pred. No. 9.3e+05;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGRPPF 8

Db 1 MLLGRPPF 8

RESULT 7

AA074213

ID AA074213 standard; peptide: 10 AA.

XX

AC AA074213;

DT 05-MAY-1999 (first entry)

XX

DE HJ loop peptide K038H101.

XX

KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;

KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;

KW inflammatory disorder; central nervous system disease; septic shock;

KW Parkinson's disease; hypertension.

OS Synthetic.

XX

PH Key Location/Qualifiers

FT Modified-site 1 /note= "myristylated"

FT Modified-site 10 /note= "amidated"

XX

PN WO9853050-A2.

XX

PD 26-NOV-1998.

XX

PF 20-MAY-1998; 98WO-US10119.

XX

PR 21-MAY-1997; 97US-0861338.

XX

PA (CHIL-) CHILDRENS MEDICAL CENT.

PA (VISS) VISSUM RES & DEV CO.

XX

PI Ben-Sasson SA;

XX

DR WPI: 1999-070142/06.

PT inflammatory disorders or autoimmune disorders
 PS Claim 14; Fig 4; 70pp; English.
 XX
 CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury and
 CC hyperaesthesia), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.
 XX
 SQ Sequence 11 AA;
 Query Match 93.2%; Score 41; DB 20; Length 11;
 Best Local Similarity 87.5%; Pred. No. 0.47;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPF 8
 DB 1 MLLGRPPF 8
 RESULT 10
 AA098319
 ID AA098319 standard; Peptide; 11 AA.
 XX
 AC AA098319;
 XX
 DT 13 AUG-2002 (first entry)
 XX
 DE Pdc kinase serine-threonine kinase HJ loop peptide J 46.
 XX
 KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 KW anti-inflammatory; immunosuppressive; cardiac; haemostatic;
 KW modulating STK activity; pdc kinase; J 46.
 XX
 OS Unidentified.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl"
 FT Misc difference 9
 FT /note= "Benzyl ester of Glutamic acid"
 FT Modified-site 11
 FT /note= "C-terminal amide"
 XX
 XX US2002049301-A1.
 XX
 XX 25-APR-2002.
 XX
 FF 13-DEC-2000; 2000US-0736076.
 XX
 PR 21-MAY-1997; 97US-0861338.
 XX
 PA (CHIL-); CHILDRENS MEDICAL CENT.
 XX
 PI Ben-Sasson SA;
 XX
 CR WPI; 2002-462787/49.

XX
 PT New peptide from the HJ loop of serine-threonine kinase, useful for
 PT treating e.g. cancer and for producing diagnostic antibodies -
 XX
 PS Disclosure; Fig 4; 41pp; English.
 XX
 CC The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the pdc kinase
 CC serine-threonine kinase HJ loop peptide J-46. This sequence is one of
 CC the short peptides of the invention that selectively modulate the
 CC activity of STK.
 XX
 SQ Sequence 11 AA;
 Query Match 93.2%; Score 41; DB 23; Length 11;
 Best Local Similarity 87.5%; Pred. No. 0.47;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPF 8
 DB 1 MLLGRPPF 8
 RESULT 11
 AA094717
 ID AAB94717 standard; Protein; 469 AA.
 XX
 AC AAB94717;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human protein sequence SEQ ID NO:15726.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 KW Homo sapiens.
 OS
 XX EPI074617-A2.
 PN
 XX 07-FEB-2001.
 PD
 XX 28-JUL-2000; 2000EP-0116126.
 PF
 XX 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99CP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI; 2001-318749/34.
 DR
 XX Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 8; SEQ ID 15726; 2537pp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95493 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

XX SQ Sequence 469 AA;

Query Match 93.2%; Score 41; DB 22; Length 469;
 Best Local Similarity 87.5%; Pred. No. 18;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLLGKPPF 8
 ||| |||
 Db 57 MLLGRRPF 64

RESULT 13

AAAG57426
 ID AAG57426 standard; Protein: 469 AA.

XX AC AAG57426;

XX CT 26-NOV-2001 (first entry)

DE Amino acid sequence of a human protein kinase/protein phosphatase.

XX KW Human; protein kinase; protein phosphatase; signal transduction;
 KW intracellular signalling pathway.

XX OS Homo sapiens.

XX ZN W0200109345-A1.

XX XX 08 FEB-2001.

XX PF 28 JUL-2000; 2000WO-3P05260.

XX PR 29-JUL-1999; 99JP-0248036.

XX FR 18-OCT-1999; 99US-0159590.

XX PR 12-JAN-2000; 2000JP-0118776.

XX PR 17-FEB-2000; 2000US-0183322.

XX PR 22-MAY-2000; 2000JP-0183767.

XX PA (HELI-); HELIX RES INST.

XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;

XX PI Senoo C, Nezu J;

XX DR WPI; 2001-564736/63.

XX DR N-PSDB; AAH78069.

XX XX New genes encoding protein kinase and protein phosphatase, useful for
 PT identifying modulators which can be used to treat human or animal
 PT disorders associated with the expression or function of these enzymes .
 XX XX Claim 2; Page 136-139; 336pp; Japanese.

XX CC The present sequence represents a human protein kinase/protein
 CC phosphatase. The polypeptides are expected to participate in signal
 CC transduction in cells. The kinase phosphatases are connected with
 CC intracellular signalling pathways. Antisense oligonucleotides and
 CC compounds identified by screening (agonists or antagonists) can be
 CC used to treat human or animal disorders associated with the expression
 CC or function of the protein. In addition, the polypeptides may be used
 CC as target molecules for drug development.

XX SQ Sequence 469 AA;

Query Match 93.2%; Score 41; DB 22; Length 469;
 Best Local Similarity 87.5%; Pred. No. 18;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLLGKPPF 8
 ||| |||

Db 57 MLLGRRPF 64

RESULT 13

AAAY00915
 ID AAAY00915 standard; Protein: 685 AA.

XX AC AAAY00915;

XX DT 28-MAY-1999 (first entry)

XX DE Human serum inducible kinase.

XX KW Serum inducible kinase; SNK protein; human; proliferative disease;
 KW leukaemia; solid tumour cancer; metastasis; chronic inflammatory;
 KW psoriasis; rheumatoid arthritis; proliferative cardiovascular disease;
 KW restenosis; ocular disorder; diabetic retinopathy; haemangioma;
 KW benign hyperproliferative disease; diagnosis.

XX OS Homo sapiens.

XX PN W09909:46-A1.

XX PD 25-FEB-1999.

XX PF 20-AUG-1998; 98WO-US-7248.

XX PR 20-AUG-1997; 97US-0056112.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Anderson KM, Bouzyk M, Hansbury MJ, Jackson JR;

XX PI Nerurkar SS, Roshak AK;

XX DR WPI; 1999-181027/15.

XX DR N-PSDB; AAX27227.

XX PT New serum inducible kinase (Snk) polypeptides and polynucleotides -
 XX useful for treating proliferative diseases
 XX Claim 1; Page 39-40; 41pp; English.

XX CC This sequence is a human serum inducible kinase (SNK) of the
 CC invention. The invention relates to diagnostic assays or kits for
 CC detecting diseases associated with inappropriate SNK activity or levels.
 CC Disease states that can be diagnosed include proliferative diseases such
 CC as leukaemia, solid tumour cancers and metastases, chronic inflammatory
 CC proliferative diseases such as psoriasis and rheumatoid arthritis,
 CC ocular disorders such as diabetic retinopathy and benign
 CC hyperproliferative diseases such as haemangiomas. The polynucleotides can
 CC be used as hybridisation probes for cDNA and genomic DNA or as primers
 CC for a nucleic acid amplification (PCR) reaction, to isolate full-length
 CC cDNAs and genomic clones encoding polypeptides of this invention and to
 CC isolate cDNA and genomic clones of other genes which have a high sequence

CC similarity to the SNK coding sequence. The differences between cDNA and
 CC genomic sequences can be observed and therefore mutations detected. Any
 CC mutations may then be attributed to likely causative agents of disease.
 CC The nucleotide sequences are also useful for chromosome identification.

XX Sequence 685 AA;

Query Match 93.2%; Score 41; DB 20; Length 685;
 Best Local Similarity 87.5%; Pred. No. 27;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 |||:||||
 Db 273 MLLGKPPF 280

RESULT 14
 AAW88432
 ID AAW88432 standard; Protein: 685 AA.

XX AAW88432;

AC AAW88432;

DT 26-APR-1999 (first entry)

DE Disease associated protein kinase DAPK-1.

XX DAPK-1; disease associated protein kinase; human; diagnosis;
 KW therapy; adult respiratory distress syndrome; allergy; asthma;
 KW arteriosclerosis; bronchitis; emphysema; hyperosinophilia;
 KW myocardial inflammation; pericardial inflammation; anaemia;
 KW rheumatoid arthritis; Addison's disease; AIDS; arteriosclerosis;
 KW atopic dermatitis; dermatomyositis; diabetes mellitus;
 KW glomerulonephritis; gout; Grave's disease; lupus erythematosus;
 KW multiple sclerosis; myasthenia gravis; osteoarthritis;
 KW osteoporosis; pancreatitis; polycystic kidney disease;
 KW polymyositis; scleroderma; Sjogren's syndrome;
 KW autoimmune thyroiditis; cancer; infection; trauma;
 KW cell proliferation.

XX Homo sapiens.

CS Homo sapiens.

PH Key Location/Qualifiers
 ET Binding-site 99..96
 ET Peptide /note= "potential ATP binding site"
 FT 508..511
 FT /note= "presumed regulatory sequence common to
 PC-6 family protein kinases"

XX W09859352.A2.

PN 25 DEC-1998.

PD 19-JUN-1999; 93WO-US12813.

PF 19-JUN-1997; 97US-0878989.

PR (INCY) INCYTE PHARM INC.

PA Bandman O, Corley NC, Goli SK, Guegler RJ, Hillman CL;
 PI Lee P, Shah P;

XX WFI: 1999-080352/07.

DR N-PSDB; AAW88432.

XX New disease associated protein kinases - used to stimulate cell
 PT proliferation and to treat the immune response and cancer

XX Claim 1; Page 54-56; 93pp; English.

XX This is the amino acid sequence of human disease associated protein
 CC kinase DAPK-1, as deduced from a consensus sequence (see AAW88432);
 CC of overlapping cDNA clones from libraries which are immortalised
 CC or cancerous and show inflammatory or immune responses. DAPK-1

CC shows 53% homology to human proliferation-related protein kinase
 CC PRK (GI 1488263). The invention provides DAPK-1 to DAPK-7
 CC polypeptides (see AAW88432-38) and cDNA clones encoding them (see
 CC AAX06831-36 and AAX06882), as well as expression vectors, host cells,
 CC agonists, antagonists and antibodies. The invention further
 CC provides uses of such products in the diagnosis, prevention and
 CC treatment of diseases associated with cell proliferation,
 CC especially cancer or an immune response (claimed). Conditions
 CC that may be treated include adult respiratory distress syndrome,
 CC allergies, asthma, arteriosclerosis, bronchitis, emphysema,
 CC hyperosinophilia, myocardial or pericardial inflammation,
 CC rheumatoid arthritis, Addison's disease, AIDS, anaemia,
 CC atherosclerosis, various diseases of the digestive system, atopic
 CC dermatitis, dermatomyositis, diabetes mellitus, glomerulonephritis,
 CC gout, Grave's disease, lupus erythematosus, multiple sclerosis,
 CC myasthenia gravis, osteoarthritis, osteoporosis, pancreatitis,
 CC polycystic kidney disease, polymyositis, scleroderma, Sjogren's
 CC syndrome, autoimmune thyroiditis, complications of cancer,
 CC extracorporeal circulation, viral, bacterial, fungal, parasitic,
 CC protozoal and helminthic infections, and trauma (disclosed).

XX Sequence 685 AA;

Query Match 93.2%; Score 41; DB 20; Length 685;

Best Local Similarity 87.5%; Pred. No. 27;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 |||:||||
 Db 273 MLLGKPPF 280

RESULT 15

ABP61474

ID ABP61474 standard; Protein: 685 AA.

XX ABP61474;

XX 30-SEP-2002 (first entry)

DE Human NF-kB activating protein SEQ ID NO 101.

XX Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
 KW immunomodulator; cytostatic; antineoplastic; osteopathic; neoplastic;
 KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
 KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.

XX Homo sapiens.

PN W0200253737.A1.

PD 11-JUL-2002.

XX 25-DEC-2001; 2001WO-JP11389.

XX 28-DEC-2000; 2000JP-0402288.

PR 26-MAR-2001; 2001JP-0088912.

PR 24-AUG-2001; 2001JP-0254016.

XX (ASAH) ASAH KASEI KOGYO KK.

XX Matsuda A, Honda G, Muramatsu S, Nagano Y;

DR WPI: 2002-583617/62.

XX N-PSDB; AB091962.

XX NF-approximatelykB activating gene and expressed protein, applicable in
 PT diagnosis and screening inhibitors or promoters to control excessive
 PT activation or inhibition for treating e.g. inflammations, autoimmune
 PT diseases and cancer.

PS Claim 1; Page 448-453; 841pp; Japanese.

PR	21-OCT-1999;	99US-0160768.	PR	14-MAY-1999;	99US-0134219.
PR	21-OCT-1999;	99US-0160770.	PR	14-MAY-1999;	99US-0134221.
PR	21-OCT-1999;	99US-0160814.	PR	14-MAY-1999;	99US-0134370.
PR	21-OCT-1999;	99US-0160815.	PR	18-MAY-1999;	99US-0134768.
PR	22-OCT-1999;	99US-0160980.	PR	19-MAY-1999;	99US-0134941.
PR	22-OCT-1999;	99US-0160981.	PR	20-MAY-1999;	99US-0135124.
PR	22-OCT-1999;	99US-0160989.	PR	21-MAY-1999;	99US-0135353.
PR	22-OCT-1999;	99US-0161404.	PR	24-MAY-1999;	99US-0135629.
PR	25-OCT-1999;	99US-0161405.	PR	25-MAY-1999;	99US-0136021.
PR	25-OCT-1999;	99US-0161406.	PR	27-MAY-1999;	99US-0136392.
PR	26-OCT-1999;	99US-0161359.	PR	28-MAY-1999;	99US-0136782.
PR	26-OCT-1999;	99US-0161360.	PR	01-JUN-1999;	99US-0137222.
PR	26-OCT-1999;	99US-0161361.	PR	03-JUN-1999;	99US-0137528.
PR	28-OCT-1999;	99US-0161920.	PR	04-JUN-1999;	99US-0137502.
PR	28-OCT-1999;	99US-0161992.	PR	07-JUN-1999;	99US-0137724.
PR	28-OCT-1999;	99US-0161993.	PR	08-JUN-1999;	99US-0138094.
PR	29 OCT-1999;	99US-0162142.	PR	10-JUN-1999;	99US-0138540.
PR	29 OCT-1999;	99US-0162142.	PR	10-JUN-1999;	99US-0138847.
PR	29 OCT-1999;	99US-0162142.	PR	14-JUN-1999;	99US-0139119.
PR	29 OCT-1999;	99US-0162142.	PR	16-JUN-1999;	99US-0139452.
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PR	29 OCT-1999;	99US-0162142.	PR	18-JUN-1999;	99US-0139454.
PR	29 OCT-1999;	99US-0162142.	PR	18-JUN-1999;	99US-0139455.
PR	29 OCT-1999;	99US-0162142.	PR	18-JUN-1999;	99US-0139456.
PR	29 OCT-1999;	99US-0162142.	PR	18-JUN-1999;	99US-0139457.
PR	29 OCT-1999;	99US-0162142.	PR	18-JUN-1999;	99US-0139458.
PR	29 OCT-1999;	99US-0162142.	PR	18-JUN-1999;	99US-0139459.
PR	29 OCT-1999;	99US-0162142.	PR	18-JUN-1999;	99US-0139460.
PR	29 OCT-1999;	99US-0162142.	PR	18-JUN-1999;	99US-0139461.
PR	29 OCT-1999;	99US-0162142.	PR	18-JUN-1999;	99US-0139462.
PR	29 OCT-1999;	99US-0162142.	PR	18-JUN-1999;	99US-0139463.
PR	29 OCT-1999;	99US-0162142.	PR	18-JUN-1999;	99US-0139763.
PR	29 OCT-1999;	99US-0162142.	PR	18-JUN-1999;	99US-0139763.
PR	29 OCT-1999;	99US-0162142.	PR	21-JUN-1999;	99US-0139817.
PR	29 OCT-1999;	99US-0162142.	PR	22-JUN-1999;	99US-0139899.
PR	29 OCT-1999;	99US-0162142.	PR	23-JUN-1999;	99US-0140353.
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PR	29 OCT-1999;	99US-0162142.	PR	24-JUN-1999;	99US-0140395.
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PR	29 OCT-1999;	99US-0162142.	PR	29-JUN-1999;	99US-0140991.
PR	29 OCT-1999;	99US-0162142.	PR	30-JUN-1999;	99US-0141287.
PR	29 OCT-1999;	99US-0162142.	PR	01-JUL-1999;	99US-0141842.
PR	29 OCT-1999;	99US-0162142.	PR	01-JUL-1999;	99US-0142154.
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PR	29 OCT-1999;	99US-0162142.	PR	06-JUL-1999;	99US-0142390.
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PR	29 OCT-1999;	99US-0162142.	PR	09-JUL-1999;	99US-0142920.
PR	29 OCT-1999;	99US-0162142.	PR	12-JUL-1999;	99US-0142977.
PR	29 OCT-1999;	99US-0162142.	PR	13-JUL-1999;	99US-0143542.
PR	29 OCT-1999;	99US-0162142.	PR	14-JUL-1999;	99US-0143624.
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PR	29 OCT-1999;	99US-0162142.	PR	16-JUL-1999;	99US-0144085.
PR	29 OCT-1999;	99US-0162142.	PR	16-JUL-1999;	99US-0144086.
PR	29 OCT-1999;	99US-0162142.	PR	19-JUL-1999;	99US-0144325.
PR	29 OCT-1999;	99US-0162142.	PR	19-JUL-1999;	99US-0144331.
PR	29 OCT-1999;	99US-0162142.	PR	19-JUL-1999;	99US-0144332.
PR	29 OCT-1999;	99US-0162142.	PR	19-JUL-1999;	99US-0144333.
PR	29 OCT-1999;	99US-0162142.	PR	19-JUL-1999;	99US-0144334.
PR	29 OCT-1999;	99US-0162142.	PR	19-JUL-1999;	99US-0144335.
PR	29 OCT-1999;	99US-0162142.	PR	20-JUL-1999;	99US-0144352.
PR	29 OCT-1999;	99US-0162142.	PR	20-JUL-1999;	99US-0144632.
PR	29 OCT-1999;	99US-0162142.	PR	20-JUL-1999;	99US-0144884.
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PR	29 OCT-1999;	99US-0162142.	PR	22-JUL-1999;	99US-0145085.
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PR	29 OCT-1999;	99US-0162142.	PR	22-JUL-1999;	99US-0145089.
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PR	29 OCT-1999;	99US-0162142.	PR	23-JUL-1999;	99US-0145145.
PR	29 OCT-1999;	99US-0162142.	PR	23-JUL-1999;	99US-0145218.
PR	29 OCT-1999;	99US-0162142.	PR	23-JUL-1999;	99US-0145224.

Query Match 88.68; Score 39; DR 21; Length 304;
Best local Similarity 87.51; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 MLLGKPPF 8
Db 163 MLLGKPPF 170

RESULT 18
AAG37267
ID AAG37267 standard; Protein: 304 AA.
XX AAG37267;
XX
XX 18-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 45796.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
XX
XX EPIC33405-AZ.
XX
XX 16-SEP-2000.
XX
XX 25-FEB-2000; 200SEP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 28-APR-1999; 99US-0130891.
XX 30-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
XX 30-APR-1999; 99US-0132407.
XX 04-MAY-1999; 99US-0132484.
XX 05-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
XX 06-MAY-1999; 99US-0132487.
XX 27-MAY-1999; 99US-0132863.
XX 11-MAY-1999; 99US-0134256.
XX 14-MAY-1999; 99US-0134218.
XX 14-MAY-1999; 99US-0134219.

PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 31-JUN-1999; 99US-0137222.
PR 33-JUN-1999; 99US-0137528.
PR 34-JUN-1999; 99US-0137502.
PR 37-JUN-1999; 99US-0137724.
PR 38-JUN-1999; 99US-0138094.
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PR 12-JUN-1999; 99US-0138847.
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PR 28-JUN-1999; 99US-0140823.
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PR 23-JUL-1999; 99US-0145145.
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PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
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PR 04-AUG-1999; 99US-0147204.
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PR 20-AUG-1999; 99US-0149722.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 31-AUG-1999; 99US-0151910.
PR 01-SEP-1999; 99US-0151910.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
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PR 04-OCT-1999; 99US-0157117.
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PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.

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PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match: 88.6%; Score 39; DB 21; Length 105;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY i MLJGKPPF 8
|||.||
DC 163 MLJGKPPF 170

RESULT 20
AAG36346
ID AAG36346 standard; Protein; 129 AA.
XX
AC
XX AAG36346;
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 44529
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; Genetic mapping; gene expression control; promoter;
XX termination sequence.
CS Arabidopsis thaliana.
XX
XX EP-033405 A2.
XX
PC
XX
XX
XX
XX 25-FEB-2000; 2000EP-030439.
XX
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KW termination sequence.
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX CS Arabidopsis thaliana.
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Query Match 88.6%; Score 39; ES 21; Length 330;
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 Db 188 MLTKPPF 195

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 DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 44528.
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 XX termination sequence.
 OS Arabidopsis thaliana.
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 PD 06-SEP-2000.
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 PF 25-FEB-2000; 200CEP-030:439.
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Query Match      88.6%; Score 39; DB 21; Length 465;
Best Local Similarity 87.5%; Pred. No. 43;
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QY 1 MLGKPPF 8
DB 324 MLGKPPF 331

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DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 45794.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.

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05-OCT-1999	99US-0157753		
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22-OCT-1999	99US-0160980		
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Query Match	Score 19	DB 21	Length 485
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22-SEP-1999	99US-0153139		
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07-OCT-1999	99US-0158329		
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PR 04-OCT-1999; 99US-0157117.
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Query Match 88.6%; Score 39; DB 21; Length 466;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 324 MLTGKPPF 331

RESULT 26

AA93500
ID AA93500 standard; Protein; 592 AA.

XX AC AA93500;

XX DT 25-SEP-2000 (first entry)

XX DE Amino acid sequence of the protein kinase KSG1 polypeptide.

XX KW Protein kinase; Pkh1, Pkh2; Ypk1; Ypk2; protein kinase B-alpha;

XX KW human serum and glucocorticoid induced protein kinase; SGK; PKBalpha;

XX KW 3-phosphoinositide-dependent protein kinase-1; PDK1; fungal infection;

XX KW thrush; cancer; diabetes; obesity; antifungal; Candida infection.

XX OS Schizosaccharomyces pombe.

XX PN WO200036135-A2.

XX PD 22-JUN-2000.

XX PF 14-DEC-1999; 99WO-GB04228.

XX PR 14-DEC-1998; 98US-0112114.

XX PA (MEDI-) MEDICAL RES COUNCIL.

XX PA (REGC) UNIV CALIFORNIA.

PI Thorner JW, Alessi DR, Torrance PD, Casamayor A;

```

XX WPI: 2000-442391/38.
DR N-PSDB: AAA46568.
XX
PT Screening method identifying compounds which modulate protein kinase
PT activity for use in treating fungal infections and cancer.
XX
XX Disclosures: Page 21: 155pp; English.
XX
CC The present sequence represents a protein kinase Kcs1. The specification
CC describes a screening method to identify a compound which modulates the
CC activity of protein kinases from different sources, using host yeast
CC cells. The method is used to identify a compound which modulates
CC inhibits the activity of a protein kinase. Pkh1 or Pkh2 phosphorylate
CC and activate Ypk1, Yrk2, human serum and glucocorticoid induced protein
CC kinase (SGK) or protein kinase B-alpha (PKBalpha). 3-phosphoinositide-
CC dependent protein kinase-1 (PDK1) is used to phosphorylate and activate
CC Ypk1 and Yrk2 or SGK but not PKBalpha or p70S6 kinase. Compounds
CC identified by the methods are used to treat fungal infections e.g.
CC thrush, and to treat cancer. To treat cancer, the compounds inhibit PKB,
CC PDK1 or the activation of PKB by PDK1. Compounds which activate PKB or
CC PDK1 can be used in the treatment of diabetes or obesity, and compounds
CC which inhibit a fungal functional homologue of PDK1 (Pkh1 or Pkh2) or
CC SGK (Ypk1 or Yrk2) can be used as an antifungal agent to treat Candida
CC infections, e.g. thrush.
XX
XX Sequence 592 AA:
SQ
Query Match 98.6%; Score 39; DB 21; Length 592;
Best Local Similarity 87.5%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
DB 305 MLGKPPF 312
|||
|

RESULT 27
AAU74657
ID AAU74657 standard; Protein: 604 AA.
XX
AC AAU74657;
XX
DT 09 APR-2002 (first entry)
XX
DE Yeast cyclin dependent kinase 5 (cdcs5).
XX
KW Polo-like kinase; PK1; polo-box; cytoskeletal neoplasm;
KW hyperproliferative disorder; cytokinesis; solid tumour;
KW carcinoma; sarcoma; cancer; small cell carcinoma; adenocarcinoma;
KW Mullerian tumour; squamous cell carcinoma; protein yeast;
KW cyclin dependent kinase; cdc5.
XX
OS Saccharomyces cerevisiae.
XX
XX Key Location/Qualifiers
XX Region 513..542
XX /label= Polo-box
XX /note= "Core polo-box consensus sequence"
XX
PN WO2001190401-A2.
XX
XX 29-NOV-2001.
XX
XX 23-MAY-2001; 2001WO-US16903.
XX
XX 23-MAY-2000; 2000US-206588P.
XX
XX (HARD) HARVARD COLLEGE.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (USSH) US NAT INST OF HEALTH.
XX Lee KS, Song S, Erikson R;
PI

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XX WPI: 2002-106210/14.
XX
PT Identifying polo-like kinase modulators by contacting eukaryotic cells
PT expressing polo-box peptides with test compounds and evaluating changes
PT in dominant negative cytokinesis-defective growth patterns.
XX
XX Example 2; Fig 5; 57pp; English.
XX
CC The invention describes a novel method of detecting compounds with
CC polo-like kinase (PK) modulating activity. This comprises contacting
CC eukaryotic cells expressing polo-box or polo-box related peptides,
CC binding peptides comprising 25 contiguous residues from a polo-like
CC kinase C-terminal region, with a test compound. Ectopic expression of a
CC polo-box in a eukaryotic cell causes a severe cytokinetic defect in the
CC cell. These eukaryotic cells can also be tested with the test compound
CC used in the method of the invention. The polo-box related peptides and
CC polo-like kinase activity modulatory compounds can be used to inhibit or
CC enhance cellular proliferation and subsequently for treating
CC hyper-proliferative disorders including neoplasm, solid tumours,
CC carcinomas, sarcomas and cancers e.g. small cell carcinoma,
CC adenocarcinoma, Mullerian tumours and squamous cell carcinomas. This is
CC the amino acid sequence of yeast cyclin dependent kinase cdc5, identified
CC in budding yeast as encoding a polo-like kinase and used to study the
CC effects of the polo-box on cytokinesis, described in the method of the
CC invention.
XX
XX Sequence 604 AA:
SQ
Query Match 88.6%; Score 39; DB 23; Length 604;
Best Local Similarity 75.0%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
DB 234 LLGKPPF 211
|||
|

RESULT 28
AAU93498
ID AAU93498 standard; Protein: 766 AA.
XX
AC AAU93498;
XX
DT 25-SEP-2000 (first entry)
XX
DE Amino acid sequence of the protein kinase Pkl1 polypeptide.
XX
KW Protein kinase; Pkh1; Pkh2; Ypk1; Yrk2; protein kinase B-alpha;
KW human serum and glucocorticoid induced protein kinase; SGK; PKBalpha;
KW 3-phosphoinositide-dependent protein kinase-1; PDK1; fungal infection;
KW thrush; cancer; diabetes; obesity; antifungal; Candida infection.
XX
OS Saccharomyces cerevisiae.
XX
XX WO200036135-A2.
XX
XX 22-JUN-2000.
XX
XX 14-DEC-1999; 99WO-GB04228.
XX
XX 14-DEC-1998; 98US-0112114.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX (REGC) UNIV CALIFORNIA.
XX
XX Thorne JW, Alessi DR, Torrance PD, Casamayor A;
XX
XX WPI: 2000-442391/38.
XX N-PSDB: AAA46566.
XX
PT Screening method identifying compounds which modulate protein kinase
PT activity for use in treating fungal infections and cancer.

```

XX Disclosure, Page 15; 155pp; English.

XX

XX The present sequence represents a protein kinase Pkl1. The specification describes a screening method to identify a compound which modulates the activity of protein kinases from different sources, using host yeast cells. The method is used to identify a compound which modulates (inhibits) the activity of a protein kinase. Pkl1 or Pkl2 phosphorylate and activate Ypk1, Yrk2, human serum and glucocorticoid induced protein kinase (SGK) or protein kinase B-alpha (PKBalpha). 3-phosphoinositide-dependent protein kinase-1 (PDK1) is used to phosphorylate and activate Ypk1 and Yrk2 or SGK but not PKBalpha or PDK1. Compounds identified by the methods are used to treat fungal infections e.g. thrush, and to treat cancer. To treat cancer, the compounds inhibit PKB, PDK1 or the activation of PKB by PDK1. Compounds which activate PKB or PDK1 can be used in the treatment of diabetes or obesity, and compounds which inhibit a fungal functional homologue of PDK1 (Pkl1 or Pkl2) or SGK (Ypk1 or Yrk2) can be used as an antifungal agent to treat Candida infections, e.g. thrush.

XX

XX Sequence 766 AA;

XX Query Match 88.6%; Score 19; DB 21; Length 766;
Best Local Similarity 87.5%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : MLLGKPPF 8
 |||
DB 310 MLAGKPPF 337

RESULT 29
AAW74211

ID AAW74211 standard; peptide; 8 AA.

XX

XX AAW74211;

XX

XX 05-MAY 1999 (first entry)

XX

XX HJ loop peptide K035H001.

XX

XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy; haemorrhagic shock; cardiovascular disease; immunosuppressive disorder; inflammatory disorder; central nervous system disease; septic shock; Parkinson's disease; hypertension.

XX

XX Synthetic

XX

XX Key Location/Qualifiers

XX Modified-site 1 /note= "acetylated"

XX Modified-site 8 /note= "amidated"

XX

XX WC98-3050-A2.

XX

XX 26-NOV-1998.

XX

XX 20-MAY-1998; 98WC-US-0319.

XX

XX 21-MAY-1997; 97US-0861338.

XX

XX (CHILD-) CHILDRENS MEDICAL CENT.

XX (YIES) YIESUM RES & DEV CO.

XX

XX Ben-Sasson SA;

XX

XX WPI; 1999-070142/06.

XX

XX New peptides for modulating serine/threonine kinase activity - comprise a sequence corresponding to the HJ loop of a serine/threonine kinase, used for treating, e.g. cancers, inflammatory disorders or autoimmune disorders

XX Disclosure, Fig 6; 70pp; English.

XX

XX This sequence represents a peptide of the invention, and is a derivative of the HJ loop of a serine/threonine kinase (STK). The peptides can be used for the treatment of disorders caused by overactivity or underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis, arteriosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury and hypertension), immunosuppressive and inflammatory disorders (e.g. asthma, psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression of organ transplant rejection, multiple sclerosis, inflammatory bowel disease and AIDS), central nervous system diseases (e.g. Alzheimer's disease, stroke and trauma), septic shock, Parkinson's disease or hypertension. The peptides can also be used to produce antibodies which can be used to identify cells expressing the STK and to study the intracellular distribution of the STK. In addition, the peptides can be used to identify and quantitate ligands which bind the HJ loop of the STK from which the peptide was derived.

XX

XX Sequence 8 AA;

XX Query Match 86.4%; Score 38; DB 20; Length 8;
Best Local Similarity 75.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY : MLLGKPPF 8
 |||
DB 1 LLVGKPPF 8

RESULT 30
AAU98355

ID AAU98355 standard; Peptide; 8 AA.

XX

XX AAU98355;

XX

XX 13-AUG-2002 (first entry)

XX

XX Polo kinase P1k serine-threonine kinase HJ loop peptide K035H001.

XX

XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity; central nervous system disorder; inflammatory disorder; autoimmune disorder; cardiovascular disorder; haemorrhagic shock; lipid metabolism; cytostatic; antidiabetic; anorectic; neurological; antiinflammatory; immunosuppressive; cardiant; haemostatic; modulating STK activity; polo kinase; P1k; K035H001.

XX

XX Unidentified.

XX Synthetic.

XX

XX Key Location/Qualifiers

XX Modified-site 1 /note= "N-terminal acetyl"

XX Modified-site 8 /note= "C-terminal amide"

XX

XX US2002049301-A1.

XX

XX 25-APR-2002.

XX

XX 13-DEC-2000; 2000US-0736076.

XX

XX 21-MAY-1997; 97US-0861338.

XX

XX (CHILD-) CHILDRENS MEDICAL CENT.

XX Ben-Sasson SA;

XX

XX WPI; 2002-462787/49.

XX

XX New peptide from the HJ loop of serine-threonine kinase, useful for treating e.g. cancer and for producing diagnostic antibodies.

XX Disclosure; Fig 6; 41pp; English.

XX The present invention relates to new peptides derived from the HJ loop

CC of a serine/threonine kinase (STK). The peptides of the invention are

CC used to modulate STK activity, especially for treating cancer, diabetes,

CC obesity or a wide variety of central nervous system, inflammatory,

CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for

CC regulating lipid metabolism. The peptides are also used to generate

CC antibodies that bind specifically to the parent STK, used e.g. for

CC identifying STK-expressing cells and to study intracellular distribution

CC of STK, and to identify or quantify ligands that bind to the HJ loop.

CC The present amino acid sequence represents the polo kinase Plx

CC serine/threonine kinase HJ loop peptide K035800. This sequence is one

CC of the short peptides of the invention that selectively modulate the

CC activity of STK.

XX

SQ Sequence 5 AA;

Query Match 86.4%; Score 38; DB 23; Length 8;

Best Local Similarity 75.0%; Pred. No. 9.3e+05;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 3;

QY 1 MLLGKPPF 8

DB : LLVGKPPF 8

AAW74173

AAW74173 standard; peptide: 20 AA.

AAW74173;

25-MAY-1999 (first entry)

HJ loop peptide POLO.

HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;

haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;

inflammatory disorder; central nervous system disease; septic shock;

Parkinson's disease; hypertension.

Synthetic.

W030553050-A2.

26-NOV-1998.

20-MAY-1998; 98WQ-US10319.

21-MAY-1997; 97US-0861338.

(CHIL-) CHILDRENS MEDICAL CENT.

(VISC-) YISSUM RES & DEV CO.

Ben-Sasson SA;

WPI; 1999-07042/06.

New peptides for modulating serine/threonine kinase activity -

comprise a sequence corresponding to the HJ loop of a

serine/threonine kinase, used for treating, e.g. cancers,

inflammatory disorders or autoimmune disorders

Claim 47; Fig 3b; 70pp; English.

This sequence represents a peptide of the invention, and is a derivative

of the HJ loop of a serine/threonine kinase (STK). The peptides can be

used for the treatment of disorders caused by overactivity or

underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic

shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,

arteriosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury and

CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,

CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression

CC of organ transplant rejection, multiple sclerosis, inflammatory bowel

CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's

CC disease, stroke and trauma), septic shock, Parkinson's disease or

CC hypertension. The peptides can also be used to produce antibodies which

CC can be used to identify cells expressing the STK and to study the

CC intracellular distribution of the STK. In addition, the peptides can be

CC used to identify and quantitate ligands which bind the HJ loop of the STK

CC from which the peptide was derived.

XX

SQ Sequence 20 AA;

Query Match 86.4%; Score 38; DB 20; Length 20;

Best Local Similarity 75.0%; Pred. No. 3.1;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8

DB 3 LLVGKPPF 10

AAU98306

AAU98306 standard; Peptide; 20 AA.

AAU98306;

13-AUG-2002 (first entry)

Peptide sequence of HJ loop of serine-threonine kinase polo kinase.

HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;

central nervous system disorder; inflammatory disorder;

autoimmune disorder; cardiovascular disorder; haemorrhagic shock;

lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;

antiinflammatory; immunosuppressive; cardiant; haemostatic;

modulating STK activity; polo kinase.

Unidentified.

US2002049301-A1.

25-APR-2002.

13-DEC-2000; 2000US-0736076.

21-MAY-1997; 97US-0861338.

(CHIL-) CHILDRENS MEDICAL CENT.

Ben-Sasson SA;

WPI; 2002-462787/49.

New peptide from the HJ loop of serine-threonine kinase, useful for

treating e.g. cancer and for producing diagnostic antibodies -

Claim 33; Fig 3; 41pp; English.

The present invention relates to new peptides derived from the HJ loop

of a serine/threonine kinase (STK). The peptides of the invention are

used to modulate STK activity, especially for treating cancer, diabetes,

obesity or a wide variety of central nervous system, inflammatory, and for

autoimmune or cardiovascular disorders, also haemorrhagic shock, and for

regulating lipid metabolism. The peptides are also used to generate

antibodies that bind specifically to the parent STK, used e.g. for

identifying STK-expressing cells and to study intracellular distribution

of STK, and to identify or quantify ligands that bind to the HJ loop.

The present amino acid sequence represents the peptide sequence of the HJ

loop of serine-threonine kinase polo kinase. This sequence is one of the

short peptides of the invention that selectively modulate the activity

of STK.

XX SQ Sequence 20 AA;
 Query Match 86.4%; Score 38; DB 23; Length 20;
 Best Local Similarity 75.0%; Pred. No. 3.1;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 : : : : :
 DB 3 LLVGKPPF 10
 : : : : :
 : : : : :

RESULT 34
 AAU83127
 ID AAU83127 standard; Protein; 419 AA.
 AC AAU83127;
 XX
 DT 08-MAY-2002 (first entry)
 DE Novel secreted protein Z835510GSP.
 XX
 KW Protein secretion: mammalian secreted polypeptide; MSP.
 XX
 OS Homo sapiens.
 XX
 PW WO200202621-A2.
 XX
 PD 10-JAN-2002.
 XX
 PF 28-JUN-2001; 2001WO-US20638.
 XX
 PR 30-JUN-2000; 2000US-215446P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sheppard PO, Presnell SR;
 XX
 DR WPI; 2002-147999/19.
 DR N-PSDB; ABK33C42.
 XX
 PT Novel isolated mammalian secreted polypeptide useful in therapeutic and
 PT diagnostic methods, to direct secretion of other proteins of interest
 PT from host cell, as educational tools, and as laboratory practicum kits
 PT .
 XX
 PS Claim 12; Page 171-173; 397pp; English.
 XX
 CC The invention describes an isolated mammalian secreted polypeptide (MSP)
 CC (1). (1) is useful to direct the secretion of other proteins of interest
 CC from a host cell, to monitor secretion of proteins, to degenerate
 CC sequences comprising all nucleotide sequences encoding a particular
 CC polypeptide, to screen for cell metabolism effecting receptors, for
 CC identifying new target receptors and drug design, for identifying, for
 CC protein purification, for determining the weight of expressed MSP
 CC polypeptides as a ratio to total protein expressed, for identifying
 CC peptide cleavage sites, for coupling amino and carboxy terminal tags, for
 CC amino acid sequence analysis, for monitoring biological activities of the
 CC protein in vitro and in vivo, and to teach analytical skills and as
 CC reagents for the study of cells, receptors, and other binding molecules.
 CC The polynucleotide is useful for radiation hybrid mapping, and somatic
 CC cell genetic technique developed for constructing high-resolution.
 CC contiguous maps of mammalian chromosomes. Reagents disclosed in the
 CC invention may be used to detect metabolic abnormalities characterised by
 CC over or under production of the protein. This is the amino acid sequence
 CC of a mammalian secreted polypeptide, described in the method of the
 CC invention.
 XX
 SQ Sequence 419 AA;

Query Match 86.4%; Score 38; DB 23; Length 419;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPP 7
 : : : : :
 DB :70 MLGKPP 176
 : : : : :
 : : : : :

XX SQ Sequence 20 AA;
 Query Match 86.4%; Score 38; DB 23; Length 20;
 Best Local Similarity 75.0%; Pred. No. 3.1;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 : : : : :
 DB 3 LLVGKPPF 10
 : : : : :
 : : : : :

RESULT 34
 AAB56690
 ID AAB56690 standard; Protein; 329 AA.
 AC AAB56690;
 XX
 DT 13 MAR-2001 (first entry)
 DE Human prostate cancer antigen protein sequence SEQ ID NO:1268.
 XX
 KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
 KW uroterary; gastrointestinal; nephrotoxic; anti-infective; gynaecological;
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease.
 XX
 OS Homo sapiens.
 XX
 PW WO20005574-A1.
 XX
 PD 21 SEP-2000.
 XX
 PF CA MAR-2000; 2000WO-US05988.
 XX
 PR 12 MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C.A.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2000-587513/55.
 DR N-PSDB; AAF1593.
 XX
 PT Prostate cancer associated gene sequences, related to an prostate
 PT cancer antigens, useful for treatment, prevention and diagnosis of
 PT disorders such as prostate cancer.
 XX
 PS Claim 11; Page 1691-1692; 234pp; English.
 XX
 CC AAF15666 to AAF16505 encode the human prostate cancer associated
 CC proteins, called prostate cancer antigens, given in AAB56163 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytostatic,
 CC cardioactive, immunomodulatory, muscular, uroterary, gastrointestinal,
 CC nephrotoxic, anti-infective, gynaecological, and antimicrobial activities,
 CC and can be used in gene therapy. The prostate cancer antigen
 CC polynucleotides may be used for detection of prostate cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The prostate cancer antigens may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AAF15666 to AAF16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 329 AA;

Query Match 86.4%; Score 38; DB 23; Length 329;
 Best Local Similarity 75.0%; Pred. No. 4.7;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT IS

ABP73734

ID AB:73724 standard; Protein; 528 AA.

XX

AC A5273734;

XX
DT 30-JAN-2003 (first entry)

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DE *Candida albicans* essential protein SEQ ID NO 757.

XX

KW Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;

KW signal transduction; DNA replication; cell division; growth;

KW proliferation; Candida albicans; fungicide; antifungal

✕✕

OS *Candida albicans*.

XX

P.N. WC200253728-A2.

XX

PC 11 JUL 2002.

XX

PF 26-DEC-2001; 2001WC-US49486.

XX

PR 29-DEC-2000; 2000US-259128P.

PR 20-FEB-2007; 2007US-

PR 22-AUG-2001; 2001US-314050P.

XX

PA (ELIT-); ELITRA PHARM INC.

XX

PT Roemer T, Jiang B, Bocne C, Bussey H, Chlsen KL;

XX

DR WPI; 2002-566694/60.

DR N-PSDB; AB232284;

XX
XX
X

100

PT Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele
PT of a gene and placing other allele of the gene under conditional
PT expression

XX

PS Claim 44; SEQ ID NC 7571; 167pp + Sequence Listing; English.

 $\times \times$

The invention relates to constructing (M2) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination of a promoter replacement fragment with a heterologous promoter, so that expression of the second allele is regulated by the promoter (M2) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that

CC contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (vi) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transport, transcriptional, translational, signal transduction, DNA replication and cell division activity. The method is useful for identifying a compound having the ability to inhibit growth or proliferation of *C. albicans* cells and for treating infection by *C. albicans*. The present sequence is that of an essential *Candida albicans* protein used in the method of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Berwert by the European Patent Office.

XX XX

Sequence 528 AA:

Query Match	Score	Length
86.4%	33.23	38

	Matches	6: Conservative	2: Mismatches	0: Gaps
QY	1	MLLGKPPF	8	

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FT      /label= Unknown
FT      Misc-difference 361
FT      /label= Unknown
FT      Misc-difference 362
FT      /label= Unknown
FT      Misc-difference 363
FT      /label= Unknown
FT      Misc-difference 364
FT      /label= Unknown
FT      Misc-difference 365
FT      /label= Unknown
FT      Region:
FT      410..439
FT      /label= Polo-box
FT      /note= "Core polo-box consensus sequence"
XX
XX      WQ20019C401-A2.
XX
XX      29-NOV-2001.
XX
XX      23-MAY 2001; 2001WO-US16903.
XX
XX      23-MAY-2000; 2000US-206588P.
XX
XX      (HRC) ; HARVARD COLLEGE.
XX      (USSH) ; US DEPT HEALTH & HUMAN SERVICES.
XX      (USSH) ; US NAT INST OF HEALTH.
XX
XX      Lee KS, Song S, Erikson R;
XX      WPI; 2002-06210/14.
XX
XX      Identifying polo-like kinase modulators by contacting eukaryotic cells
XX      expressing polo-box peptides with test compounds and evaluating changes
XX      in dominant negative cytokinesis-defective growth patterns.
XX
XX      Example 2; Fig 5; 57pp; English.
XX
XX      The invention describes a novel method of detecting compounds with
XX      polo-like kinase (PLK) modulating activity. This comprises contacting
XX      eukaryotic cells expressing polo-box or polo-box related peptides,
XX      binding peptides comprising 25 contiguous residues from a polo-like
XX      kinase C-terminal region, with a test compound. Ectopic expression of a
XX      polo-box in a eukaryotic cell causes a severe cytotoxic defect in the
XX      cell. These eukaryotic cells can also be tested with the test compound
XX      used in the method of the invention. The polo-box related peptides and
XX      polo-like kinase activity modulatory compounds can be used to inhibit or
XX      enhance cellular proliferation and subsequently for treating
XX      hyper-proliferative disorders including neoplasms, solid tumours,
XX      carcinomas, sarcomas and cancers and small cell carcinoma.
XX      adenocarcinoma, Mullerian tumours and squamous cell carcinomas. This
XX      is the amino acid sequence of a mammalian polo-like kinase (PLK),
XX      uncontrolled expression of the PLK family is implicated in the
XX      development of human cancers, discussed in the method of the invention.
XX
XX      Sequence 531 AA:
XX
XX      Query Match      86.4%; Score 38; DB 23; Length 531;
XX      Best Local Similarity 75.0%; Pred. No. 75;
XX      Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 MLLGKPPF 8
XX      :|:|:|:|
XX      Db      204 LLVGKPPF 211
XX
XX      RESULT 37
XX      AAR74620
XX      ID AAR74620 standard; Protein: 603 AA.
XX      AC AAR74620;
XX      DT 25-MAR-2003 (updated)
XX      DE Mouse polo-like kinase (Plk).
XX      26-OCT-1995 (first entry)
XX      KW Polo box; PB; cytosstatic; fungicide; protozoacide; antihelminthic;

```

```

XX      Human lung tumour Polo-like kinase.
XX
XX      Polo-like kinase; Plk; serine threonine kinase; human; lung tumour;
XX      autoimmune disease; lymphocyte activity.
XX
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      Binding-site 60..86
XX      /label= ATP-binding_motif
XX      Region      174..177
XX      /note= "motif that is highly conserved in protein
XX      kinases"
XX
XX      Region      194..196
XX      /note= "motif that is highly conserved in protein
XX      kinases"
XX
XX      DE4329177-A1.
XX
XX      02-MAR-1995.
XX
XX      30-AUG-1993; 93DE-4329177.
XX
XX      30-AUG-1993; 93DE-4329177.
XX
XX      (CHEV-) CHEMOTHERAPEUTISCHES FORSCHUNG.
XX
XX      Holtrich U, Rubsamen-Waigmann H, Strebhardt K;
XX      Rubsamen-Waigmann H;
XX      WPI; 1995-099454/14.
XX      N-PSDB; AAQ88155.
XX
XX      A polo-like serine threonine kinase-protein - isolated from
XX      proliferating human tissue, useful in the determ of lymphocyte
XX      activity, eg in auto-immune diseases
XX
XX      Claim 1; Page 8-10; 11pp; German.
XX
XX      A human lung tumour-derived cDNA (AAQ88155) was found to have high
XX      homology with sequences from members of the serine/threonine kinase
XX      family. Due to the strong homology with the Drosophila polo gene,
XX      the protein encoded by the new cDNA (AAR74620) was designated a polo-
XX      like kinase (PLK). PLK mRNA is expressed in proliferating cells such
XX      as placenta, colon and tumours of the lung, oesophagus, gut and
XX      intestine. Resting lymphocytes do not express the PLK gene but after
XX      stimulation with phytohaemagglutinin, PLK is expressed and can be
XX      used as an indicator of lymphocyte stimulation.
XX      (Updated on 25-MAR-2003 to correct PN field.)
XX
XX      Query Match      86.4%; Score 38; DB 16; Length 603;
XX      Best Local Similarity 75.0%; Pred. No. 85;
XX      Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 MLLGKPPF 8
XX      :|:|:|:|
XX      Db      244 LLVGKPPF 251
XX
XX      RESULT 38
XX      AAU79306
XX      ID AAR79306 standard; Peptide; 603 AA.
XX      AC AAU79306;
XX      DT 02-JUL-2002 (first entry)
XX      DE Mouse polo-like kinase (Plk).
XX      KW Polo box; PB; cytosstatic; fungicide; protozoacide; antihelminthic;

```

KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk.
 XX
 CS Mus musculus.
 XX
 XX US6358738-B1.
 XX
 PD 19-MAR-2002.
 XX
 XX 13-MAY-1999; 99US-0311311.
 XX
 PD 13-MAY-1998; 98US-085296P.
 XX
 XX (HARD) HARVARD COLLEGE.
 XX
 PI Erikson RL, Lee KS;
 DR WPI: 2002-3:4756/35.
 XX
 PT Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections -
 XX
 PS Example 1; Column 59-64; 47pp; English.
 XX
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of the polo-like kinase (Plk), a
 CC protein from which mitotic protein polo kinase inhibitory peptides are
 CC derived.
 XX
 SQ Sequence 603 AA;
 Query Match 86.4%; Score 38; DB 23; Length 603;
 Best Local Similarity 75.0%; Pred. No. 85;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGKPPF 8
 DB 244 LVGKPPF 251
 DE
 DE Mouse polo-like kinase (Plk) T210D mutant.
 XX
 XX Polo box; PBI; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutin.
 XX
 CS Mus musculus.

OS Synthetic.
 PH Key Location/Qualifiers
 FT Misc-difference 210 /note= "Wild type Thr substituted by Asp"
 XX US6358738-B1.
 XX
 PD 19-MAR-2002.
 XX
 XX 13-MAY-1999; 99US-0311311.
 XX
 PD 13-MAY-1998; 98US-085296P.
 XX
 XX (HARD) HARVARD COLLEGE.
 XX
 PI Erikson RL, Lee KS;
 DR WPI: 2002-3:4756/35.
 XX
 PT Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections -
 XX
 PS Example 1; Page 47pp; English.
 XX
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information
 CC given in the invention.
 XX
 SQ Sequence 603 AA;
 Query Match 86.4%; Score 38; DB 23; Length 603;
 Best Local Similarity 75.0%; Pred. No. 85;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGKPPF 8
 DB 244 LVGKPPF 251
 DE
 DE Mouse polo-like kinase (Plk) T210E mutant.
 XX
 XX Polo box; PBI; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutin.
 XX
 CS Mus musculus.
 OS Synthetic.

RESULT 40

AAU79309
 ID AAU79309 standard; Peptide: 603 AA.

XX
 AC AAU79309;

DT 02-JUL-2002 (first entry)

DE Mouse polo-like kinase (Plk) T210E mutant.

XX Polo box; PBI; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutin.
 XX
 CS Mus musculus.
 OS Synthetic.

FH Key Location/Qualifiers
FT Misc-difference 210 /note= "Wild type Thr substituted by Glu"
XX
XX US6158738-B1.
XX
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 14-MAY-1998; 98US-085296P.
XX
XX (HASC : HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections
XX
XX Example 1; Page : 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporum), protozoans, leishmanias, and arthropods.
XX This is the amino acid sequence of a mouse polo like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AA03506 using information
XX given in the invention.
XX
XX Sequence 603 AA;
XX
XX Query Match 86.4%; Score 38; DB 23; Length 633;
XX Best Local Similarity 75.0%; Pred No. 65;
XX Matches 6; Conservative 2; Mismatches 3; Indels 3; Gaps 0;
XX
XX 1 MLGKPPF 8
XX : : : : :
XX 244 LLVGKPPF 251

Search completed: November 14, 2003, 13:59:05
Cdb time : 31.957. secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OX protein - protein search, using sw model

Run on: November 14, 2003, 13:23:00 ; Search time 10,543 Seconds
(without alignments)
32.193 Million cell updates/sec

Title: US-09-736-076-16

Perfect score: 44

Sequence: 1 MGLGKPPF 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 2.5

Searched: 328717 seqs, 4230859 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
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7: /cgn2_6/prodata/iaa/6E_COMB.pep.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	8	3	US-08-861-338-16
2	44	100.0	9	3	US-08-861-338-17
3	41	93.2	9	3	US-08-861-338-18
4	41	93.2	11	3	US-08-861-338-19
5	41	93.2	272	1	US-08-861-338-12
6	41	93.2	272	2	US-08-861-338-13
7	41	93.2	685	2	US-08-861-338-14
8	41	93.2	685	3	US-08-861-338-15
9	41	93.2	685	3	US-08-861-338-16
10	41	93.2	685	3	US-08-861-338-17
11	39	88.6	275	1	US-08-861-338-18
12	39	88.6	275	2	US-08-861-338-19
13	38	86.4	272	1	US-08-861-338-20
14	38	86.4	272	2	US-08-861-338-21
15	38	86.4	603	3	US-08-861-338-22
16	38	86.4	603	3	US-08-861-338-23
17	38	86.4	603	3	US-08-861-338-24
18	37	84.1	264	2	US-08-861-338-25
19	37	84.1	499	4	US-08-861-338-26
20	37	84.1	588	4	US-08-861-338-27
21	37	84.1	668	4	US-08-861-338-28
22	37	84.1	962	4	US-08-861-338-29
23	37	84.1	962	4	US-08-861-338-30
24	37	84.1	980	4	US-08-861-338-31
25	37	84.1	980	4	US-08-861-338-32
26	37	84.1	1088	4	US-08-861-338-33
27	37	84.1	1088	4	US-08-861-338-34

28	84.1	1099	4	US-09-442-100-2	Sequence 2, Appli
29	84.1	1099	4	US-09-442-100-2	Sequence 2, Appli
30	84.1	1130	4	US-09-442-100-4	Sequence 4, Appli
31	84.1	1130	4	US-09-442-100-4	Sequence 4, Appli
32	84.1	1130	4	US-09-442-100-4	Sequence 4, Appli
33	84.1	1130	4	US-09-442-100-4	Sequence 4, Appli
34	84.1	1130	4	US-09-442-100-4	Sequence 4, Appli
35	84.1	1130	4	US-09-442-100-4	Sequence 4, Appli
36	84.1	1130	4	US-09-442-100-4	Sequence 4, Appli
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45	84.1	1130	4	US-09-442-100-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-861-338-16
; Sequence 16, Application US/29861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /note= "Phenylalanine-NH2"
US-08-861-338-16

Query Match 100.0% Score 44; DB 3; Length 8;

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,338
FILING DATE: 21-MAY-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CMCC-593
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "N-Acetyl Methionine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: /note= "Glutamic Acid Benzyl Ester"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: /note= "Serine-NH2"
US-08-861-338-19

Query Match 93.2%; Score 41; DB 3; Length 11;
Best Local Similarity 87.5%; Pred. No. 3.11;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGKPPF 8
Db : MLLGKPPF 8

RESULT 5
US-08-252-9950-12
Sequence 12, Application US/08/2529950
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
City: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DCS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,9950
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-252-9950-12

Query Match 93.2%; Score 41; DB 1; Length 272;
Best Local Similarity 87.5%; Pred. No. 2.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGKPPF 8
Db 199 MLLGKPPF 206

RESULT 6
US-08-834-108-12
Sequence 12, Application US/08834108
Patent No. 5978893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
City: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-834-108-12

Query Match 93.2%; Score 41; DB 2; Length 272;
Best Local Similarity 87.5%; Pred. No. 2.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGKPPF 8
Db 199 MLLGKPPF 206


```

RESULT 7
US-09-736-989 1
; Sequence 1, Application US/08878989
; Patent No. 5985803
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/98/878,989
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: FF-012; US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415 845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVENOB01
; CIGNE: 39043
US 09 878-989-1

```

```

Query Match 93.2%; Score 41; DB 2; Length 685;
Best Local Similarity 87.5%; Pred. No. 7.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

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QY 1 MLLGKPPF 8
DB 273 MLLGKPPF 280

```

```

RESULT 8
US-09-136-282-2
; Sequence 2, Application US/0916282
; Patent No. 6083699
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, KAREN
; APPLICANT: JACKSON, JEFFREY
; APPLICANT: HANSBURY, MICHAEL
; APPLICANT: NERJUKAR, SANDHYA

```

```

; APPLICANT: ROSHAK, AMY
; APPLICANT: BOUZYK, MARK
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,282
; FILING DATE: 20-AUG-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/356,112
; FILING DATE: 20-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-136-282-2

```

```

Query Match 93.2%; Score 41; DB 3; Length 685;
Best Local Similarity 87.5%; Pred. No. 7.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MLLGKPPF 8
DB 273 MLLGKPPF 280

```

```

RESULT 9
US-09-272-796-1
; Sequence 1, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

```

```

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272.796
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,989
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-945-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 685 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: HUVENOB01
CLONE: 39043

```

```

US-09-736-16.1
Query Match: 93.2%; Score 41; DB 3; Length 685;
Best Local Similarity 87.5%; Pred. No. 7.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MLLGKPPF 8
|:|:|:|
DB 273 MLLGKPPF 290

```

```

RESULT 10
US-09-505-744-2
Sequence 2, Application US/09505744
Patent No. 6245544
GENERAL INFORMATION:
APPLICANT: Karen M. Anderson
APPLICANT: Mark W. Bouzyk
APPLICANT: Michael J. Hansbury
APPLICANT: Jeffrey R. Jackson
APPLICANT: Sandhya S. Nerutkar
APPLICANT: Amy K. Roshak
TITLE OF INVENTION: HUMAN SERINE INDUCIBLE KINASE GEN-
FILE REFERENCE: GH-70233-A-D1
CURRENT APPLICATION NUMBER: US/09/505,744
CURRENT FILING DATE: 2000-02-16
EARLIER APPLICATION NUMBER: 09/136,280
EARLIER FILING DATE: 1998-08-20
EARLIER APPLICATION NUMBER: 60/056,112
EARLIER FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASTSEQ for Windows Version 1.0
SEQ ID NO 2
LENGTH: 685
TYPE: PRT
ORGANISM: HOMO SAPIENS

```

```

US-09-505-744-2
Query Match: 93.2%; Score 41; DB 3; Length 685;
Best Local Similarity 87.5%; Pred. No. 7.1;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MLLGKPPF 8
|:|:|:|
DB 273 MLLGKPPF 290

```

```

RESULT 11
US-08-252-995D-13
Sequence 13, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Hefferman, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 362-1398
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
US-08-252-995D-13

```

```

Query Match: 88.6%; Score 39; DB 1; Length 275;
Best Local Similarity 75.0%; Pred. No. 6.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MLLGKPPF 8
|:|:|:|
DB 200 MLLGKPPF 207

```

```

RESULT 12
US-08-834-108-13
Sequence 13, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Hefferman, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834.108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-213
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 364-1398
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
US-08-834-108-13

Query Match 88.6%; Score 39; DB 2; Length 275;
Best Local Similarity 75.0%; Pred. No. 6.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 200 LLVGKPPF 207

RESULT 13
US-08-861-338-6
Sequence 5, Application US/08861338
Patent No. 6174993
GENERAL INFORMATION:
APPLICANT: Ben-Gasson, Shmuel A.
TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Multifa Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861.338
FILING DATE: 21-MAY-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CMCC-550
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide

US-08-861-338-6
Query Match 86.4%; Score 38; DB 3; Length 20;
Best Local Similarity 75.0%; Pred. No. 0.75;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 3 LLVGKPPF 10

RESULT 14
US-08-252-995D-14
Sequence 14, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252.995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-252-995D-14

Query Match 86.4%; Score 38; DB 1; Length 272;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 199 LLVGKPPF 206

RESULT 15
US-08-834-108-14
Sequence 14, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE

```

; FILING DATE: 23-FEB-1996
; APPLICATION NUMBER: PC7/EP94/02863
; FILING DATE: 30-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4329177
; FILING DATE: 30-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 9516-KGB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-09-198-122-2

Query Match 86.4%; Score 38; DB 3; Length 603;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Indels 0

QY 1 MLGKPPF 8
Db 244 LLVGKPPF 251

RESULT 17
US-09-311-311C-26
; Sequence 26, Application US/09311311C
; Patent No. 6358718
; GENERAL INFORMATION:
; APPLICANT: Erikson, et al.
; TITLE OF INVENTION: POLO BOX THERAPEUTIC COMPOSITIONS,
; TITLE OF INVENTION: METHODS, AND USES THEREFOR
; FILE REFERENCE: 1874/117
; CURRENT APPLICATION NUMBER: US/09/311.311C
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,296
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(603)
; OTHER INFORMATION: Plk protein
US-09-311-311C-26

Query Match 86.4%; Score 38; DB 4; Length 603;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Indels 0

QY 1 MLGKPPF 8
Db 244 LLVGKPPF 251

RESULT 18
US-07-857-224B-17
; Sequence 17, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
; FEATURE: Protein kinase; Table 8 Column 18
; PUBLICATION INFORMATION:
; AUTHORS:
; AUTHORS: Hanks, S. K.
; AUTHORS: Quinn, A. M.
; AUTHORS: Hunter, T.
; TITLE: The protein kinase family
; JOURNAL: Science
; VOLUME: 241
; PAGES: 42-52
; DATE: 1988
; US-07-857-224B-17

Query Match 84.1%; Score 37; DB 2; Length 264;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
|||:|
DB 195 MLVGPPF 202

RESULT 19
US-09-509-902A-12
; Sequence 12, Application US/09503902A
; Patent No. 6387676
; GENERAL INFORMATION:
; APPLICANT: Virca, Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Marken, John S.
; TITLE OF INVENTION: Human cDNAs Encoding Polypeptides Having Kinase Functions
; FILE REFERENCE: 2877-US
; CURRENT APPLICATION NUMBER: US/09/509,902A
; CURRENT FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 12
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-509-902A-12

Query Match 84.1%; Score 37; DB 4; Length 499;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
|||:|
DB 407 MLVGPPF 414

RESULT 20
US-09-509-902A-16
; Sequence 16, Application US/09509902A
; Patent No. 6387676
; GENERAL INFORMATION:
; APPLICANT: Virca, Duke
; APPLICANT: Bird, Timothy A.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Marken, John S.
; TITLE OF INVENTION: Human cDNAs Encoding Polypeptides Having Kinase Functions
; FILE REFERENCE: 2877-US
; CURRENT APPLICATION NUMBER: US/09/509,902A
; CURRENT FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 16
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-509-902A-16

Query Match 84.1%; Score 37; DB 4; Length 588;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
|||:|
DB 406 MLVGPPF 413

RESULT 21
US-09-134-001C-4816
; Sequence 4816, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO: 4816
; LENGTH: 668
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-4816

Query Match 84.1%; Score 37; DB 4; Length 668;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
|||:|
DB 203 MLVGPPF 210

RESULT 22
US-09-442-100-6
; Sequence 6, Application US/09442100

```

; Patent No. 6359193
; GENERAL INFORMATION:
; APPLICANT: Xu, Tian
; APPLICANT: Tao, Wufan
; APPLICANT: Wang, Weiyl
; APPLICANT: Zhang, Sheng
; APPLICANT: Yu, Wan
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
; TITLE OF INVENTION: GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/442,100
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/411,111
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 962 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-442-100-6

Query Match      84.1%   Score 37; DB 4; Length 962;
Best Local Similarity 75.0%; Pred. No. 55;
Matches      6; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

Cy      1 MLIGKPPF 8
Db      775 MLVGQPPF 782

RESULT 23
US-08-939-106-6
; Sequence 6, Application US/08939106
; Patent No. 6559285
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/442,100
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/411,111
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 962 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-442-100-6

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,106
; FILING DATE: 26-Nov-6559285-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-007-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 962 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-939-106-6

Query Match      84.1%   Score 37; DB 4; Length 962;
Best Local Similarity 75.0%; Pred. No. 55;
Matches      6; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

Cy      1 MLIGKPPF 8
Db      775 MLVGQPPF 782

RESULT 24
US-09-442-100-8
; Sequence 8, Application US/09442100
; Patent No. 6359193
; GENERAL INFORMATION:
; APPLICANT: Xu, Tian
; APPLICANT: Tao, Wufan
; APPLICANT: Wang, Weiyl
; APPLICANT: Zhang, Sheng
; APPLICANT: Yu, Wan
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
; TITLE OF INVENTION: GENES AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/442,100
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/411,111
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6523-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:

```

```
? SEQUENCE CHARACTERISTICS:
? LENGTH: 980 amino acids
? TYPE: amino acid
? TOPOLOGY: unknown
? MOLECULE TYPE: protein
US-09-442-100-8
Query Match      84.1%; Score 37; DB 4; Length 980;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLGKPPF 8
      ||:|:|
DB      802 MLVGQPPF 809

RESULT 25
US-09-339-106-8
? Sequence 8, Application US/09939106
? Patent No. 6559285
? GENERAL INFORMATION:
? APPLICANT: Yale University
? TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
? NUMBER OF SEQUENCES: 16
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Pennie & Edmonds
? STREET: 1155 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: USA
? ZIP: 10036-2711
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent in Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/88/934,106
? FILING DATE: 26-Nov-85
? CLASSIFICATION: <Unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Misrock, S. Leslie
? REGISTRATION NUMBER: 8,872
? REFERENCE/DOCKET NUMBER: 652, 007-228
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 790 9249
? TELEFAX: (212) 969-9741/8844
? TELEX: 66141 PENNIE
? INFORMATION FOR SEQ ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 980 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-339-106-8
Query Match      84.1%; Score 37; DB 4; Length 980;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLGKPPF 8
      ||:|:|
DB      802 MLVGQPPF 809

RESULT 26
US-09-233-857-4
? Sequence 4, Application US/09233857
? Patent No. 6495353
? GENERAL INFORMATION:
? APPLICANT: Plovman, Gregory
? TITLE OF INVENTION: HUMAN ORTHOLOGUES OF WART
? FILE REFERENCE: 239/251
? CURRENT APPLICATION NUMBER: US/09/233.857
? CURRENT FILING DATE: 1999-01-20
? EARLIER APPLICATION NUMBER: USSN 60/072,023
? EARLIER FILING DATE: 1998-01-21
? NUMBER OF SEQ ID NOS: 18
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 4:
? LENGTH: 1088
? TYPE: PRT
? ORGANISM: HUMAN
US-09-233-857-4
Query Match      84.1%; Score 37; DB 4; Length 1088;
Best Local Similarity 75.0%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLGKPPF 8
      ||:|:|
DB      906 MLVGQPPF 913

RESULT 27
US-09-233-857-13
? Sequence 13, Application US/09233857
? Patent No. 6495353
? GENERAL INFORMATION:
? APPLICANT: Plovman, Gregory
? TITLE OF INVENTION: HUMAN ORTHOLOGUES OF WART
? FILE REFERENCE: 239/251
? CURRENT APPLICATION NUMBER: US/09/233.857
? CURRENT FILING DATE: 1999-01-20
? EARLIER APPLICATION NUMBER: USSN 60/072,023
? EARLIER FILING DATE: 1998-01-21
? NUMBER OF SEQ ID NOS: 18
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 13:
? LENGTH: 1088
? TYPE: PRT
? ORGANISM: HUMAN
US-09-233-857-13
Query Match      84.1%; Score 37; DB 4; Length 1088;
Best Local Similarity 75.0%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLGKPPF 8
      ||:|:|
DB      951 MLVGQPPF 958

RESULT 28
US-09-442-100-2
? Sequence 2, Application US/09442100
? Patent No. 6359193
? GENERAL INFORMATION:
? APPLICANT: Xu, Tian
? APPLICANT: Tao, Wufan
? APPLICANT: Wang, Weiyl
? APPLICANT: Zhang, Sheng
? APPLICANT: Yu, Wan
? TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
? NUMBER OF SEQUENCES: 16
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Pennie & Edmonds
? STREET: 1155 Avenue of the Americas
? CITY: New York
? STATE: New York
? COUNTRY: USA
```



```
RESULT 31
US-09-233-857-3
; Sequence 3, Application US/09233857
; Patent No. 6495353
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Flanagan, Peter
; TITLE OF INVENTION: HUMAN ORTHOLOGUES OF WART
; FILE REFERENCES: 239/251
; CURRENT APPLICATION NUMBER: US/09/233-857
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: USSN 60/072,023
; EARLIER FILING DATE: 1998-01-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1130
; TYPE: PRT
; ORGANISM: HUMAN
LS-09-233-857-3

Query Match      84.1%; Score 37; DB 4; Length 1130;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLGKPPF 8
Db      943 MLVGQPPF 950

RESULT 32
US-08-919-106-4
; Sequence 4, Application US/08919106
; Patent No. 6559285
; GENERAL INFORMATION:
; APPLICANT: Yale University
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydko, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-252-995D-10

Query Match      81.8%; Score 36; DB 1; Length 273;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLGKPPF 8
Db      200 LLIGRPFF 207

RESULT 34
US-08-834-108-10
; Sequence 10, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; SEQ ID NO 4
; LENGTH: 1130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-08-834-108-4

Query Match      84.1%; Score 37; DB 4; Length 1130;
```

```
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLGKPPF 8
Db      943 MLVGQPPF 950

RESULT 33
US-08-252-995D-10
; Sequence 10, Application US/08252995D
; Patent No. 5630501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydko, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-252-995D-10

Query Match      81.8%; Score 36; DB 1; Length 273;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLGKPPF 8
Db      200 LLIGRPFF 207

RESULT 34
US-08-834-108-10
; Sequence 10, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
```

STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version: #1.33
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Rudydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-834-108-10

Query Match 81.8%; Score 36; DB 2; Length 273;
Best Local Similarity 82.5%; Pred. No. 24;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
DB 200 LIGRPPF 207

RESULT 35
US-08-755-728-4
Sequence 4, Application US/08/755728
Patent No. 5962312
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR 1
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,728
FILING DATE: No. 5962312ember 25, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,809
FILING DATE: December 18, 1995

FILING DATE: August 14, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/113
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-755-728-4

Query Match 81.8%; Score 36; DB 2; Length 403;
Best Local Similarity 85.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPF 8
DB 323 LVGKPPF 329

RESULT 36
US-08-974-655-4
Sequence 4, Application US/08/974655
Patent No. 5972676
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,655
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/755,728
FILING DATE: No. 5972676ember 25, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/113
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
 LENGTH: 403 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYDROTHERMAL: NO
 ANTI-SENSE: NO

US-08-974 655-4

Query Match 81.8%; Score 36; DB 2; Length 403;
 Best Local Similarity 85.7%; Pred. No. 35;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPF 8
 DB 323 LVGKPPF 329

RESULT 37

US-09-283-011-4
 ; Sequence 4, Application US/0928301
 ; Patent No. 6207401
 ; GENERAL INFORMATION:
 ; APPLICANT: Plowman, Gregory
 ; APPLICANT: Mossie, Kevin
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AIR-1
 ; TITLE OF INVENTION: AND/OR AIR-2 RELATED DISORDERS
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyen & Lyen
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: Storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: FastSeq for Windows 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/283,011
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/012,135
 ; FILING DATE: January 22, 1998
 ; APPLICATION NUMBER: 28/755,726
 ; FILING DATE: No. 6207401, December 28, 1996
 ; APPLICATION NUMBER: 60/023,943
 ; FILING DATE: August 14, 1996
 ; APPLICATION NUMBER: 60/008,509
 ; FILING DATE: December 18, 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 231/282
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510

SEQUENCE CHARACTERISTICS:
 LENGTH: 403 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYDROTHERMAL: NO
 ANTI-SENSE: NO

US-09-283-011-4

Query Match 81.8%; Score 36; DB 3; Length 403;
 Best Local Similarity 85.7%; Pred. No. 35;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPF 8
 DB 323 LVGKPPF 329

RESULT 38

US-08-252-995D-2
 ; Sequence 2, Application US/08252995D
 ; Patent No. 5650501
 ; GENERAL INFORMATION:
 ; APPLICANT: Dennis, James W
 ; APPLICANT: Heffernan, Mike
 ; APPLICANT: Fode, Carol
 ; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BERESKIN & PARR
 ; STREET: 40 King Street West
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5H 3Y2
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/252.995D
 ; FILING DATE: 02-JUN-1994
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kurdydk, Linda M
 ; REGISTRATION NUMBER: 34,971
 ; REFERENCE/DOCKET NUMBER: 3:53-96
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 364-7311
 ; TELEFAX: (416) 361-1398
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 416 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-252-995D-2

Query Match 81.8%; Score 36; DB 1; Length 416;
 Best Local Similarity 62.5%; Pred. No. 37;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 DB 204 LLIGRPPF 211

RESULT 39

US-08-834-108-2
 ; Sequence 2, Application US/08834108
 ; Patent No. 5976893
 ; GENERAL INFORMATION:
 ; APPLICANT: Dennis, James W
 ; APPLICANT: Heffernan, Mike
 ; APPLICANT: Fode, Carol
 ; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BERESKIN & PARR

STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/934,108
 FILING DATE:
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Kurdydyk, Linda M
 REGISTRATION NUMBER: 34,971
 REFERENCE/DOCKET NUMBER: 3153-210
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 416 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 OS-CA 834108-2

Query Match 81.8%; Score 36; DB 2; Length 416;
 Best Local Similarity 62.5%; Pred. No. 37;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 DI 204 LLIGRFFP 211

RESULT 40
 US-06-252-995D-6
 Sequence 6, Application US/08252995D
 Patent No. 5653501
 GENERAL INFORMATION:
 APPLICANT: Dennis, James W
 APPLICANT: Heffernan, Mike
 APPLICANT: Fode, Carol
 TITLE OR INVENTION: NOVEL SERINE-THREONINE KINASE
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PERESKIN & FARR
 STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/252,995D
 FILING DATE: 02-JUN-1994
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Kurdydyk, Linda M
 REGISTRATION NUMBER: 34,971
 REFERENCE/DOCKET NUMBER: 3153-96
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:

LENGTH: 464 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-252-995D-6
 Query Match 81.8%; Score 36; DB 1; Length 464;
 Best Local Similarity 62.5%; Pred. No. 41;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGKPPF 8
 DI 204 LLIGRFFP 211
 Search completed: November 14, 2003, 13:29:50
 Job time : 11.5143 secs

GenCore version: 5.1.6
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CM protein: protein search, using sw model

Run on: November 14, 2003, 13:29:05 ; Search time 19.6817 Seconds
without alignments:
71.443 Million cell Updates/sec

Title: US 09-736-076-16
Perfect score: 44
Sequence: 1 MLLGKPPF 8

Scoring table: RASCM62
Gapop 10.0, Gapext 0.5

Seatched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum PR seq length: 0
Maximum DR seq length: 200000000

Post processing: Minimum Match 98
Maximum Match 100
Listing first 45 summaries

Database: Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOVB.pep.*
- 2: /cgn2_6/ptodata/1/pubaa/PCR_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOVB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubaa/PTUS_PUBCOVB.pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOVB.pep.*
- 9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOVB.pep.*
- 10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOVB.pep.*
- 11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOVB.pep.*
- 12: /cgn2_6/ptodata/1/pubaa/US09A_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOVB.pep.*
- 14: /cgn2_6/ptodata/1/pubaa/US09_PUBCOVB.pep.*
- 15: /cgn2_6/ptodata/1/pubaa/US10_PUBCOVB.pep.*
- 16: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubaa/US09C_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubaa/US09_PUBCOVB.pep.*

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the t.d.a. score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	8	9	US-09-736-076-16
2	44	100.0	9	9	US-09-736-076-17
3	41	93.2	9	9	US-09-736-076-15
4	41	93.2	10	9	US-09-736-076-57
5	41	93.2	11	9	US-09-736-076-19
6	41	93.2	400	15	US-10-036-021-5
7	41	93.2	469	15	US-10-059-585-14
8	41	93.2	685	10	US-09-771-161A-249
9	41	93.2	685	10	US-09-771-161A-250
10	41	93.2	685	10	US-09-771-161A-251
11	41	93.2	685	12	US-10-024-299A-101
12	41	93.2	685	12	US-09-769-970-1
13	41	93.2	685	12	US-10-042-21A-101
14	39	86.6	40	10	US-09-842-582-9
15	39	86.6	122	10	US-09-015-806-24

16	39	88.6	183	15	US-10-172-088-12	Sequence 12, Appl
17	39	88.6	256	11	US-09-898-837A-32	Sequence 32, Appl
18	38	86.4	8	9	US-09-736-076-55	Sequence 55, Appl
19	38	86.4	20	9	US-09-736-076-6	Sequence 6, Appl
20	38	86.4	329	10	US-09-925-300-1268	Sequence 1268, Ap
21	38	86.4	367	15	US-10-026-021-6	Sequence 6, Appl
22	38	86.4	419	10	US-09-893-737-106	Sequence 106, App
23	38	86.4	516	10	US-09-771-161A-123	Sequence 123, App
24	38	86.4	528	12	US-10-032-585-7571	Sequence 7571, Ap
25	38	86.4	603	10	US-09-771-161A-214	Sequence 214, App
26	38	86.4	603	15	US-10-171-311-186	Sequence 186, App
27	37	84.1	445	10	US-09-836-392-15	Sequence 15, Appl
28	37	84.1	499	15	US-10-024-828-12	Sequence 12, Appl
29	37	84.1	588	15	US-10-024-828-16	Sequence 16, Appl
30	37	84.1	660	9	US-09-815-242-5470	Sequence 5470, Ap
31	37	84.1	664	9	US-09-815-242-12179	Sequence 12179, A
32	37	84.1	1089	12	US-10-390-303-3	Sequence 3, Appl
33	37	84.1	1088	12	US-10-390-303-4	Sequence 4, Appl
34	36	81.8	48	9	US-09-922-138-19	Sequence 19, Appl
35	36	81.8	133	9	US-09-916-790-26	Sequence 26, Appl
36	36	81.8	180	9	US-09-910-150-29	Sequence 29, Appl
37	36	81.8	194	9	US-09-910-150-28	Sequence 28, Appl
38	36	81.8	230	9	US-09-797-039-11	Sequence 11, Appl
39	36	81.8	230	12	US-10-170-789-11	Sequence 11, Appl
40	36	81.8	231	10	US-09-515-806-13	Sequence 13, Appl
41	36	81.8	231	10	US-09-515-806-14	Sequence 14, Appl
42	36	81.8	231	10	US-09-882-166-5	Sequence 5, Appl
43	36	81.8	231	10	US-09-934-406-6	Sequence 6, Appl
44	36	81.8	231	12	US-10-170-789-18	Sequence 18, Appl
45	36	81.8	231	12	US-10-170-789-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-09-736-076-16
; Sequence 16, Application US/09736076
; Patent No. US20020049301A:
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Samuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242,10:5-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(10)
; NAME/KEY: AMIDATION
; LOCATION: (3)...(8)
; OTHER INFORMATION: J43
; US-09-736-076-16

Query Match 100.0% Score 44; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5,9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLLGKPPF 8

Db 1 MLLGKPPF 8

RESULT 2

US-09-736-076-17

```

; Sequence 17, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242.1015-009
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: J43.1
; US-09-736-076 17

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```

Query Match 100.0% Score 41; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MLLGKPPF 8
   |||
Db 1 MLLGKPPF 8

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RESULT 1

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; US-09-736-076-15
; Sequence 15, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: J42
; US-09-736-076-15

```

```

Query Match 93.2% Score 41; DB 9; Length 9;
Best Local Similarity 87.5%; Pred. No. 5.9e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MLLGKPPF 8
   |||
Db 1 MLLGKPPF 8

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RESULT 4

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; US-09-736-076-57
; Sequence 57, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MYRISTATE
; LOCATION: (1)...(10)
; OTHER INFORMATION: position 10 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (10)...(10)
; OTHER INFORMATION: SNK
; US-09-736-076-57

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```

Query Match 93.2% Score 41; DB 9; Length 10;
Best Local Similarity 87.5%; Pred. No. 0.52;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MLLGKPPF 8
   |||
Db 2 MLLGKPPF 9

```

RESULT 5

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; US-09-736-076-19
; Sequence 19, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(10)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (10)...(11)
; OTHER INFORMATION: J46
; US-09-736-076-19

```

```

Query Match 93.2% Score 41; DB 9; Length 11;
Best Local Similarity 87.5%; Pred. No. 0.57;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 MLLGKPPF 8
   |||
Db 1 MLLGKPPF 8

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RESULT 6
 US-10-026 021-5
 ; Sequence 5, Application US/10026021
 ; Publication No. US2003027756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genkings, Yonchu
 ; APPLICANT: Demc, Susan
 ; APPLICANT: Rigel Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
 ; TITLE OF INVENTION: Treatment of Cancer
 ; FILE REFERENCE: 021044-201210US
 ; CURRENT APPLICATION NUMBER: US/01026.021
 ; CURRENT FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/309,632
 ; PRIOR FILING DATE: 2001-08-01
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: DOMAIN
 ; LOCATION: (1...400)
 ; OTHER INFORMATION: human SNK mitotic kinase domain
 US 10 026 021-5

Query Match 93.2%; Score 41; DB 15; Length 403;
 Best Local Similarity 87.5%; Pred. No. 19;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLJCKPFF 8
 |||:|
 Db 273 MLJGRPFF 280

RESULT 7
 US-10-059-585-14
 ; Sequence 14, Application US/10059585
 ; Publication No. US20030382776A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ota, Toshio
 ; APPLICANT: Isogai, Takao
 ; APPLICANT: Nishikawa, Tetsuo
 ; APPLICANT: Hayashi, Koji
 ; APPLICANT: Otsuka, Kaoru
 ; APPLICANT: Yamamoto, Jun-ichi
 ; APPLICANT: Ishii, Shizuko
 ; APPLICANT: Sugiyama, Tomoyasu
 ; APPLICANT: Wakamatsu, Ai
 ; APPLICANT: Nagai, Keiichi
 ; APPLICANT: Otsuki, Tetsuji
 ; APPLICANT: Funahashi, Shin-ichi
 ; APPLICANT: Senoo, Chiaki
 ; APPLICANT: Nezu, Jun-ichi
 ; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
 ; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
 ; FILE REFERENCE: 06501-090001
 ; CURRENT APPLICATION NUMBER: US/10/059,585
 ; CURRENT FILING DATE: 2002-01-29
 ; PRIOR APPLICATION NUMBER: PCT/JP00/05060
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: US 60/183,322
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: US 60/159,590
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: JP 2000-118776
 ; PRIOR FILING DATE: 2000-01-11
 ; PRIOR APPLICATION NUMBER: JP 2000-183767
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: JP 11-248036
 ; PRIOR FILING DATE: 1999-07-29

; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 469
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-059-585-14
 Query Match 93.2%; Score 41; DB 15; Length 469;
 Best Local Similarity 87.5%; Pred. No. 23;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLJCKPFF 8
 |||:|
 Db 57 MLJGRPFF 64

RESULT 8
 US-09-771-161A-249
 ; Sequence 249, Application US/09771161A
 ; Patent No. US20020110811A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, et al.
 ; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 ; FILE REFERENCE: 802620-2005.1
 ; CURRENT APPLICATION NUMBER: US/09/771,161A
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 09/724,676
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 136776
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 135619
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 273
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 249
 ; LENGTH: 685
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-771-161A-249

Query Match 93.2%; Score 41; DB 10; Length 685;
 Best Local Similarity 87.5%; Pred. No. 33;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLJCKPFF 8
 |||:|
 Db 273 MLJGRPFF 280

RESULT 9
 US-09-771-161A-250
 ; Sequence 250, Application US/09771161A
 ; Patent No. US20020110811A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, et al.
 ; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 ; FILE REFERENCE: 802620-2005.1
 ; CURRENT APPLICATION NUMBER: US/09/771,161A
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 09/724,676
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 136776
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 135619
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 273
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 250
 ; LENGTH: 685
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-771-161A-250

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? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-024-298A-101

Query Match          93.2%; Score 41; DB 10; Length 685;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGKPPF 8
DB      273 MLLGKPPF 280

RESULT 10
US-09-771-161A-251
? Sequence 251: Application US/03771161A
? Patent No. US2003010811A1
? GENERAL INFORMATION:
? APPLICANT: LEVINE, et al.
? TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
? FILE REFERENCE: 802620-2005.1
? CURRENT APPLICATION NUMBER: US/09/771.161A
? CURRENT FILING DATE: 2001-01-26
? PRIOR APPLICATION NUMBER: 09/724,676
? PRIOR FILING DATE: 2000-11-28
? PRIOR APPLICATION NUMBER: 136776
? PRIOR FILING DATE: 2000-06-15
? PRIOR APPLICATION NUMBER: 135619
? PRIOR FILING DATE: 2000-04-12
? NUMBER OF SEQ ID NOS: 273
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 251
? LENGTH: 685
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-771-161A-251

Query Match          93.2%; Score 41; DB 10; Length 685;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGKPPF 8
DB      273 MLLGKPPF 280

RESULT 11
US-10-024-298A-101
? Sequence 101: Application US/10024298A
? Publication No. US20030143540A1
? GENERAL INFORMATION:
? APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
? APPLICANT: AKIO MATSUDA
? APPLICANT: GOICHI HONDA
? APPLICANT: SHUJI YURAMATSU
? APPLICANT: YUKIKO NAGANO
? TITLE OF INVENTION: NF-K B Activating Gene
? FILE REFERENCE: 1254-0191P
? CURRENT APPLICATION NUMBER: US/10/024.298A
? CURRENT FILING DATE: 2003-04-08
? PRIOR APPLICATION NUMBER: 60/314,385
? PRIOR FILING DATE: 2001-08-24
? PRIOR APPLICATION NUMBER: 60/278,641
? PRIOR FILING DATE: 2001-03-26
? PRIOR APPLICATION NUMBER: 60/258,315
? PRIOR FILING DATE: 2000-12-28
? PRIOR APPLICATION NUMBER: JP254018/2001
? PRIOR FILING DATE: 2001-08-24
? PRIOR APPLICATION NUMBER: JP0089312/2001
? PRIOR FILING DATE: 2001-03-26
? PRIOR APPLICATION NUMBER: JP402288/2000
? PRIOR FILING DATE: 2000-12-28
? NUMBER OF SEQ ID NOS: 182
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 101
? LENGTH: 685
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? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-024-298A-101

Query Match          93.2%; Score 41; DB 12; Length 685;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGKPPF 8
DB      273 MLLGKPPF 280

RESULT 12
US-09-769-970-1
? Sequence 1: Application US/09769970
? Publication No. US20030170219A1
? GENERAL INFORMATION:
? APPLICANT: Bandman, Olga
? APPLICANT: Hillman, Jennifer L.
? APPLICANT: Corley, Neil C.
? APPLICANT: Guegler, Karl G.
? APPLICANT: La, Preeti
? APPLICANT: Goli, Surya K.
? APPLICANT: Shah, Purvi
? TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
? NUMBER OF SEQUENCES: 21
? CORRESPONDENCE ADDRESS:
? ADDRESS: Incyte Pharmaceuticals, Inc.
? STREET: 3174 Porter Drive
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/769,970
? FILING DATE: 24-Jan-2001
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/272,796
? FILING DATE: <Unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Billings, Lucy J J
? REGISTRATION NUMBER: 36,749
? REFERENCE/DOCKET NUMBER: PF-0321 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-855-0555
? TELEFAX: 415-845-4166
? TELEX: <Unknown>
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 685 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: HUVEB081
? CLONE: 39C43
? SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-769-970-1

QY      1 MLLGKPPF 8
DB      273 MLLGKPPF 280

Query Match          93.2%; Score 41; DB 12; Length 685;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Ch 273 MLGKPPF 280

RESULT 13

US-10-042-211A-101
 ; Sequence 101, Application US/10042211A
 ; Publication No. US20030170719A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MATSUDA, Aki et al.
 ; TITLE OF INVENTION: NFkB Activating Gene
 ; FILE REFERENCE: 1254-0192P
 ; CURRENT APPLICATION NUMBER: US/10042211A
 ; CURRENT FILING DATE: 2002-01-11
 ; PRIOR APPLICATION NUMBER: JP 2000-40288
 ; PRIOR FILING DATE: 2000-12-26
 ; PRIOR APPLICATION NUMBER: JP 2001-089512
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: JP 2001-254318
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/258,315
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: US 60/278,640
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: US 60/314,165
 ; PRIOR FILING DATE: 2001-08-24
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 101
 ; LENGTH: 685
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-042-211A-101

Query Match 93.2%; Score 41; DB 12; Length 685;
 Best Local Similarity 87.5%; Pred. No. 33;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGKPPF 8

Db 273 MLGKPPF 280

RESULT 14

US-09-842-582-9
 ; Sequence 9, Application US/09842582
 ; Patent No. US2002015570A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: 2246 NOVEL PROTEIN KINASE MOLECULES AND
 ; FILE REFERENCE: 38155-20054.00
 ; CURRENT APPLICATION NUMBER: US/09/842,582
 ; CURRENT FILING DATE: 2001-04-25
 ; PRIOR APPLICATION NUMBER: US 60/199,391
 ; PRIOR FILING DATE: 2000-04-25
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 40
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Consensus: amino acid
 US-09-842-582-9

Query Match 88.6%; Score 39; DB 10; Length 40;
 Best Local Similarity 87.5%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLGKPPF 8

Db 33 MLGKPPF 40

RESULT 15

US-09-515-806-24
 ; Sequence 24, Application US/09515806
 ; Patent No. US20020132321A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COOK, WILLIAM J.
 ; TITLE OF INVENTION: KAPELLE-LIBERMAN, ROSANA
 ; FILE REFERENCE: 38155-20002.C0
 ; CURRENT APPLICATION NUMBER: US/09/515,806
 ; CURRENT FILING DATE: 2000-02-29
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 24
 ; LENGTH: 122
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Consensus
 ; OTHER INFORMATION: Kinase sequence
 US-09-515-806-24

Query Match 88.6%; Score 39; DB 10; Length 122;
 Best Local Similarity 87.5%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLGKPPF 8

Db 30 MLGKPPF 37

RESULT 16

US-10-172-088-12
 ; Sequence 12, Application US/10172088
 ; Publication No. US20030008370A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: MEYERS, Rachel
 ; FILE REFERENCE: 13295 NOVEL PROTEIN KINASE MOLECULES AND
 ; TITLE OF INVENTION: US8 THEREOF
 ; FILE REFERENCE: 38155-20010.01
 ; CURRENT APPLICATION NUMBER: US/10/172,088
 ; CURRENT FILING DATE: 2002-09-13
 ; PRIOR APPLICATION NUMBER: US/09/596,071
 ; PRIOR FILING DATE: 2003-06-16
 ; PRIOR APPLICATION NUMBER: US 60/199,391
 ; PRIOR FILING DATE: 2000-04-25
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 183
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Consensus: amino acid sequence
 US-10-172-088-12

Query Match 88.6%; Score 39; DB 15; Length 183;
 Best Local Similarity 87.5%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLGKPPF 8

Db 176 MLGKPPF 183

RESULT 17

US-09-898-837A-32
 ; Sequence 32, Application US/09898937A
 ; Publication No. US20030077697A1
 ; GENERAL INFORMATION:

; LOCATION: (59);
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (307)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (308)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (314)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (317)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (323)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (327)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (328)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (329)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-928-300-1268
 Query Match 86.4%; Score 38; DB 10; Length 329;
 Best Local Similarity 75.0%; Pred. No. 55;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy : MLGKPPF 8
 : |||||
 Db 260 LLVGKPPF 267

RESULT 21
 US-10-026-021-6
 ; Sequence 6, Application US/1002602;
 ; Publication No. US03002756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hitoshi, Yasumichi;
 ; APPLICANT: Demo, Susan;
 ; APPLICANT: Jenkins, Yonchu
 ; APPLICANT: Rigel Pharmaceuticals, Inc.;
 ; TITLE OF INVENTION: SAK: Modulation of cellular proliferation for
 ; FILE REFERENCE: 021044-00121005
 ; CURRENT APPLICATION NUMBER: US/10/026-021
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR FILING DATE: 2001-06-31
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 367
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: DOMAIN
 ; LOCATION: (1)...(367)
 ; OTHER INFORMATION: human PLK1 mitotic kinase kinase domain

US-10-026-021-6
 Query Match 86.4%; Score 38; DB 10; Length 367;
 Best Local Similarity 75.0%; Pred. No. 61;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy : MLGKPPF 8
 : |||||
 Db 244 LLVGKPPF 251

RESULT 22
 US-09-893-737-106
 ; Sequence 106, Application US/09893737
 ; Patent No. US20020110855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Presnell, Scott R.
 ; TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
 ; FILE REFERENCE: 00-41
 ; CURRENT APPLICATION NUMBER: US/09/893,737
 ; CURRENT FILING DATE: 2001-06-28
 ; PRIOR APPLICATION NUMBER: US 60/215,446
 ; PRIOR FILING DATE: 2000-06-30
 ; NUMBER OF SEQ ID NOS: 329
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 106
 ; LENGTH: 419
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-893-737-106

Query Match 86.4%; Score 38; DB 10; Length 419;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGKPPF 7
 : |||||
 Db 170 MLGKPPF 176

RESULT 23
 US-09-771-161A-123
 ; Sequence 123, Application US/09771161A
 ; Patent No. US20020110811A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, et al.
 ; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 ; FILE REFERENCE: 802620-2035-1
 ; CURRENT APPLICATION NUMBER: US/09/771,161A
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 09/724,676
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 136776
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 135619
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 273
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 123
 ; LENGTH: 516
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-771-161A-123

Query Match 86.4%; Score 38; DB 10; Length 516;
 Best Local Similarity 75.0%; Pred. No. 85;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGKPPF 8
 : |||||
 Db 157 LLVGKPPF 164

RESULT 24
 US-10-032-585-7571
 ; Sequence 7571, Application US/10032585
 ; Publication No. US20030180953A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Terry, Roemer D.
 ; APPLICANT: Bo, Jiang
 ; APPLICANT: Charles, Boone
 ; APPLICANT: Howard, Bussey

; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
 ; FILE REFERENCE: 10182-005-999
 ; CURRENT APPLICATION NUMBER: US/10/032,585
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 8000
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7571
 ; LENGTH: 528
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-10-032-585-7571

Query Match 86.4%; Score 38; DB 12; Length 528;
 Best Local Similarity 75.0%; Pred. No. 97;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 Db 454 LLVGKPPF 461

RESULT 25
 US-09-771-161A-214
 ; Sequence 214, Application US/09771161A
 ; Patent No. US2002011821A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, et al.
 ; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 ; FILE REFERENCE: 802620-2005.1
 ; CURRENT APPLICATION NUMBER: US/09/771,61A
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: C97/724,676
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 136776
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 135619
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 273
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 214
 ; LENGTH: 603
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-771-161A-214

Query Match 86.4%; Score 38; DB 10; Length 603;
 Best Local Similarity 75.0%; Pred. No. 99;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 Db 244 LLVGKPPF 251

RESULT 26
 US-10-071-311-186
 ; Sequence 186, Application US/10171311
 ; Publication No. US20030087270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Chen, Yan
 ; APPLICANT: Zhao, Xumei
 ; APPLICANT: Morahan, John
 ; APPLICANT: Kamatkar, Shubhangi
 ; APPLICANT: Glatt, Karen
 ; APPLICANT: Gannavarapu, Manjula
 ; APPLICANT: Hoersb, Sebastian
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
 ; OF CERVICAL CANCER
 ; FILE REFERENCE: WRI-035
 ; CURRENT APPLICATION NUMBER: US/10/171,311
 ; CURRENT FILING DATE: 2002-06-12

; PRIOR APPLICATION NUMBER: US 60/298,159
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/298,155
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/335,936
 ; PRIOR FILING DATE: 2001-11-14
 ; NUMBER OF SEQ ID NOS: 238
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 186
 ; LENGTH: 603
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-171-311-186

Query Match 86.4%; Score 38; DB 15; Length 603;
 Best Local Similarity 75.0%; Pred. No. 99;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 Db 244 LLVGKPPF 251

RESULT 27
 US-09-836-392-15
 ; Sequence 15, Application US/09836392
 ; Patent No. US20020173458A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptide
 ; FILE REFERENCE: PT020PI
 ; CURRENT APPLICATION NUMBER: US/09/836,392
 ; CURRENT FILING DATE: 2001-04-18
 ; PRIOR APPLICATION NUMBER: PCT/US00/28866
 ; PRIOR FILING DATE: 2000-10-11
 ; PRIOR APPLICATION NUMBER: 60/159,542
 ; PRIOR FILING DATE: 1999-10-15
 ; PRIOR APPLICATION NUMBER: 60/165,914
 ; PRIOR FILING DATE: 1999-11-17
 ; PRIOR APPLICATION NUMBER: 60/189,027
 ; PRIOR FILING DATE: 2000-03-14
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 15
 ; LENGTH: 445
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-836-392-15

Query Match 84.1%; Score 37; DB 10; Length 445;
 Best Local Similarity 75.0%; Pred. No. 11e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 Db 263 MLVGQPPF 270

RESULT 28
 US-10-024-828-12
 ; Sequence 12, Application US/10024828
 ; Publication No. US2003003605A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Virca, Duke
 ; APPLICANT: Bird, Timothy A.
 ; APPLICANT: Anderson, Dirk M.
 ; APPLICANT: Marken, John S.
 ; TITLE OF INVENTION: Human cDNAs Encoding Polypeptides Having Kinase
 ; FUNCTIONALITY
 ; FILE REFERENCE: 2877-US
 ; CURRENT APPLICATION NUMBER: US/10/024,828
 ; CURRENT FILING DATE: 2001-12-18

; PRIOR APPLICATION NUMBER: US/C9/509,902A
 ; PRIOR FILING DATE: 1999-08-03
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 499
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-024 828 12

Query Match 84.1%; Score 37; DB 15; Length 499;
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 3;

QY 1 MLGKPPF 8
 Db 407 MLVGPPF 414

RESULT 29
 ; US-10-024-828-16
 ; Sequence 16, Application US/10024828
 ; Publication No. US2003036051A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Virco, Duke
 ; APPLICANT: Bird, Timothy A.
 ; APPLICANT: Anderson, Dirk M.
 ; APPLICANT: Marken, John S.
 ; TITLE OF INVENTION: Human cDNAs Encoding Polypeptides Having Kinase
 ; TITLE OF INVENTION: Functions
 ; FILE REFERENCE: 2877-US
 ; CURRENT APPLICATION NUMBER: US/10/024,828
 ; PRIOR FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: US/C9/509,902A
 ; PRIOR FILING DATE: 1999-08-03
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 16
 ; LENGTH: 598
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-024 828-16

Query Match 84.1%; Score 37; DB 15; Length 588;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 3; Gaps 0;

QY 1 MLGKPPF 8
 Db 406 MLVGPPF 413

RESULT 30
 ; US-09-815-242-5470
 ; Sequence 5470, Application US/C9815242
 ; Patent No. US2002061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; TITLE OF INVENTION: Prokaryotes
 ; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5470
 ; LENGTH: 660
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-09-815-242-5470

Query Match 84.1%; Score 37; DB 9; Length 660;
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 Db 201 MLVGPPF 208

RESULT 31
 ; US-09-815-242-12179
 ; Sequence 12179, Application US/09815242
 ; Patent No. US2002061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; TITLE OF INVENTION: Prokaryotes
 ; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12179
 ; LENGTH: 664
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-09-815-242-12179

Query Match 84.1%; Score 37; DB 9; Length 664;
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8

```

Db      202 MLVGQPPF 209
||:||||
; SEQ ID NO 19
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-09-922-138-19

RESULT 32
US-10-390-303-3
; Sequence 3, Application US/10390303
; Publication No. US2003071569A1
; GENERAL INFORMATION:
; APPLICANT: JCR Pharmaceuticals Co., Ltd.
; TITLE OF INVENTION: Human Tumor Suppressing Gene
; FILE REFERENCE: 38155-20330.03
; CURRENT APPLICATION NUMBER: US/10/290,303
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 3
; LENGTH: 1088
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-390-303-3

Query Match      84.1%   Score 371   DB 12; Length 1088;
Best Local Similarity 75.0%; Pred. No. 27e+22;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLUGKPPF 8
||:||||
Db      906 MLVGQPPF 913

RESULT 33
US-10-390-303-4
; Sequence 4, Application US/10390303
; Publication No. US2003071569A1
; GENERAL INFORMATION:
; APPLICANT: JCR Pharmaceuticals Co., Ltd.
; TITLE OF INVENTION: Human Tumor Suppressing Gene
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/390,303
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 4
; LENGTH: 1088
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-390-303-4

Query Match      84.1%   Score 371   DB 12; Length 1088;
Best Local Similarity 75.0%; Pred. No. 27e+22;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MLUGKPPF 8
||:||||
Db      906 MLVGQPPF 913

RESULT 34
US-09-922-138-19
; Sequence 19, Application US/09922138
; Patent No. US20020061574A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 16658, 14223, AND 16022, NOVEL HUMAN
; FILE REFERENCE: 38155-20330.03
; CURRENT APPLICATION NUMBER: US/09/922,138
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/223,295
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version: 4.0
; LENGTH: 180
; TYPE: PRT

```

```

; SEQ ID NO 19
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-09-922-138-19

Query Match      81.8%   Score 36; DB 9; Length 48;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLUGKPPF 8
||:||||
Db      35 LLTGKPPF 42

RESULT 35
US-09-916-790-26
; Sequence 26, Application US/09916790
; Patent No. US20020061573A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachael
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 18431 AND 32374, NOVEL HUMAN PROTEIN
; FILE REFERENCE: 381552002700
; CURRENT APPLICATION NUMBER: US/09/916,790
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 6C/221,543
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-09-916-790-26

Query Match      81.8%   Score 36; DB 9; Length 133;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MLUGKPPF 8
||:||||
Db      44 LLTGKPPF 51

RESULT 36
US-09-910-150-29
; Sequence 29, Application US/09910150
; Patent No. US20020068698A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: 13237, 18480, 2245 OR 16228 NOVEL HUMAN
; FILE REFERENCE: 38155-20020.00
; CURRENT APPLICATION NUMBER: US/09/910,150
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,028
; PRIOR FILING DATE: 2000-07-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 180
; TYPE: PRT

```


1 PRIOR FILING DATE: 2001-03-06
 2 PRIOR APPLICATION NUMBER: PCT/US01/07074
 3 PRIOR FILING DATE: 2001-03-05
 4 PRIOR APPLICATION NUMBER: US 60/187,428
 5 PRIOR FILING DATE: 2000-03-07
 6 NUMBER OF SEQ ID NOS: 63
 7 SOFTWARE: FastSeq for Windows Version 4.0
 8 SEQ ID NO 1:
 9 LENGTH: 230
 10 TYPE: PRT
 11 ORGANISM: Artificial Sequence
 12 FEATURE:
 13 OTHER INFORMATION: consensus sequence
 US-10 170-189-11

Query Match 81.8% Score 16 DB 12 Length 230
 Best Local Similarity 75.0% Pct Id 87
 Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 1 MLLCKPPF 8
 DB 175 LLLCKPPF 182

RESULT 40
 US-09-515-806 13
 1 Sequence 13, Application US/09515806
 2 Patent No. US200201232A1
 3 GENERAL INFORMATION:
 4 APPLICANT: COOK, WILLIAM J.
 5 TITLE OF INVENTION: 14790, NOVEL PROTEIN KINASE MOLECULE AND USES THEREFOR
 6 FILE REFERENCE: 38155-20002.20
 7 CURRENT APPLICATION NUMBER: US/09/515,806
 8 CURRENT FILING DATE: 2000-02-29
 9 NUMBER OF SEQ ID NOS: 22
 10 SOFTWARE: Patentia Ver. 2.1
 11 SEQ ID NO 13
 12 LENGTH: 231
 13 TYPE: PRT
 14 ORGANISM: Artificial Sequence
 15 FEATURE:
 16 OTHER INFORMATION: Description of Artificial Sequence: Consensus
 17 OTHER INFORMATION: Kinase sequence
 US-09 515-806 13

Query Match 81.8% Score 16 DB 12 Length 231
 Best Local Similarity 75.0% Pct Id 87
 Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 1 MLLCKPPF 8
 DB 176 LLLCKPPF 193

Search completed: November 14, 2003, 13:43:47
 Job time : 20.5857 secs

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY : MLGKPPF 8
 Db 251 MLGKPPF 258

RESULT 3
 S68462
 C:Species: Arabidopsis thaliana (mouse ear cross)
 C:Accession: S68462; A54141
 R:MiZoguchi, T.; Hayashida, N.; Yamaguchi, Shinozaki, K.; Kawada, H.; Shinozaki, K.
 FEBS Lett. 358, 199-204, 1995
 A:Title: Two genes that encode ribosomal protein S6 kinase homologs are induced by cold
 A:Reference number: S68462; MUID:95129712; PMID:7828736
 A:Accession: S68462
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-465 <M12>
 A:Cross-references: EMBL:D42056; NID:g867996; P1DN:BAAC7656.1; PID:d1008238; PID:g867997
 R:Zhang, S.H.; Lawton, M.A.; Hunter, T.; Lamb, C.J.
 J. Biol. Chem. 269, 17586-17592, 1994
 A:Title: atpK1, a novel ribosomal protein kinase gene from Arabidopsis. I. Isolation, characterization and expression
 A:Reference number: A54141; MUID:94292519; PMID:7912697
 A:Contents: ecotype Landsberg erecta
 A:Accession: A54141
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-465 <ZHA>
 A:Cross-references: GB:D29030; NID:g509307; PID:AA21142.1; PID:g508308
 A:Note: sequence extracted from NCBI; backbone (NCBIN:149344, NCBI:P149415)
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 C:Keywords: AtP; phosphotransferase; serine/threonine-specific protein kinase
 F:132-389/Domain: protein kinase homology <KIN>
 F:140-148/Region: protein kinase ATP-binding motif

Query Match 88.6%; Score 39; DB 2; Length 465;
 Best Local Similarity 87.5%; Pred. No. 7;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : MLGKPPF 8
 Db 324 MLGKPPF 331

RESULT 4
 S68463
 C:Species: Arabidopsis thaliana (mouse ear cross)
 C:Accession: S68463
 R:MiZoguchi, T.; Hayashida, N.; Yamaguchi, Shinozaki, K.; Kawada, H.; Shinozaki, K.
 FEBS Lett. 358, 199-204, 1995
 A:Title: Two genes that encode ribosomal protein S6 kinase homologs are induced by cold
 A:Reference number: S68462; MUID:95129712; PMID:7828736
 A:Accession: S68463
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-471 <M12>
 A:Cross-references: EMBL:D42061; NID:g1526412; PIDN:BAAC766.1; PID:d1008243; PID:g867999
 C:Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolog
 C:Keywords: AtP; phosphotransferase; serine/threonine specific protein kinase
 F:138-395/Domain: protein kinase homology <KIN>
 F:146-154/Region: protein kinase ATP-binding motif

Query Match 88.6%; Score 39; DB 2; Length 471;
 Best Local Similarity 87.5%; Pred. No. 7.8;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : MLGKPPF 8
 Db 324 MLGKPPF 331

Db 330 MLGKPPF 337

RESULT 5
 S56639
 C:Species: ribosomal protein S6 kinase homolog (clone AspKil) - oat
 N:Alternate names: mitogen-activated protein kinase pp70 homolog
 C:Species: Avena sativa (cat)
 C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 24-Sep-1999
 C:Accession: S56639
 R:Huttly, A.K.; Phillips, A.L.
 Plant Mol. Biol. 27, 1043-1052, 1995
 A:Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that
 A:Reference number: S56638; MUID:95284341; PMID:7766874
 A:Accession: S56639
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-480 <HUT>
 A:Cross-references: EMBL:X79992; NID:g871985; PIDN:CAA56313.1; PID:g871986
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 C:Keywords: ATP; phosphotransferase; protein kinase
 F:149-407/Domain: protein kinase homology <KIN>
 F:157-165/Region: protein kinase ATP-binding motif

Query Match 88.6%; Score 39; DB 2; Length 480;
 Best Local Similarity 87.5%; Pred. No. 8;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : MLGKPPF 8
 Db 341 MLGKPPF 348

RESULT 6
 T43402
 C:Species: Schizosaccharomyces pombe
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
 C:Accession: T43402; T41425
 R:Niederberger, C.
 submitted to the EMBL Data Library, July 1998
 A:Reference number: Z22486
 A:Accession: T43402
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-592 <NIE>
 A:Cross-references: EMBL:X99280; PIDN:CAA67672.1
 A:Experimental source: strain h90
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
 submitted to the EMBL Data Library, September 1998
 A:Reference number: Z21954
 A:Accession: T41425
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-592 <WOG>
 A:Cross-references: EMBL:AL031798; PIDN:CAA211194.1; GSPDB:GN00068; SPDB:SPCC576.15C
 A:Experimental source: strain 972b; cosmid c576
 C:Genetics:
 A:Gene: KSG1; SPCC576.15C
 A:Map position: 3
 A:Introns: 191/3
 C:Keywords: phosphotransferase

Query Match 88.6%; Score 39; DB 2; Length 592;
 Best Local Similarity 87.5%; Pred. No. 9.9;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : MLGKPPF 8
 Db 305 MLGKPPF 312

RESULT 7

T38254
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
 C:Accession: T38254; T45128
 R:Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, N.A.; Wood, V.
 Submitted to the EMBL Data Library, August 1995
 A:Reference number: 221781
 A:Accession: T38254
 A:Status: preliminary; translated from GB/EXBL/DBEJ
 A:Molecule type: DNA
 A:Residues: 1-483 <BRO>
 A:Cross-references: EMBL:Z98559; PIDN:CA811167.1; GSPDB:KNC0366; SPDB:SPAC23C11.16
 A:Experimental source: strain 972H; cosmid c23C11
 R:Okkura, H.; Hagar, L.M.; Glover, D.M.
 Genes Dev. 9, 1059-1073, 1995
 A:Title: The conserved Schizosaccharomyces pombe kinase pcd1, required to form a bipolar
 A:Reference number: 222921; MUID:95262899; PMID:7744248
 A:Accession: T45128
 A:Status: preliminary; translated from GB/EXBL/DBEJ
 A:Molecule type: DNA
 A:Residues: 1-693 <CHK>
 A:Cross-references: EMBL:X85758; NID:9887640; PIDN:CAA59766.1; PID:9887641
 A:Experimental source: strain 972 derivative
 C:Genetics:
 A:Gene: pcd1; SPAC23C11.16
 A:Map position: 1
 C:Function:
 A:Description: required to form a bipolar spindle and early in the regulatory cascade th
 C:Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolo
 C:Keywords: phosphotransferase; protein kinase

Query Match 88.6%; Score 39; DB 2; Length 653;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLGKPPF 3
 |||||
 DB 233 LLGKPPF 240

RESULT 8
 A48144
 protein kinase CDC5 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein kinase PKX2; protein YMR220C; protein YMR001C
 C:Species: Saccharomyces cerevisiae
 C:Date: 30-Jun-1995 #sequence_revision 30-Jun-1995 #text_change 24-Sep-1999
 C:Accession: A48144; S53030; S27445
 R:Kitada, K.; Johnson, A.L.; Johnston, L.H.; Sugino, A
 Mol. Cell. Biol. 13, 4445-4457, 1993
 A:Title: A multicopy suppressor gene of the Saccharomyces cerevisiae G-1 cell cycle muta
 A:Reference number: A48144; MUID:93109479; PMID:831244
 A:Accession: A48144
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-705 <KIT>
 A:Cross-references: EMBL:M84420; NID:9172186; PIDN:AA483576.1; PID:g172187
 R:Devlin, K.; Churcher, C.M.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53028
 A:Accession: S53030
 A:Molecule type: DNA
 A:Residues: 1-705 <DEV>
 A:Cross-references: EMBL:Z48613; NID:9725645; PIDN:CAA85516.1; PID:g728648; MIPS:YMR001C
 A:Experimental source: strain AB972
 C:Genetics:
 A:Gene: SGD: CDC5, PKX2
 A:Cross-references: SGD: S0004603; MIPS: YMR001C
 A:Map position: 13R
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
 C:Keywords: ATP; cell cycle control; phosphotransferase; protein kinase
 F:80-137/Domain: protein kinase homology <KIT>

Query Match 88.6%; Score 39; DB 2; Length 705;
 Best Local Similarity 75.0%; Pred. No. 12;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 |||||
 DB 274 LLGKPPF 281

RESULT 9
 S69657
 hypothetical protein YDR490C - yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002
 C:Accession: S69657
 R:Dietrich, F.S.
 submitted to the EMBL Data Library, August 1995
 A:Description: The sequence of S. cerevisiae cosmid 9410, 8035, 8166, and 9787.
 A:Reference number: S69554
 A:Accession: S69657
 A:Molecule type: DNA
 A:Residues: 1-766 <DIE>
 A:Cross-references: EMBL:U33C50; NID:g927726; PIDN:AAB64917.1; PID:g927745; MIPS:YDR4
 C:Genetics:
 A:Gene: SGD: PKH1
 A:Cross-references: SGD: S0002898
 A:Map position: 4R
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho
 C:Keywords: ATP
 F:123-391/Domain: protein kinase homology <KIN>
 F:131-139/Region: protein kinase ATP-binding motif

Query Match 88.6%; Score 39; DB 2; Length 766;
 Best Local Similarity 87.5%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 |||||
 DB 330 MLGKPPF 337

RESULT 10
 S45894
 probable serine/threonine-specific protein kinase (EC 2.7.1.1) - yeast (Sacc
 N:Alternate names: protein YBR312
 C:Species: Saccharomyces cerevisiae
 C:Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002
 C:Accession: S45884; S46558
 R:Grivelli, L.A.; de Haan, M.; Maat, M.J.; Smits, P.H.M.
 submitted to the Protein Sequence Database, August 1994
 A:Reference number: S45875
 A:Accession: S45884
 A:Molecule type: DNA
 A:Residues: 1-525 <GRI>
 A:Cross-references: EMBL:Z35897; NID:g536370; PIDN:CAA84970.1; PID:g536371; MIPS:YBR
 A:Experimental source: strain S288C
 R:Smits, P.H.M.; de Haan, M.; Maat, C.; Grivelli, L.A.
 Yeast 10(Suppl.A), S75-S80, 1994
 A:Title: The complete sequence of a 33 kb fragment on the right arm of chromosome II
 ly identified genes and a homologue of the SCOL gene.
 A:Reference number: S46551; MUID:94378725; PMID:8091864
 A:Accession: S46558
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-525 <SMI>
 A:Cross-references: EMBL:X76078; NID:g498748; PIDN:CAA53684.1; PID:g498756
 A:Experimental source: strain S288C
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 199
 C:Genetics:
 A:Cross-references: SGD: S0000232
 A:Map position: 2R
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F126-423/Domain: protein kinase homology <KIN>
 F134-142/Region: protein kinase ATP-binding motif
 F1277/Active Site: Asp #status predicted

Query Match 86.4% Score 38; DB 2; Length 525;
 Best Local Similarity 75.0%; Pred. No. 16;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGKPPF 8

|||||

Db 355 MLGKPPY 362

RESULT 11

S34130

serine/threonine-specific protein kinase PLK (EC 2.7.1.1) - human

N:Alternate names: polo-like protein kinase; protein kinase ptk-1

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999

C:Accession: S34130; 138123; S61543

R:Golsteyn, R.M.; Schultz, S.C.; Bartek, J.; Ziemiedzi, A.; Ried, T.; Nigg, E.A.

submitted to the EMBL Data Library, June 1993

A:Description: Cloning and characterization of a novel human protein kinase ptk-1 a potent inducer of mitosis

A:Reference number: S34130

A:Accession: S34130

A:Molecule type: mRNA

A:Residues: 1-603 <GOL>

A:Cross-references: EMBL:X73458; NID:9312977; PIDN:CAA61871.1; PIR:G312998

R:Horstrich, U.; Wolf, G.; Brauninger, A.; Karn, T.; Borne, H.; Subramaniam-Waigmann, H.; S

Proc. Natl. Acad. Sci. U.S.A. 91, 1736-1740, 1994

A:Title: Induction and down-regulation of PLK, a human serine/threonine kinase expressed

A:Reference number: A53134; MUID:9417394; PMID:8127874

A:Accession: 138123

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-140, 'P', 142-226, 'E', 228-603 <RES>

A:Cross-references: EMBL:X75912; NID:9460745; PIDN:CAA61871.1; PID:G460769

R:Bräuninger, A.; Strebhardt, K.; Ruebner-Waigmann, H.

Oncogene 11, 1793-1800, 1995

A:Title: Identification and functional characterization of the human and murine polo-like

A:Reference number: S61543; MUID:96058906; PMID:7478607

A:Accession: S61543

A:Molecule type: DNA

A:Residues: 1-122, 'T', 124-136 <BRA>

A:Cross-references: EMBL:X50725; NID:9416113; PIDN:CAA61871.1; PID:G1061144

A:Experimental source: placenta

A:Note: the authors translated the codon AAT for leucine but as Val

C:Genetics:

A:Gene: GOL, PLK

A:Cross-references: CDB:331003

A:Map position: 17p11-17p12

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology

C:Keywords: ATP; phosphotransferase; serine/threonine specific protein kinase

F151-325/Domain: protein kinase homology <KIN>

Query Match

Best Local Similarity 86.4% Score 38; DB 2; Length 603;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGKPPF 8

|||||

Db 244 LLVGKPPF 251

RESULT 12

A47545

protein kinase (EC 2.7.1.37) ptk - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999

C:Accession: A47545

R:Clay, F.J.; McEwen, S.J.; Bertonecello, I.; Wilks, A.F.; Dunn, A.R.
 Proc. Natl. Acad. Sci. U.S.A. 90, 4882-4886, 1993
 A:Title: Identification and Cloning of a protein kinase-encoding mouse gene, Plk, re
 A:Reference number: A47545; MUID:93281660; PMID:8099445

A:Accession: A47545

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-603 <CLA>

A:Cross-references: GB:L06144; NID:9309461; PIDN:AAA39948.1; PID:G309462

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hc

C:Keywords: ATP; phosphotransferase

F:51-305/Domain: protein kinase homology <KIN>

Query Match 86.4% Score 38; DB 2; Length 603;

Best Local Similarity 75.0%; Pred. No. 16;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGKPPF 8

|||||

Db 244 LLVGKPPF 251

RESULT 13

A54596

Protein kinase - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999

C:Accession: A54596

R:Lake, R.J.; Jelinek, W.R.

Mol. Cell. Biol. 13, 7793-7801, 1993

A:Title: Cell cycle- and terminal differentiation-associated regulation of the mouse

A:Reference number: A54596; MUID:94567140; PMID:7902533

A:Accession: A54596

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-603 <RES>

A:Cross-references: GB:L19558; NID:9403473; PIDN:AAA16071.1; PID:G403474

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hc

F:51-305/Domain: protein kinase homology <KIN>

Query Match

Best Local Similarity 86.4% Score 38; DB 2; Length 603;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGKPPF 8

|||||

Db 244 LLVGKPPF 251

RESULT 14

A32545

Protein kinase C (EC 2.7.1.1) - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 19-Jun-1999

C:Accession: A32545

R:Rosenthal, A.; Rhee, L.; Yadegari, R.; Paro, R.; Ullrich, A.; Goeddel, D.V.

EMBO J. 6, 433-441, 1987

A:Title: Structure and nucleotide sequence of a Drosophila melanogaster protein kin

A:Reference number: A32545; MUID:87218499; PMID:3107983

A:Accession: A32545

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-639 <ROS>

A:Cross-references: GB:X05076; NID:98352; PIDN:CAA26736.1; PID:G8353; GB:Y00042

C:Genetics:

A:Gene: FlyBase:PKC3E

A:Cross-references: FlyBase:FBgn0003091

C:Superfamily: protein kinase C alpha; protein kinase C2 region homology; protein

C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F:46-95/Domain: protein kinase C zinc-binding repeat homology <K21>

F:11-160/Domain: protein kinase C zinc-binding repeat homology <K22>

F:161-273/Domain: protein kinase C2 region homology <K2>

F:339-599/Domain: protein kinase homology <KIN>

F:347-355/Region: protein kinase ATP-binding motif

Query Match: 84.1%; Score 37; DB 2; Length 639;
Best Local Similarity: 75.0%; Pred. No. 27;
Matches: 6; Conservative: 2; Mismatches: 0; Indels: 0; Gaps: 0;

QY : MLGKPPF 8
||:||||
DB 513 MLVGPPF 540

RESULT 15

G89894 protein kinase [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 16 May 2001 #text_change 22-Oct-2001
C:Accession: G89894

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yurawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, M.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of "elicitin-resistant" Staphylococcus aureus.

A:Reference number: A89758; MUID:21311953; PMID:1141846

A:Accession: G89894

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-664 <KUR>

A:Cross-references: GB:BA000018; FID:51370120; PIDN:BAF42315.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: SA1063

Query Match: 84.1%; Score 37; DB 2; Length 664;
Best Local Similarity: 75.0%; Pred. No. 28;
Matches: 6; Conservative: 2; Mismatches: 0; Indels: 0; Gaps: 0;

QY : MLGKPPF 8
||:||||
DB 202 MLVGPPF 209

RESULT 16

T22318 hypothetical protein F46F6.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15 Oct-1999 #text_change 16-Feb-2000
C:Accession: T22318; T27624

R:Coftage, A.

submitted to the EMBL Data Library, July 1996

A:Reference number: Z19547

A:Accession: T22318

A>Status: preliminary; translated from GB:EMBL:U00028

A:Molecule type: DNA

A:Residues: 1-1018 <W1>

A:Cross-references: EMBL:Z50028; PIDN:CAA93445.1; GSPDB:GN00028; GESP:F46F6.2

A:Experimental source: Clone F46F6

R:Kershaw, J.

submitted to the EMBL Data Library, July 1995

A:Reference number: Z20394

A:Accession: T27624

A>Status: preliminary; translated from GB:EMBL:U00028

A:Molecule type: DNA

A:Residues: 1-1018 <W12>

A:Cross-references: EMBL:Z50029; PIDN:CAA93445.1; GSPDB:GN00028; GESP:F46F6.2

A:Experimental source: clone ZC504

C:Genetics:

A:Gene: GESP:F46F6.2

A:Map position: X

A:Introns: 41/2; 139/2; 446/3; 520/1; 601/3; 859/1; 923/3; 972/3; 1017/2

A:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match: 84.1%; Score 37; DB 2; Length 1018;

Best Local Similarity: 75.0%; Pred. No. 41;

Matches: 6; Conservative: 2; Mismatches: 0; Indels: 0; Gaps: 0;

QY : MLGKPPF 8
||:||||
DB 883 MLVGPPF 890

RESULT 17

S51899

probable protein kinase HRC1081 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein G0784; protein YOL100w

C:Species: Saccharomyces cerevisiae

C:Date: 05-May-1995 #sequence_revision 03-Aug-1995 #text_change 19-Apr-2002

A:Accession: S51899; S59175; S66796

R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.

submitted to the EMBL Data Library, January 1995

A:Description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV including

and a Delta.

A:Reference number: S51848

A:Accession: S51899

A:Molecule type: DNA

A:Residues: 1-1081 <VAN>

A:Cross-references: EMBL:Z48149; NID:G663234; PIDN:CAA88162.1; PID:G663254

R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.

Yeast 11, 1069-1075, 1995

A:Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including a

delta element.

A:Reference number: S59156; MUID:96076631; PMID:7502582

A:Accession: S59175

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1081 <VAN>

A:Cross-references: EMBL:Z48149; NID:G663234; PIDN:CAA88162.1; PID:G663254

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995

R:Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S66793

A:Accession: S66796

A:Molecule type: DNA

A:Residues: 1-1081 <DJR>

A:Cross-references: EMBL:Z74842; NID:G1419951; PIDN:CAA99113.1; PID:e251892; PID:G14

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:PKH2

A:Cross-references: SGD:SC005460

A:Map position: 15L

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho

C:Keywords: ATP; phosphotransferase

F:177-443/Domain: protein kinase homology <KIN>

F:185-193/Region: protein kinase ATP-binding motif

Query Match: 84.1%; Score 37; DB 2; Length 1081;

Best Local Similarity: 75.0%; Pred. No. 46;

Matches: 6; Conservative: 1; Mismatches: 1; Indels: 0; Gaps: 0;

QY : MLGKPPF 8
||:||||
DB 382 MLGKPPF 389

RESULT 18

A56155

tumor suppressor protein warts (EC 2.7.1.-) - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 24-Sep-1999

A:Accession: A56155

R:Gustice, R.W.; Zilian, O.; Woods, D.F.; Noll, M.; Bryant, P.J.

Genes Dev. 9, 534-546, 1995

A:Title: The Drosophila tumor suppressor gene warts encodes a homolog of human mycto

A:Reference number: A56155; MUID:95212904; PMID:7698644

A:Accession: A56155

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1099 <JUS>
 A:Cross-references: GB:L98837; NID:G755007; PIDN:AAA73959.1; PID:G755008
 C:Genetics:
 A:Gene: wts
 A:Cross-references: FlyBase:FBgn001733
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology
 C:Keywords: ATP; phosphotransferase
 F:711-1014/Domain: protein kinase homology <XIN>
 F:719-727/Region: protein kinase ATP-binding motif

Query Match 84.1%; Score 37; DB 2; Length 1039;
 Best Local Similarity 75.0%; Pred. No. 46;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 I:|||||
 DB 948 MLVGQPPF 955

RESULT 19
 S28754
 MADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 blue mussel mitochondrion (fragment)
 C:Species: Mitochondrion Mytilus edulis (blue mussel)
 C>Date: 12-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 03-Jun-2002
 C:Accession: S28754; S28755
 R:Heffmann, R.J.; Boore, J.L.; Brown, W.M.
 C:Genetics: 131, 397, 412, 1992
 A:Title: A novel mitochondrial genome organization for the blue mussel, Mytilus edulis.
 A:Reference number: S28743; MUID:92354892; PMID:1186586
 A:Accession: S28754
 A:Molecule type: DNA
 A:Residues: 1-131; 32-217 <BRC>
 A:Cross-references: EMBL:M83760; EMBL:M83761
 C:Genetics:
 A:Gene: MD2
 A:Genome: Mitochondrion
 A:Genetic code: SGC4
 C:Superfamily: MADH dehydrogenase (ubiquinone) chain 2
 C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 81.8%; Score 36; DB 2; Length 217;
 Best Local Similarity 75.0%; Pred. No. 14;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 I:|||||
 DB 135 MLVGQPPF 142

RESULT 20
 T43221
 serine/threonine-specific protein kinase (EC 2.7.1.1) - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 14-Mar-2000
 C:Accession: T43221
 R:Schumacher, C.M.; Golden, A.; Donovan, P.J.
 J. Cell. Biol. 143, 1635-1646, 1998
 A:Title: AIR-2: An aurora/Tip1-related protein kinase associated with chromosomes and mitosis
 A:Reference number: Z22347; MUID:99069487; PMID:952157
 A:Accession: T43221
 A:Status: preliminary; translated from GS/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-305 <SCH>
 A:Cross-references: EMBL:AF071207; PIDN:AA070945.1
 C:Genetics:
 A:Gene: AIR-2
 A:Map position: 1
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: phosphotransferase

Query Match 81.8%; Score 36; DB 2; Length 355;
 Best Local Similarity 85.7%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPF 8
 I:|||||
 DB 220 LVGKPPF 226

RESULT 21

B87790
 protein B0207.4 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
 C:Accession: B87790
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999.
 A:Accession: B87790
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-329 <STO>
 A:Cross-references: GB:chr_I; PIDN:AA852459.1; PID:G1943805; GSPDB:GN00019; CESP:B0207.4
 C:Genetics:
 A:Gene: B0207.4
 A:Map position: 1
 C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 81.8%; Score 36; DB 2; Length 329;
 Best Local Similarity 85.7%; Pred. No. 21;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPF 8
 I:|||||
 DB 244 LVGKPPF 250

RESULT 22

S52242
 protein kinase (EC 2.7.1.1) p46XIEg22 - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 18-Jun-1999
 C:Accession: S52242
 R:Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
 submitted to the EMBL Data Library, October 1992
 A:Description: Eg2, selected by differential screening encodes a new Xenopus protein kinase
 A:Reference number: S52242
 A:Accession: S52242
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-389 <POG>
 A:Cross-references: EMBL:Z17206; NID:G609279; PIDN:CAA78914.1; PID:G609280
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphotransferase
 F:119-371/Domain: protein kinase homology <XIN>
 F:127-135/Region: protein kinase ATP-binding motif

Query Match 81.8%; Score 36; DB 2; Length 389;
 Best Local Similarity 85.7%; Pred. No. 25;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPF 8
 I:|||||
 DB 311 LVGKPPF 317

RESULT 23

JC5974
 aurora-related kinase 1 (EC 2.7.1.1) - human
 C:Species: Homo sapiens (man)
 C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jan-2000
 C:Accession: JC5974
 R:Shindo, M.; Nakano, H.; Kuroyanagi, H.; Shirasawa, T.; Mihara, M.; Gilbert, D.J.,

Query Match 81.8%; Score 36; DB 2; Length 355;
 Best Local Similarity 85.7%; Pred. No. 19;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Biochem. Biophys. Res. Commun. 244, 285-292, 1998
 A:Title: cDNA cloning, expression, subcellular localization, and chromosomal assignment
 A:Reference number: JC5974; MUID:98183439; PMID:9514916
 A:Accession: JC5974
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-403 <SH1>
 A:Cross-references: GB:A008551
 C:Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolog
 C:Keywords: phosphotransferase
 F:131-383/Domain: protein kinase homology <KIN>
 Query Match 81.8%; Score 36; DB 2; Length 433;
 Best Local Similarity 85.7%; Pred. No. 26;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LLGKPPF 8
 Db 323 LVGKPPF 329
 RESULT 24
 S52243
 P46Eg265 protein - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 24-Sep-1999
 C:Accession: S52243; S34642; I51695
 R:Kohgi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
 submitted to the EMBL Data Library, October 1992
 A:Description: Egg, selected by differential screening encodes a new Xenopus protein kin
 A:Reference number: S52242
 A:Accession: S52243
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-407 <ROG>
 A:Cross-references: EMBL:Z17207; NID:9603281; PIDN:CAA80926.1; PID:G394757
 R:Bouvet, P.; Omilli, F.; Axiot-Bornemai, V.; Legagneux, V.; Roghi, C.; Bassett, T.; Osb
 submitted to the EMBL Data Library, June 1993
 A:Description: Targeted deadenylation of specific mRNAs in Xenopus embryos by a mechani
 A:Reference number: S34642
 A:Accession: S34642
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 328-407 <BOU>
 A:Cross-references: EMBL:Z24453; NID:9394756; PIDN:CAA80926.1; PID:G394757
 R:Bouvet, P.; Omilli, F.; Axiot-Bornemai, V.; Legagneux, V.; Roghi, C.; Bassett, T.; Osb
 Cell, Biol. 14, 1893-1900, 1994
 A:Title: The deadenylation conferred by the 3' untranslated region of a developmentally
 A:Reference number: I51695; MUID:94158861; PMID:8114721
 A:Accession: I51695
 A:Status: preliminary; translated from JN/EMBL/2526
 A:Molecule type: mRNA
 A:Residues: 328-407 <BOU>
 A:Cross-references: EMBL:Z24453; NID:9394756; PIDN:CAA80926.1; PID:G394757
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 C:Keywords: ATP; phosphotransferase; protein kinase
 F:138-393/Domain: protein kinase homology <KIN>
 F:146-154/Region: protein kinase ATP-binding motif
 Query Match 81.8%; Score 36; DB 2; Length 437;
 Best Local Similarity 85.7%; Pred. No. 26;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LLGKPPF 8
 Db 330 LVGKPPF 336
 RESULT 25
 B55748
 protein kinase (EC 2.7.1.37); Sak-b - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 19-Dec-1997

C:Accession: B55748
 R:Rode, C.; Motro, B.; Yousefi, S.; Heffernan, M.; Dennis, J.W.
 Proc. Natl. Acad. Sci. U.S.A. 91, 6388-6392, 1994
 A:Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosoph
 A:Reference number: A55748; MUID:94294387; PMID:8022793
 A:Accession: B55748
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-465 <FOO>
 A:Cross-references: GB:L29480
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
 C:Keywords: ATP; phosphotransferase
 F:1C-265/Domain: protein kinase homology <KIN>
 F:18-26/Region: protein kinase ATP-binding motif
 Query Match 81.8%; Score 36; DB 2; Length 465;
 Best Local Similarity 62.5%; Pred. No. 30;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGKPPF 8
 Db 204 LLGKPPF 211
 RESULT 26
 D88640
 protein F55A8.2 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
 C:Accession: D88640
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bic
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C-
 A:Reference number: Science 283, 35, 1999; Science 283, 2103, 1999;
 A:Accession: D88640
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-521 <STO>
 A:Cross-references: GB:chr_IV; PIDN:AAC19186.1; PID:G3193148; GSPDB:GN00022; GSP:F55
 C:Genetic:cs
 A:Gene: F55A8.2
 A:Map position: 4
 C:Superfamily: cGMP-dependent protein kinase; cAMP receptor protein cyclic nucleotide
 Query Match 81.8%; Score 36; DB 2; Length 521;
 Best Local Similarity 62.5%; Pred. No. 34;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGKPPF 8
 Db 401 LLGKPPF 408
 RESULT 27
 T41509
 serine/threonine-protein kinase - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
 R:Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, March 1999
 A:Reference number: Z21939
 A:Accession: T41509
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-830 <MUR>
 A:Cross-references: EMBL:ALC049522; PIDN:CA840012.1; GSPDB:GN00068; SPDB:SPCC63.08C
 A:Experimental source: strain 972h-; cosmid c63
 C:Genetics:
 A:Gene: SPDB:SPCC63.08C
 A:Map position: 3

A: Intons: 34/3
C: Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 81.8%; Score 36; DB 2; Length 830;
Best Local Similarity 75.0%; Pred. No. 55;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||||
DB 242 NAVGKPPF 249

RESULT 28
A55748
protein kinase (EC 2.7.1.37) Sak-a - mouse
C: Species: Mus musculus (house mouse)
C: Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 24-Sep-1999
C: Accession: A55748
R: Pöde, C.; Nictro, B.; Yousefi, S.; Hefferman, M.; Dennis, J.W.
Proc. Natl. Acad. Sci. U.S.A. 91: 6368-6392, 1994
A: Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosophila
A: Reference number: A55748; MUID:94294387; PMID:8022793
A: Accession: A55748
A: Status: Preliminary
A: Molecule type: mRNA
A: Residues: 1-925 <FOD>
A: Cross-references: GB:L29479; NID:9497869; PIDN:AA037648.1; PID:9487870
C: Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolo
C: Keywords: ATP; phosphotransferase
F: 10-265/Domain: protein kinase homology <KIN>
F: 18-26/Region: protein kinase ATP-binding motif

Query Match 81.8%; Score 36; DB 2; Length 925;
Best Local Similarity 62.5%; Pred. No. 61;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||||
DB 204 MLLGRPPF 211

RESULT 19
S32947
hupK protein - Rhodobacter capsulatus
C: Species: Rhodobacter capsulatus
C: Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C: Accession: S32947; B38532; S25691
R: Colbeau, A.; Richard, P.; Foussaint, B.; Caballero, F.; Elster, C.; Delphin, C.; Sm
Mol. Microbiol. 15: 29, 1991
A: Title: Organization of the genes necessary for hydrogenase expression in Rhodobacter c
A: Reference number: S32947; MUID:93326620; PMID:1414119
A: Accession: S32947
A: Status: Preliminary
A: Molecule type: DNA
A: Residues: 1-294 <COL>
A: Cross-references: EMBL:215089; NID:9313668; PIDN:AA78603.1; PID:946048
R: Xu, H.W.; Walli, J.D.
J. Bacteriol. 173: 2401-2405, 1991
A: Title: Clustering of genes necessary for hydrogen oxidation in Rhodobacter capsulatus
A: Reference number: A38532; MUID:91177833; PMID:2007559
A: Accession: B38532
A: Status: Preliminary
A: Molecule type: DNA
A: Residues: 1-69, 'A', 71-294 <XUA>
A: Cross-references: GB:M55089; NID:9151949; PIDN:AA72604.1; PID:9151951
C: Genetics:
A: Gene: hupK

Query Match 79.5%; Score 35; DB 2; Length 294;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 7
|||||

Db 31 LLLGKPP 37
|||||

RESULT 30
I38133
protein kinase (EC 2.7.1.37) Ndr - human
C: Species: Homo sapiens (man)
C: Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 24-Sep-1999
C: Accession: I38133
R: Millward, T.; Cron, P.; Hemmings, B.A.
Proc. Natl. Acad. Sci. U.S.A. 92: 5022-5026, 1995
A: Title: Molecular cloning and characterization of a conserved nuclear serine/threon
A: Reference number: I38133; MUID:95281588; PMID:7761441
A: Accession: I38133
A: Status: Preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-465 <RES>
A: Cross-references: EMBL:235102; NID:9854169; PIDN:CAA844485.1; PID:9854170
C: Genetics:
A: Gene: GDB:NDR
A: Cross-references: GDB:696268
C: Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho
C: Keywords: ATP; phosphotransferase
F: 87-182/Domain: protein kinase homology <KIN>
F: 95-103/Region: protein kinase ATP-binding motif

Query Match 79.5%; Score 35; DB 2; Length 465;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
|||||
DB 315 MLLGYPPF 322

RESULT 31
F82190
sigma-54 dependent response regulator VC1522 [imported] - Vibrio cholerae (strain N1
C: Species: Vibrio cholerae
C: Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Mar-2003
C: Accession: F82190
R: Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R
Chardson, D.; Ermoeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Seller
L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406: 477-483, 2000
A: Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A: Reference number: AB2035; MUID:23408833; PMID:10952301
A: Accession: F82190
A: Status: Preliminary
A: Molecule type: DNA
A: Residues: 1-484 <HEI>
A: Cross-references: GB:AE004230; GB:AE003852; NID:9656018; PIDN:AAF94676.1; GSPDB:G
A: Experimental source: serogroup O1; strain N16961; biotype El Tor
C: Genetics:
A: Gene: VC1522
A: Map position: 1
C: Superfamily: response regulator of the NtrC type; response regulator homology; RNA

Query Match 79.5%; Score 35; DB 2; Length 484;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPP 7
|||||
DB 382 LLLGKPP 388

RESULT 32
T17298
hypothetical protein DKFP586M2123.1 - human (fragment)
C: Species: Homo sapiens (man)
C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000

C:Accession: J17298
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 C:Accession: J17298
 A:Reference number: J17298
 A:Accession: J17298
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-511 <KNS>
 A:Cross-references: EMBL:AL117551
 A:Experimental source: adult uterus; clone DKF2P586X2121
 C:Genetics:
 A:Note: DKF2P586M2123.1
 C:Superfamily: unassigned EGF-related proteins; EGF homology

Query Match 79.5%; Score 35; DB 2; Length 511;
 Best Local Similarity 85.7%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 7
 DB 410 LLLGKPPF 416

RESULT 33
 K1HUCA

C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 C:Accession: S09496
 R:Finckenzieher, G.; Waxme, D.; Hsu, H.
 Nucleic Acids Res. 18, 2183, 1990
 A:Title: Sequence of human protein kinase C alpha
 A:Reference number: S09496; MUID:90245676; PMID:2336401
 A:Accession: S09496
 A:Molecule type: mRNA
 A:Residues: 1-672 <FIN>
 A:Cross-references: EMBL:X52479; NID:G35492; PIDN:CAA16718.1; PID:G35483
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-specific inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters.
 C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may
 C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
 C:Genetics:
 A:Gene: GDB:PRKCA
 A:Cross-references: GDB:128015; OMIM:176360
 A:Map position: 17q22-17q23.2
 C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C
 C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding
 F:19-22/Region: pseudophosphorylation motif
 F:22-27/Region: protein kinase C zinc-binding repeat homology <K21>
 F:37-66/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:102-151/Domain: protein kinase C C2 region homology <KIN>
 F:152-264/Domain: protein kinase C C2 region homology <K21>
 F:337-597/Domain: protein kinase C C2 region homology <KIN>
 F:345-353/Region: protein kinase C C2 region homology <K21>
 F:368/Active site: Lys #status predicted
 F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 79.5%; Score 35; DB 1; Length 672;
 Best Local Similarity 75.0%; Pred. No. 69;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 DB 531 MLGKPPF 538

RESULT 35
 K1MSCA

C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 C:Accession: S07104; JS0078
 R:McGidish, T.; Vazurek, N.
 Nature 342, 807-811, 1989
 A:Title: A mutant protein kinase C that can transform fibroblasts.
 A:Reference number: S07104; MUID:90099082; PMID:2601739
 A:Accession: S07104
 A:Molecule type: mRNA
 A:Residues: 1-672 <MEG>
 A:Cross-references: GB:X51603; NID:949938; PIDN:CAA36908.1; PID:949939
 A:Experimental source: strain Balb/C
 R:Rose-John, S.; Dietrich, A.; Marks, F.
 Gene 74, 465-471, 1988
 A:Title: Molecular cloning of mouse protein kinase C (PKC) cDNA from Swiss 3T3 fibroblasts
 A:Reference number: JS0078; MUID:89232737; PMID:2469625
 A:Accession: JS0078
 A:Molecule type: mRNA
 A:Residues: 1-146, 'D', 148-217, 'N', 219-276, 'AH', 279-312, 'V', 314-466, 'N', 468-471, 'N', 471
 A:Cross-references: GB:X25811
 A:Note: The authors translated the codon AAC for residue 141 as Lys; the sequence shc
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-specific inositol phospholipids. This protein is a receptor for tumor-promoting phorbol ester
 C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane
 C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
 C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C
 C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bin
 F:19-29/Region: pseudophosphorylation motif
 F:22-27/Region: protein kinase C zinc-binding repeat homology <K21>
 F:37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:102-151/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:152-264/Domain: protein kinase C C2 region homology <K21>
 F:337-597/Domain: protein kinase C C2 region homology <KIN>

N:Alternate names: protein kinase C type III
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 C:Accession: S02248; SC2620
 R:Ono, Y.; Fujii, T.; Igarashi, K.; Kikkawa, U.; Ogita, K.; Nishizuka, Y.
 Nucleic Acids Res. 16, 5199-5200, 1988
 A:Title: Nucleotide sequences of cDNAs for alpha and gamma subtypes of rat brain pr
 A:Reference number: S02129; MUID:88262515; PMID:3387228
 A:Accession: S02248
 A:Molecule type: mRNA
 A:Residues: 1-672 <ONC>
 A:Cross-references: EMBL:X07285; NID:G56913; PIDN:CAA30286.1; PID:G56914
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-specific inositol phospholipids. This protein is a receptor for tumor-promoting phorbol ester
 C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane
 C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
 C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C
 C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bin
 F:19-29/Region: pseudophosphorylation motif
 F:22-27/Region: protein kinase C zinc-binding repeat homology <K21>
 F:37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:102-151/Domain: protein kinase C C2 region homology <K21>
 F:152-264/Domain: protein kinase C C2 region homology <KIN>
 F:337-597/Region: protein kinase C C2 region homology <KIN>
 F:345-353/Region: protein kinase C C2 region homology <KIN>
 F:368/Active site: Lys #status predicted
 F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 79.5%; Score 35; DB 1; Length 672;
 Best Local Similarity 75.0%; Pred. No. 69;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 DB 531 MLGKPPF 538

RESULT 35
 K1MSCA

C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 C:Accession: S07104; JS0078
 R:McGidish, T.; Vazurek, N.
 Nature 342, 807-811, 1989
 A:Title: A mutant protein kinase C that can transform fibroblasts.
 A:Reference number: S07104; MUID:90099082; PMID:2601739
 A:Accession: S07104
 A:Molecule type: mRNA
 A:Residues: 1-672 <MEG>
 A:Cross-references: GB:X51603; NID:949938; PIDN:CAA36908.1; PID:949939
 A:Experimental source: strain Balb/C
 R:Rose-John, S.; Dietrich, A.; Marks, F.
 Gene 74, 465-471, 1988
 A:Title: Molecular cloning of mouse protein kinase C (PKC) cDNA from Swiss 3T3 fibroblasts
 A:Reference number: JS0078; MUID:89232737; PMID:2469625
 A:Accession: JS0078
 A:Molecule type: mRNA
 A:Residues: 1-146, 'D', 148-217, 'N', 219-276, 'AH', 279-312, 'V', 314-466, 'N', 468-471, 'N', 471
 A:Cross-references: GB:X25811
 A:Note: The authors translated the codon AAC for residue 141 as Lys; the sequence shc
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-specific inositol phospholipids. This protein is a receptor for tumor-promoting phorbol ester
 C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane
 C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
 C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C
 C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bin
 F:19-29/Region: pseudophosphorylation motif
 F:22-27/Region: protein kinase C zinc-binding repeat homology <K21>
 F:37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:102-151/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:152-264/Domain: protein kinase C C2 region homology <K21>
 F:337-597/Domain: protein kinase C C2 region homology <KIN>

F:345-353/Region: protein kinase ATP-binding motif
 F:37-67,70,86/Binding site: zinc (His, Cys, Cys) #status predicted
 F:50-53,75,78/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:102-132,135,151/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:115,118,140,143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:368/Active site: lys #status predicted
 F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 79.5% Score 35; DB 1; Length 672;
 Best Local Similarity 75.0% Pred. No. 69;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 |||
 DB 531 MLAGQPPF 538

RESULT 36
 KIBOC
 protein kinase C (EC 2.7.1.1) alpha - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 C:Accession: C26537
 R:Oono, S.; Kawasaki, H.; Imajoh, S.; Suzuki, K.; Inagaki, M.; Yokokura, H.; Sakoh, T.;
 Nature 325, 161-166, 1997
 A:Title: tissue-specific expression of three distinct types of rabbit protein kinase C.
 A:Reference number: A26037; MUID:87115883; PMID:9039073
 A:Accession: C26037
 A:Molecule type: mRNA
 A:Residues: 1-672 <GN>
 A:Cross-references: EMBL:X04796; NID:gl672; PDC:CAA28483.1; PID:gl673
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-sp
 f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters,
 C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may
 C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
 C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kin
 C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bindi
 F:19-29/Region: phospholipid binding #status experimental
 F:22-27/Region: pseudophosphorylation motif
 F:37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:102-151/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:152-264/Domain: protein kinase C C2 region homology <K2>
 F:337-597/Domain: protein kinase homology <KIN>
 F:345-353/Region: protein kinase ATP-binding motif
 F:37-67,70,86/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:50-53,75,78/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:102-132,135,151/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:115,118,140,143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:368/Active site: lys #status predicted
 F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 79.5% Score 35; DB 1; Length 672;
 Best Local Similarity 75.0% Pred. No. 69;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 |||
 DB 531 MLAGQPPF 538

RESULT 37
 KIBOC
 protein kinase C (EC 2.7.1.1) alpha - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 17-Mar-1997 #sequence_revision 17-Mar-1997 #text_change 11-Jun-1999
 C:Accession: A00621
 R:Parker, P.J.; Coussens, L.; Totty, N.; Rhee, L.; Young, S.; Chen, E.; Stabel, S.; Wate
 Science 233, 853-859, 1986
 A:Title: The complete primary structure of protein kinase C - the major phorbol ester re
 A:Reference number: A00621; MUID:86289426; PMID:3755547
 A:Accession: A00621
 A:Molecule type: mRNA
 A:Residues: 1-672 <FAR>

A:Cross-references: GB:M13973; NID:gl63529; PDC:AAA30706.1; PID:gl63530
 A:Experimental source: brain
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine
 f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol ester
 C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane
 C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
 C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein k
 C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bin
 F:19-29/Region: phospholipid binding #status experimental
 F:22-27/Region: pseudophosphorylation motif
 F:37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:102-151/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:152-264/Domain: protein kinase C C2 region homology <K2>
 F:337-597/Domain: protein kinase homology <KIN>
 F:345-353/Region: protein kinase ATP-binding motif
 F:37-67,70,86/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:50-53,75,78/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:102-132,135,151/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:115,118,140,143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:368/Active site: lys #status predicted
 F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Query Match 79.5% Score 35; DB 1; Length 672;
 Best Local Similarity 75.0% Pred. No. 69;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 |||
 DB 531 MLAGQPPF 538

RESULT 38
 A37237
 protein kinase C (EC 2.7.1.1) I - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 28-Feb-1997
 C:Accession: A37237
 R:Chen, K.; Peng, Z.; Lavi, S.; Kung, H.
 Second Messengers Phosphoproteins 12, 251-260, 1989
 A:Title: Molecular cloning and sequence analysis of two distinct types of Xenopus la
 A:Reference number: A37237; MUID:90172230; PMID:3272298
 A:Accession: A37237
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
 A:Molecule type: mRNA
 A:Residues: 1-676 <CHE>
 C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein
 C:Keywords: ATP; phosphotransferase
 F:42-91/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:107-156/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:157-267/Domain: protein kinase C C2 region homology <K2>
 F:341-601/Domain: protein kinase homology <KIN>
 F:349-357/Region: protein kinase ATP-binding motif

Query Match 79.5% Score 35; DB 2; Length 676;
 Best Local Similarity 75.0% Pred. No. 70;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 |||
 DB 535 MLAGQPPF 542

RESULT 39
 KIBOC
 protein kinase C (EC 2.7.1.1) gamma - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 C:Accession: C24664
 R:Coussens, L.; Parker, P.J.; Rhee, L.; Yang-Feng, T.L.; Chen, E.; Waterfield, M.D.;
 Science 233, 859-866, 1986
 A:Title: Multiple, distinct forms of bovine and human protein kinase C suggest diver
 A:Reference number: A94291; MUID:86289426; PMID:3755548
 A:Accession: C24664

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OX protein - protein search, using sw model

Run on: November 14, 2003, 12:56:44 ; Search time 5.94256 Seconds
(without alignments)
61,105 Million cell updates/sec

Title: US-09-736-076-16

Perfect score: 44

Sequence: 1 MLCOKPPF 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	93.2	682	1 SNK_MOUSE	P53351 mus musculus
2	41	93.2	682	1 SNK_MOUSE	Q90122 rattus norv
3	41	93.2	685	1 SNK_MOUSE	Q90122 rattus norv
4	39	88.6	465	1 KPI1_ARATH	P42818 arabidopsis
5	39	88.6	471	1 KPI1_ARATH	Q90122 rattus norv
6	39	88.6	683	1 PLO1_SCHPO	P35528 schizosacch
7	39	88.6	705	1 CDC5_YEAS	P12562 saccharomyc
8	38	86.4	282	1 STK6_MOUSE	Q90122 rattus norv
9	38	86.4	525	1 KPI1_MOUSE	P42818 arabidopsis
10	38	86.4	603	1 KPI1_MOUSE	P42818 arabidopsis
11	38	86.4	603	1 KPI1_MOUSE	P42818 arabidopsis
12	38	86.4	603	1 KPI1_MOUSE	P42818 arabidopsis
13	37	84.1	679	1 KPI1_MOUSE	P42818 arabidopsis
14	37	84.1	1081	1 KOKO_MOUSE	Q90122 rattus norv
15	36	81.8	217	1 NUD2_MOUSE	Q90122 rattus norv
16	36	81.8	403	1 STK6_MOUSE	Q90122 rattus norv
17	36	81.8	407	1 STK6_MOUSE	Q90122 rattus norv
18	36	81.8	408	1 STK6_MOUSE	Q90122 rattus norv
19	36	81.8	690	1 KPI1_MOUSE	P42818 arabidopsis
20	35	79.5	294	1 KPI1_MOUSE	P42818 arabidopsis
21	35	79.5	649	1 KPI1_MOUSE	P42818 arabidopsis
22	35	79.5	658	1 KPI1_MOUSE	P42818 arabidopsis
23	35	79.5	672	1 KPI1_MOUSE	P42818 arabidopsis
24	35	79.5	672	1 KPI1_MOUSE	P42818 arabidopsis
25	35	79.5	672	1 KPI1_MOUSE	P42818 arabidopsis
26	35	79.5	672	1 KPI1_MOUSE	P42818 arabidopsis
27	35	79.5	672	1 KPI1_MOUSE	P42818 arabidopsis
28	35	79.5	682	1 KPI1_MOUSE	P42818 arabidopsis
29	35	79.5	697	1 KPI1_MOUSE	P42818 arabidopsis
30	35	79.5	697	1 KPI1_MOUSE	P42818 arabidopsis
31	35	79.5	697	1 KPI1_MOUSE	P42818 arabidopsis
32	34	77.3	363	1 MK12_MOUSE	Q90122 rattus norv
33	34	77.3	482	1 KPI1_MOUSE	P42818 arabidopsis

ALIGNMENTS

RESULT 1

ID	SNK_MOUSE	STANDARD	PRT	682 AA
AC	P53351			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Serine/threonine-protein kinase SNK (EC 2.7.1.-) (Serum inducible kinase).			
DE	kinase).			
GN	SNK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93375085; Pubmed=1508211;			
RA	Simmons D.L., Neel B.G., Stevens R., Evett G., Erikson R.L.;			
RT	"Identification of an early-growth-response gene encoding a novel putative protein kinase."			
RL	Mol. Cell. Biol. 12:4164-4169(1992).			
CC	FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS, WOUND HEALING OR NEOPLASIA.			
CC	TISSUE SPECIFICITY: BRAIN, LUNG AND HEART.			
CC	INDUCTION: BY SERUM AND PHORBOL ESTER.			
CC	SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	CDC5/POLO SUBFAMILY.			
CC	SIMILARITY: Contains 2 POLO box domains.			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).			
DR	EMBL; M96163; ; NOT_ANNOTATED_CDS.			
DR	PIR; A44493; A44493; Snk			
DR	MGI; MGI:1099790; Snk			
DR	InterPro; IPR000359; POLO_box.			
DR	InterPro; IPR000719; Prot_kinase.			
DR	InterPro; IPR002290; Ser_thr_kinase.			
DR	Pfam; PF00069; pkinase; 1.			
DR	Pfam; PF00659; POLO_box; 2.			
DR	ProDom; PD000001; Prot_kinase; 1.			
DR	SMART; SM00220; S_TKC; 1.			
DR	PROSITE; PS0078; POLO_BOX; 2.			
DR	PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS0011; PROTEIN_KINASE_ST; 1.			
KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.			
FT	DOMAIN 54 59 POLY-HIS.			
FT	DOMAIN 79 331 PROTEIN_KINASE.			
FT	NP_BIND 85 93 ATP (BY SIMILARITY).			

Q921m4 mus musculus
P16912 drosophila
P14222 homo sapien
P52104 drosophila
P54199 saccharomyc
Q9K1n2 vibrio chol
Q9JWc5 neisseria m
Q8XVn6 ralisstoria s
Q35099 mus sapien
Q35099 mus musculu
P43565 saccharomyc
Q9N0X0 sus scrofa

34 34 77.3 485 1 K6B2_MOUSE
35 34 77.3 502 1 XDC2_DROME
36 34 77.3 555 1 PERE_HUMAN
37 34 77.3 576 1 POLO_DROME
38 34 77.3 764 1 WPS1_YEAST
39 34 77.3 1297 1 PUR4_VIBCH
40 34 77.3 1320 1 PUR4_NEIMA
41 34 77.3 1369 1 PUR4_RALSO
42 34 77.3 1374 1 M3K5_HUMAN
43 34 77.3 1379 1 M3K5_MOUSE
44 34 77.3 1770 1 R115_YEAST
45 33 75.0 156 1 STKC_PIG

```

FT BINDING 108 108 ATP (BY SIMILARITY).
FT ACT_SITE 202 202 BY SIMILARITY.
FT DOMAIN 507 570 POLC BOX 1.
FT DOMAIN 603 674 POLC BOX 2.
SQ SEQUENCE 682 AA; 77911 MW; 58C5DEABFD7208A9D CRC64;

Query Match 93.2%; Score 41; DB 1; Length 682;
Best Local Similarity 87.5%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
DB 270 MLGRRPF 277

RESULT 2
SNK_RAT STANDARD; PRT; 682 AA.
AC Q9R012;
DT 16-OCT-2001 (Rel. 40, Created);
DT 16-OCT-2001 (Rel. 40, Last sequence update);
DT 16-OCT-2001 (Rel. 40, Last annotation update);
DE Serine/threonine-protein kinase SNK (EC 2.7.1.1) (Serum inducible kinase).
GN SNK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=99452763; PubMed=10521257;
RA Kauselmann G., Weiler M., Wolff P., Jessberger S., Konietzko U.,
RA Stadler J., Staubli U., Beresiter-Hahn J., Srethardt K., Kunz D.;
PT "the polo-like protein kinases Pnk and Skk associate with a Cdc2+- and
PT integrin-binding protein and are regulated dynamically with a catalytic
PT plasticity.";
RL EMBL J. 18:5528-5539(1999).
CC -- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL
CC -- TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS,
CC WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
CC -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLC SUBFAMILY.
CC -- SIMILARITY: Contains 2 POLC box domains.
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CC or send an email to license@sib-sib.ch).
CC
DR EMBL; AF136583; AAF08366.1;
DR InterPro; IPR000959; POLC box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLC box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc1;
DR PROSITE; PS00078; POLC BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP binding; Repeat.
FT DOMAIN 54 59 POLY-HIS.
FT DOMAIN 79 331 PROTEIN_KINASE.
FT NS_BIND 85 93 ATP (BY SIMILARITY).
FT BINDING 108 108 ATP (BY SIMILARITY).
FT ACT_SITE 202 202 BY SIMILARITY.
FT DOMAIN 507 570 POLC BOX 1.
FT DOMAIN 603 674 POLC BOX 2.

```

```

SQ SEQUENCE 682 AA; 77919 MW; 58C50DEBDE83D5F3 CRC64;

Query Match 93.2%; Score 41; DB 1; Length 682;
Best Local Similarity 87.5%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
DB 270 MLGRRPF 277

RESULT 3
SNK_HUMAN STANDARD; PRT; 685 AA.
AC Q9NYI3; Q60679; Q95CV7; Q9UE61;
DT 16-OCT-2001 (Rel. 40, Created);
DT 28-FEB-2003 (Rel. 41, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update);
DE Serine/threonine-protein kinase SNK (EC 2.7.1.1) (Serum inducible kinase).
GN SNK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RA Ouyang B., Dai W.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBSJ databases.
RN [2];
RP SEQUENCE FROM N.A.
RC T:SSUE=Colon;
RA Anderson K.M., Neurkar S.S., Hansbury M.J., Fornwald J., Scott G.,
RA Bouzyk M., Mui P., Imbruglia C.S., Carlson K., Marshall J.A.,
RA Roshak A.K.;
PT "Identification and characterization of human serum-inducible kinase
PT (SNK), a novel member of the polo-kinase family of cell cycle
PT regulators: potential implication for regulation of vascular smooth
PT muscle proliferation.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBSJ databases.
RN [3];
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Aitschul S.F., Ziesberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stachenko S., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney C., Heltzer E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
PT "Generation and initial analysis of more than 15,000 full-length
PT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4];
RP SEQUENCE OF 110-408 FROM N.A.
RA Fidler C., Boulwood J., Wang Jabs E., Wainscoat J.S.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBSJ databases.
CC -- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL
CC -- TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS,
CC WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
CC -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLC SUBFAMILY.

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CC  -!- SIMILARITY: Contains 2 POLQ box domains.
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CC  entities requires a license agreement. (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch.)
CC  -----
DR  EMBL: AF059617; AAC14573.1;
DR  EMBL: AF221574; AAF62897.1;
DR  EMBL: J95755; AAC00575.1;
DR  EMBL: BC013879; AAH13879.1;
DR  M.M. 607023;
DR  InterPro: IPR000959; POLQ box.
DR  InterPro: IPR000719; Prot_kinase.
DR  InterPro: IPR022290; Ser Thr_pkinase.
DR  Pfam: PF00069; pkinase; 1.
DR  Pfam: PF00659; POLQ box; 2.
DR  Pfam: PF00659; POLQ box; 2.
DR  SMART: SM00600; Prot_kinase; 1.
DR  SMART: SM00220; S_TKc; 1.
DR  PROSITE: PS00078; POLQ BOX; 2.
DR  PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR  PROSITE: PS00111; PROTEIN KINASE DOM; 1.
DR  PROSITE: PS00108; PROTEIN KINASE ST; 1.
DR  Transferase: Serine/threonine-protein kinase; ATP-binding; Repeat.
DR  DOMAIN 57 64 POLY-H-S.
FT  DOMAIN 82 334 PROTEIN KINASE.
FT  NP BIND 88 96 ATP (BY SIMILARITY).
FT  BINDING 111 111 ATP (BY SIMILARITY).
FT  ACT_SITE 205 205 BY SIMILARITY.
FT  DOMAIN 510 573 POLQ BOX 1.
FT  DOMAIN 606 677 POLQ BOX 2.
FT  CONFLICT 25 28 A -> G (IN REF. 1).
SQ  SEQUENCE 685 AA; 78236 MW; 6429F65FC83C5333 CF6A;
Query Match 93.2%; Score 41; DB 1; Length 685;
Best Local Similarity 87.5%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Cy 1 MLLGKPPF 8
Lc 233 MLLGKPPF 280
RESULT 4
RKPI ARATH
IC KPX ARATH STANDARD; PRT; 400 AA.
AC P42a18.
DT 01-NOV-1995 (Rel. 32, Created:
DT 01-NOV-1995 (Rel. 32, Last sequence update).
DT 28-FEB-2003 (Rel. 41, Last annotation update.
DE Serine/threonine-protein kinase AtPK6 (EC 2.7.11.1).
GN AtPK1 OR ATPK6 OR AT3G08730 OR F7G14.20.
OS Arabidopsis thaliana (Mouse-ear cress).
CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
CC eurosids1; Brassicales; Brassicaceae; Arabidopsi.
CC NCBI_TaxID:3702;
CC 1;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=sv. Landsberg erecta;
RX MEDLINE=94292519; PubMed=7912697;
RA Zhang S.-H., Lawton M.A., Hunter T., Lamb C.J.;
RT "AtPK1, a novel ribosomal protein kinase gene from Arabidopsis. I.
RT Isolation, characterization, and expression";
RL J. Biol. Chem. 269:17586-17592(1994).
RN 2;
RP SEQUENCE FROM N.A.
RC STRAIN=sv. Columbia;
RX MEDLINE=95129712; PubMed=7828736;
RA Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,

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RA Shinozaki K.;
RT "Two genes that encode ribosomal-protein S6 kinase homologs are
RT induced by cold or salinity stress in Arabidopsis thaliana.";
RL FEBS Lett. 358:199-204(1995).
RN 3;
RP SEQUENCE FROM N.A.
RC STRAIN=sv. Columbia;
RX MEDLINE=21016720; PubMed=1130713;
RA Salaroubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,
RA Farman B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Deiseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choise N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissbach J., Saurin W., Queciet F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Dzorek H., Effie H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Palavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Liauro C., Purnelle B., Masuy D.,
RA De Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argitkou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.-J., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,
RA Cressy T.H., Haas B., Mailli R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Miliuscher J., Sellers P., Gill J.E., Feidblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:820-822(2000).
RN 4;
RP CHARACTERIZATION.
RC STRAIN=sv. Landsberg erecta;
RX MEDLINE=94292520; PubMed=8021267;
RA Zhang S.-H., Broome M.A., Lawton M.A., Hunter T., Lamb C.J.;
RT "AtPK1, a novel ribosomal protein kinase gene from Arabidopsis. II.
RT Functional and biochemical analysis of the encoded protein.";
RL J. Biol. Chem. 269:17593-17599(1994).
CC -!- FUNCTION: COULD BE INVOLVED IN THE CONTROL OF PLANT GROWTH AND
CC DEVELOPMENT. PHOSPHORYLATES TWO RIBOSOMAL PROTEINS, P14 AND P16.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES.
CC -!- DEVELOPMENTAL STAGE: PREDOMINATES DURING HIGH METABOLIC ACTIVITY
CC IN GROWING BUDS, ROOT TIPS, LEAF MARGINS AND GERMINATING SEEDS.
CC -!- PTM: UNDERGOES SERINE-SPECIFIC AUTOPHOSPHORYLATION.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC S6 KINASE SUBFAMILY.
CC -----
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CC entities requires a license agreement. (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch.)
CC 1;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=sv. Landsberg erecta;
RX MEDLINE=94292519; PubMed=7912697;
RA Zhang S.-H., Lawton M.A., Hunter T., Lamb C.J.;
RT "AtPK1, a novel ribosomal protein kinase gene from Arabidopsis. I.
RT Isolation, characterization, and expression";
RL J. Biol. Chem. 269:17586-17592(1994).
RN 2;
RP SEQUENCE FROM N.A.
RC STRAIN=sv. Columbia;
RX MEDLINE=95129712; PubMed=7828736;
RA Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,

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DR SMART; SM00223; S-TK_X; 1.
 DR SMART; SM00223; S-TK_X; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KM Phosphorylation.
 FT DOMAIN 134 389 PROTEIN_KINASE.
 FT NP_BIND 140 248 ATP (BY SIMILARITY).
 FT BINDING 163 263 ATP (BY SIMILARITY).
 FT ACT_SITE 257 257 BY SIMILARITY.
 FT ACT_SITE 263 263 BY SIMILARITY.
 FT MUTAGEN 163 163 K->R: ACTIVITY SUBSTANTIALLY DIMINISHED.
 SQ SEQUENCE 465 AA; 52588 MW; 4071330674CA271P CRC64;

Query Match 88.6%; Score 39; DB 1; Length 471;
 Best Local Similarity 87.5%; Pred. No. 3.4;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MLGKPPF 8
 DB 324 MLGKPPF 331

RESULT 5

FP19 APATH STANDARD; PRT; 471 AA.
 AC Q49310; Q949X5; Q9C5R1;
 DT 14-DEC-2003 (Rel. 40; Created;
 DT 28-FEB-2003 (Rel. 41; Last sequence update;
 DT 28-FEB-2003 (Rel. 41; Last annotation update;
 DE Serine/threonine-protein kinase ATRK19 [EC 2.7.1.1] Mitosomal-protein
 DE S6 kinase homolog.
 GN ATRK19 OR ATRK28720 OR P17014.19.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae;
 CC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 CC NCBI_TaxID:3702;
 RN 11;
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE:95129712; PubMed:782736;
 RA Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kanada H.,
 RA Shinozaki K.;
 PT Two genes that encode ribosomal protein S6 kinase homologs are
 PT induced by cold or salinity stress in Arabidopsis thaliana.
 PS FBS Lett. 358:199-204 (1995).
 RN 12;
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE:21016720; PubMed:11130177;
 RA Salanchuk M., Lencke K., Rieger M., Ansoy W., Busch M.,
 RA Fairclough B., Valle G., Bloeker H., Perez-Aranda M., Grottel R.,
 RA Delany M., Beatty M., Grivell L.A., Vache R., Rindow-Sch P.,
 RA De Simone V., Choisy N., Artiguenave F., Robert C., Broillet P.,
 RA Winkler F., Cattolico L., Weissbach C., Saulin J., Chetier P.,
 RA Schofer F., Mueller-Auer S., Gabel C., Ecker J., Hens V.,
 RA Karmach E., Drzonek H., Erle H., Jordan N., Bangert S.,
 RA Weddelmann R., Kranz H., Voss H., Holland R., Bräuer P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simonati S.,
 RA Conrad A., Hornischer K., Kauer G., Scherff T.H., Noidseck G.,
 RA Reichelt C., Scharte M., Schoen O., Hargues M., Tsch J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Otenwaelder B., Ruchemin D.,
 RA Cooke R., Laudie M., Berger-Llauró C., Purnelle B., Masny D.,
 RA Ge Haan X., Maarse A.C., Alcaraz C.P., Corret A., Casacuberta E.,
 RA Monfort A., Argitrou A., Flores V., Maguori P., Vitale D.,
 RA Mannhaupt G., Haase D., Schöf H., Rüd S., Zaccaria P., Newes H.-W.,
 RA Mayer K.F.X., Kaut S., Town C.D., Koo H., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo W., Wais A., Utecht T., Füll C.Y., Shea T.P.,
 RA Creasy T.H., Haas B., Maiti R., Wu C., Petersen J., Van Aken S.,
 RA Pat G., Nitscher J., Sellers P., Gili E., Feldhahn T.V.,
 RA Preuss D., Lin X., Nierman W.C., Salzberg S., White O., Venter C.C.,
 RA Flisat C.M., Kureko T., Nakamura Y., Sato S., Kato T., Asanuma E.,

RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shirao S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 RT thaliana";
 RL Nature 408:820-822 (2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
 RA Palm C.J., Theologis A., Ecker J., Davis R.W.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SSP consortium (Salk/Stanford/PGECC)";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MAY BE INVOLVED IN ADAPTATION OF PLANT TO COLD OR HIGH-
 CC SALT CONDITIONS.
 CC -!- PTM: UNDERGOES SERINE-SPECIFIC AUTOPHOSPHORYLATION (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC S6 KINASE SUBFAMILY.
 CC -!- CAUTION: Ref.4 sequence differs from that shown due to a
 CC frameshift in position 391.
 CC -----
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 CC -----
 DR EMBL; D42061; BAA07661.1;
 DR EMBL; AC012562; AAC51345.1;
 DR EMBL; AF525694; AAK7162.1;
 DR EMBL; AY050826; AAK92761.1; ALT_FRAME.
 DR PIR; S68463; S68463.
 DR HSP; P05132; ICTP.
 DR InterPro; IPR000961; pkinase_C.
 DR InterPro; IPR00719; Prot_kinase.
 DR InterPro; IPR02290; Ser_Thr_kinase.
 DR Pfam; PF0069; pkinase_1.
 DR Pfam; PF0433; pkinase_C_1.
 DR ProDom; PD000001; Prot_kinase_1.
 DR SMART; SM00333; S-TK_X_1.
 DR SMART; SM02200; S-TK_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KM Phosphorylation.
 FT DOMAIN 140 395 PROTEIN_KINASE.
 FT NP_BIND 146 154 ATP (BY SIMILARITY).
 FT BINDING 169 169 ATP (BY SIMILARITY).
 FT ACT_SITE 263 263 BY SIMILARITY.
 FT ACT_SITE 250 250 A -> V (IN REF. 1).
 FT CONFLICT 359 360 LS -> VF (IN REF. 1).
 SQ SEQUENCE 471 AA; 53037 MW; 95F007B4B58DFB5 CRC64;

Query Match 88.6%; Score 39; DB 1; Length 471;
 Best Local Similarity 87.5%; Pred. No. 3.4;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MLGKPPF 8
 DB 330 MLGKPPF 337

RESULT 6
 PLOI SCHPO STANDARD; PRT: 683 AA.
 AC P3528;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 CE Serine/threonine-protein kinase ploi (EC 2.7.1.37).
 GN PLOI; OR SPAC23C11.16.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes.
 CC NCBI_TaxID=4896;
 CX [1]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=95262899; PubMed=7744248;
 RA Okura H., Hagan J.M., Glover D.M.;
 RT "The conserved Schizosaccharomyces pombe kinase ploi, required to
 form a bipolar spindle, the actin ring, and septum, can drive septum
 formation in G1 and G2 cells."
 RT Genes Dev. 9:1059-1073(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Williams R., Rajandream A.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros C., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltham T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidergott J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA McConkey P., Moule S., Mungall K., Murphy L., Niblett D., Ogdel C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Kober C., Glynn P., Berridge
 RA Wellens I., Vanterveld E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabor C., Fuchs M., Fritz C., Helzer E., Meestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirach H., Reichardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Gadye E., Dreano S., Gloux S., Delaure V., Mortier S.,
 RA Galibert F., Aves J.J., Xiang Z., Hunt S., Moore K., Hurst S.,
 RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez C., Sanchez M., del Rey P., Benito J.,
 RA Dominguez A., Revuelta J.L., Vercillo S., Armstrong J., Forsberg S.B.,
 RA Cerretti L., Lowe T., McCombie W.R., Paulsen O., Dushkin G.,
 RA Shpakovskii G.V., Ussery D., Barrell B.G., Nisenzon F.,
 RT "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-883(2002).
 CC -!- FUNCTION: REQUIRED TO FORM A BIPOLEAR SPINDLE, THE ACTIN RING AND
 CC SEPTUM. FUNCTIONS UPSTREAM OF THE WHOLE SEPTUM FORMATION PATHWAY,
 CC INCLUDING ACTIN RING FORMATION (REGULATED BY LATE SEPTATION GENES)
 CC AND SEPTAL MATERIAL DEPOSITION (REGULATED BY EARLY SEPTATION
 CC GENES). BEHAVES AS A "SEPTUM-PROMOTING FACTOR" AND COULD ALSO BE
 CC INVOLVED IN INDUCING OTHER LATE EVENTS OF CELL DIVISION.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated protein.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CD05/POLO SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 POLO box domains
 CC
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 CC or send an email to license@isb-sib.ch)
 CC
 CC EMBL: X85766.1;
 DR

DR EMBL: Z98559; CAB11167.1; -.
 DR PIR: T38254; T38254.
 DR HSSP: O63450; 1A06.
 DR GeneDB SPombe; SPAC23C11.16; -.
 DR InterPro; IPR000959; POLO_box.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00659; POLO_box; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR PROSITE; PS50078; POLO_BOX; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
 FT DOMAIN 41 296 PROTEIN KINASE.
 FT NP_BIND 47 55 ATP (BY SIMILARITY).
 FT BINDING 69 69 ATP (BY SIMILARITY).
 FT ACT_SITE 163 163 BY SIMILARITY.
 FT DOMAIN 500 567 POLO_BOX 1.
 FT DOMAIN 604 670 POLO_BOX 2.
 SQ SEQUENCE 683 AA; 77301 MW; F11CD0EF9B913917 CRC64;

Query Match 88.6%; Score 39; DB 1; Length 683;
 Best Local Similarity 75.0%; Pred. No. 5;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGKPPF 8
 Db 233 LLICKPPF 240

RESULT 7
 CDC5 YEAST
 ID CDC5 YEAST STANDARD; PRT: 705 AA.
 AC P32562;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DE Cell cycle protein kinase CDC5/MSD2 (EC 2.7.1.37).
 GN CDC5 OR PRX2 OR MSD2 OR YMR001C OR YMR270.03C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A364A;
 RX MEDLINE=93309479; PubMed=8321244;
 RA Kitada K., Sugino A., Johnston L.H., Johnson A.L.;
 RT "A multicopy suppressor gene of the Saccharomyces cerevisiae G1 cell
 RT cycle mutant gene *cdc5* encodes a protein kinase and is identified as
 RT CDC5."
 RL Mol. Cell. Biol. 13:4445-4457(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RX PubMed=9169872;
 RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
 RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
 RA Jagels K., Lyne G., Moule S., Odell C., Pearson D., Rajandream M.A.,
 RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
 RT XIII."
 RL Nature 387:90-93(1997).
 RN [3]
 RP PHOSPHORYLATION OF SCCL.
 RX PubMed=11371343;
 RA Alexandru G., Uhlmann F., Mechtler K., Poupard M.-A., Nasmyth K.;
 RT "Phosphorylation of the cohesin subunit Sccl by Polo/Cdc5 kinase
 RT regulates sister chromatid separation in yeast."
 RL Cell 105:459-472(2001).


```

CC -!- FUNCTION: Protein kinase required for the cell cycle.
CC -!- Phosphorylates SCCL/MCD1.
CC -!- CATALYTIC ACTIVITY: ATP -> a protein + ADP + a phosphoprotein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 2 POLO BOX DOMAINS.
CC -----
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CC or send an email to: license@sib-sib.ch).
CC -----
CC EMBL: Y84225; AAA02576.1; -
CC EMBL: Z48613; CAA88516.1; -
CC PIR: A49144; A48144.
CC HSSP: Q63450; 1A06.
CC SCOP: S0004603; CDC5.
CC GO: GO:0005634; C:nucleus; IDA.
CC GO: GO:0006261; P:DNA dependent DNA replication; IDA.
CC GO: GO:0006469; P:protein amino acid phosphorylation; IDA.
CC InterPro: IPR0003959; POLO BOX.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR02290; Ser_thr_kinase.
CC InterPro: IPR01245; Tyr_pkinase.
CC Pfam: PF00659; pkinase; 1.
CC PRINTS: PR0109; TYRKINASE.
CC ProDom: PD030001; Prot_kinase; 1.
CC SMART: SM00220; S_TKc; 1.
CC PROSITE: PS00378; POLO BOX; 2.
CC PROSITE: PS00137; PROTEIN KINASE ATP; 1.
CC PROSITE: PS00011; PROTEIN KINASE DOM; 1.
CC PROSITE: PS00108; PROTEIN KINASE ST; 1.
CC Cell cycle: Cell division, Serine/threonine protein kinase;
CC Transferase; ATP-binding; Repeat.
CC DOMAIN 82 337 PROTEIN KINASE.
CC NP BIND 88 96 ATP (BY SIMILARITY).
CC BINDING 110 110 ATP (BY SIMILARITY).
CC ACT SITE 204 204 BY SIMILARITY.
CC DOMAIN 520 587 POLO BOX 1.
CC DOMAIN 619 692 POLO BOX 2.
CC SEQUENCE 705 AA; 81030 MW; B5A25F15B8EAAD0 CRC64;
CC -----
Query Match 88.6%; Score 39; DB 1; Length 105;
Best Local Similarity 75.0%; Pred No. 5.1;
Matches 6; Conservative 2; Mismatches 0; Gaps 0;
QY : MLGKPPF 8
DB 274 LLGKPPF 28;
-----
Query Match 86.4%; Score 38; DB 1; Length 282;
Best Local Similarity 75.0%; Pred No. 3.2;
Matches 6; Conservative 2; Mismatches 0; Gaps 0;
QY : MLGKPPF 8
DB 205 LLGKPPF 212
-----
RESULT 8
STKD_MOUSE
ID STKD_MOUSE STANDARD; PRT: 282 AA.
AC C88445; Q9JLC2.
DT 28-FEB-2003 (Rel. 41, Created:
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase 13 (EC 2.7.1.37) (Aurora/pl1/Eg2
DE protein 1) (Aurora-C).
GN STK13 OR AIE1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Mus.
OX NCBI_taxid=10090;
EN 1.
FP SEQUENCE FROM N.A.
RP STRAIN=BALB/C;
RX MEDLINE=99025616; PubMed=9809744;

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RA Tseng T.C., Chen S.H., Hsu Y.P., Tang T.K.;
RT "Protein kinase profile of sperm and eggs: cloning and
RT characterization of two novel testis-specific protein kinases (AIE1,
RT AIE2) related to yeast and fly chromosome segregation regulators.";
RL DNA Cell Biol. 17:823-833(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RC MEDLINE=20551164; PubMed=11098217;
RA Hu H.M., Chuang C.K., Lee M.J., Tseng T.C., Tang T.K.;
RT "Genomic organization, expression, and chromosome localization of a
RT third aurora-related kinase gene, Aie1.";
RL DNA Cell Biol. 19:679-688(2000).
CC -!- FUNCTION: May play a part in organizing microtubules in relation
CC to the function of the centrosome/spindle pole during mitosis.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to spindle pole from anaphase to
CC cytokinesis (by similarity).
CC -!- TISSUE SPECIFICITY: Expressed only in testis.
CC -!- DEVELOPMENTAL STAGE: Expressed on day 14 dpc in prepubertal
CC testis, expression reached its plateau on day 21 dpc and remained
CC at a high level in adult.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC -----
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CC or send an email to: license@sib-sib.ch).
CC -----
CC EMBL: AF054620; AAC25954.1; -
CC EMBL: AF195272; AAF25838.1; -
CC HSSP: Q63450; 1A06.
CC MGD: MGI:132119; Stk13.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR02290; Ser_thr_kinase.
CC InterPro: IPR01245; Tyr_pkinase.
CC Pfam: PF00659; pkinase; 1.
CC PRINTS: PR00109; TYRKINASE.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00220; S_TKc; 1.
CC PROSITE: PS00137; PROTEIN KINASE ATP; 1.
CC PROSITE: PS00108; PROTEIN KINASE ST; 1.
CC PROSITE: PS00111; PROTEIN KINASE DOM; 1.
CC Cell cycle: Transferase; Serine/threonine-protein kinase; ATP-binding.
CC DOMAIN 16 266 PROTEIN KINASE.
CC NP BIND 22 30 ATP (BY SIMILARITY).
CC BINDING 45 45 ATP (BY SIMILARITY).
CC ACT SITE 139 139 BY SIMILARITY.
CC CONFLICT 74 74 R -> P (IN REF. 2).
CC SEQUENCE 282 AA; 32907 MW; 7C8BAEC4984B7883 CRC64;
CC -----
Query Match 86.4%; Score 38; DB 1; Length 282;
Best Local Similarity 75.0%; Pred No. 3.2;
Matches 6; Conservative 2; Mismatches 0; Gaps 0;
QY : MLGKPPF 8
DB 205 LLGKPPF 212
-----
RESULT 9
ID_KSN8_YEAST STANDARD; PRT: 525 AA.
AC P38070;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable serine/threonine-protein kinase YBR028C (EC 2.7.1.-).
GN YBR028C OR YBR0312.

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CS Saccharomyces cerevisiae (Baker's yeast).
CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CX NCB: TaxID=4912;
RN SEQUENCE FROM N.A.
RP STRAIN=S288C;
RX MEDLINE=94378725; PubMed=8091864;
RA Smith P.H.X., de Haan M., Maat C., Gravel L.A.;
RT "The complete sequence of a 33 kb fragment on the right arm of
RT chromosome II from Saccharomyces cerevisiae reveals 16 open reading
RT frames, including ten new open reading frames, five previously
RT identified genes and a homologue of the SCO1 gene.";
RL Yeast 10:575-580(1994).
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X76078; CAA53684.1; --
DR EXBL: Z35897; CAA84970.1; --
DR PIR: S45864; S45864.
DR HSP: P05132; ICTP.
DR SCJ: S000232; YBR028C.
DR InterPro: IPR000961; Pkinase C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR Pfam: PF00369; Pkinase; 1.
DR Pfam: PF00433; Pkinase; C; 1.
DR ProDom: PD003001; Prot_kinase; 1.
DR SMART: SW00133; S_TK; 1.
DR SMART: SW00223; S_TK; 1.
DR PROSITE: PS00137; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
DR PROSITE: PS00611; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00611; PROTEIN KINASE DOM; 1.
DR Hypothetical protein; Transferase; Serine/threonine protein kinase;
DR ATP-binding.
FT DCMAIN 128 424 PROTEIN KINASE.
FT NP_BIND 134 142 ATP [BY SIMILARITY].
FT BINDING 157 157 ATP [BY SIMILARITY].
FT ACT_SITE 277 277 BY SIMILARITY.
SQ SEQUENCE 525 AA; 59591 MW; 88FF6E1A46C687CF14;
Query Match 86.4%; Score 35; DB 1; Length 555.
Best Local Similarity 75.0%; Pred. No. 5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY : MLLGKPPF 8
DB : 355 MLVGKPPY 362
RESULT 10
ID PLK1_HUMAN STANDARD; PRT; 603 AA.
AC P53350;
DT 01-OCT-1996 (Rel. 34, Created;
DT 01-OCT-1996 (Rel. 34, Last sequence update;
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase PLK1 (EC 2.7.1.1) (PLK1) (Serine-
DE threonine protein kinase 13) (STPK13).
GN PLK OR PLK1.
CS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea.
CX NCB: TaxID=9606;
RN 1.
RP SEQUENCE FROM N.A.

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TISSUE=Placenta;
MEDLINE=94289293; PubMed=8018557;
RA Hamanaka R., Maloid S., Smith M.R., O'Connell C.D., Longo D.L.,
RA Ferris D.K.;
RT "Cloning and characterization of human and murine homologues of the
RT Drosophila polo serine-threonine kinase.";
RL Cell Growth Differ. 5:249-257(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94067140; PubMed=7902533;
RA Lake R.J., Jellinek W.R.;
RT "Cell cycle- and terminal differentiation-associated regulation of
RT the mouse mRNA encoding a conserved mitotic protein kinase.";
RL Mol. Cell. Biol. 13:7793-7801(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95051109; PubMed=7962193;
RA Golsteyn R.M., Schultz S.J., Bartek J., Ziemiecki A., Ried T.,
RA Nigg E.A.;
RT "Cell cycle analysis and chromosomal localization of human plk1, a
RT putative homologue of the mitotic kinases Drosophila polo and
RT Saccharomyces cerevisiae Cdc5";
RL J. Cell Sci. 107:1509-1517(1994).
RN [4]
RP SEQUENCE FROM N.A.
TISSUE=Lung;
MEDLINE=94173904; PubMed=8127874;
RA Holtrich U., Weiff G., Braeuninger A., Karn T., Boehme B.,
RA Ruebsamen-Waigmann H., Strebhardt K.;
RT "Induction and down-regulation of PLK, a human serine/threonine
RT kinase expressed in proliferating cells and tumors.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:1736-1740(1994).
RN [5]
RP SEQUENCE FROM N.A.
TISSUE=Colon, and Lung;
MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins P.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullahy S.C.,
RA Bcsak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley A.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC 1- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE.
CC 1- SUBCELLULAR LOCATION: Nuclear.
CC 1- TISSUE SPECIFICITY: PLACENTA AND COLON.
CC 1- DEVELOPMENTAL STAGE: ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
CC DURING S PHASE.
CC 1- INDUCTION: BY GROWTH-STIMULATING AGENTS.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC 1- SIMILARITY: Contains 2 POLO box domains.
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EMBL: U01038; AAA56634.1; -
EMBL: L59559; AAA36659.1; -
EMBL: X73458; CAA51837.1; -
EMBL: X75932; CAA53536.1; -
EMBL: BC023369; AAH023369.1; -
EMBL: BC033002; AAH033002.1; -
EMBL: BC014846; AAH14846.1; -
PIR: S34130; S34130; -
Genew: HGN:9077; PLK.
GK: P53350; -
XIM: 602098; -
GO: GO:0004674; F:protein,serine/threonine kinase activity; TAS.
GO: GO:0007067; P:mitosis; TAS.
GO: GO:0007048; P:cytogenesis; TAS.
GO: GO:0000074; F:regulation of cell cycle; TAS.
InterPro: IPR000959; POLO box.
InterPro: IPR002290; SerThr_kinase.
Pfam: PF000659; pkinase; 1.
Pfam: PF00659; POLO_box; 2.
ProDom: PD000001; Prot_kinase; 1.
SMART: SMC0220; S_TKC; 1.
PROSITE: PS50079; POLO_BOX; 2.
PROSITE: PS50107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE: PS50108; PROTEIN_KINASE_ST; 1.
Transferase: Serine/threonine-protein kinase; ATP binding; Repeat;
Nuclear protein.
DOMAIN 53 305 PROTEIN_KINASE.
FT NP_BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 417 480 POLO_BOX_1.
FT DOMAIN 515 584 POLO_BOX_2.
FT CONFLICT 2 2 S > T (IN REF. 1).
FT CONFLICT 11 11 A > P (IN REF. 1).
FT CONFLICT 58 58 F > L (IN REF. 1).
FT CONFLICT 60 60 G > S (IN REF. 1).
FT CONFLICT 73 73 A > V (IN REF. 2).
FT CONFLICT 141 141 L > P (IN REF. 4).
FT CONFLICT 227 227 G > E (IN REF. 4).
FT CONFLICT 301 301 N > G (IN REF. 2).
FT CONFLICT 495 495 A > G (IN REF. 2).
FT CONFLICT 501 501 E > G (IN REF. 2).
FT SEQUENCE 603 AA; 68254 MW; 10A7E01175E6A01804,
Query Match: 86.4% Score 101.13 E-100 Ident 60%
Best Local Similarity 75.0% Freq. Nucleo. 0
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
DB 244 LLYGKPPF 251
RESULT 11
PLK1_MOUSE STANDARD; PRT; 63 AA.
AC Q07832;
DT 31-FEB-1995 (Rel. 31, Created)
DT 31-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase PLK1 (PDB ID: 1PLK1) [Serine-
threonine protein kinase 13] (S-PK1).
ON PLX.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCR; Taxid: 10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Bone marrow;
RX MEDLINE=93281660; PubMed=8039445;
RA Clay F.J., McEwen S.J., Bertonecchio I., Wilks A.F., Dunn A.R.;
RT "Identification and cloning of a protein kinase-encoding mouse gene,
PLK, related to the polo gene of Drosophila.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:4882-4886(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=94289293; PubMed=8018557;
RA Hamanaka R., Malicd S., Smith M.R., O'Connell C.D., Longo D.L.,
RA Ferris D.K.;
RT "Cloning and characterization of human and murine homologues of the
Drosophila polo serine-threonine kinase.";
RL Cell Growth Differ. 5:249-257(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=94067140; PubMed=7902533;
RA Lake R.J., Jelinek W.R.;
RT "Cell cycle- and terminal differentiation-associated regulation of
the mouse mRNA encoding a conserved mitotic protein kinase.";
RL Mol. Cell. Biol. 13:7793-7801(1993).
CC -!- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
DURING G1 OR S PHASE.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: NEWBORN AND ADULT SPLEEN, FETAL AND NEWBORN
KIDNEY, LIVER, BRAIN, THYMUS AND ADULT BONE MARROW, THYMUS,
OVARY AND TESTES.
CC -!- DEVELOPMENTAL STAGE: IN THE THYMUS, LEVELS INCREASED DURING FETAL
DEVELOPMENT, WERE HIGHEST IN NEWBORN ANIMALS AND DECREASED IN THE
ADULT. IN THE TESTES, THE PLK LEVELS WERE HIGHER IN THE ADULT THAN
IN PREPUBESCENT MICE WHILE IN THE OVARY, THE LEVELS WERE HIGHER IN
THE PREPUBESCENT MICE. ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
PHASES, DECREASES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
DURING S PHASE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
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FT ACT_SITE 176 490 BY SIMILARITY.
FT DOMAIN 417 584 POLO BOX 1.
FT DOMAIN 515 584 POLO BOX 2.
FT CONFLICT 4 A -> T (IN REF. 1).
FT CONFLICT 15 A -> V (IN REF. 1).
FT CONFLICT 23 P -> L (IN REF. 1).
FT CONFLICT 27 V -> A (IN REF. 1).
FT CONFLICT 29 G -> S (IN REF. 1).
FT CONFLICT 41 F -> L (IN REF. 1).
FT CONFLICT 54 V -> I (IN REF. 1).
FT CONFLICT 495 A -> R (IN REF. 1).
FT CONFLICT 603 AA; 6830C MW; 1B98C64636EFA1C CRC64;
SQ SEQUENCE 603 AA; 6830C MW; 1B98C64636EFA1C CRC64;

Query Match 86.4%; Score 19; DB 1; Length 603;
Best Local Similarity 75.0%; Pred. NO. 6.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
DB 244 LLVGKPPF 251

RESULT 12
PK1 RAT
ID FLK1 RAT STANDARD; ERT; 603 AA.
AC Q62673.
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DE Serine/threonine-protein kinase PLK (EC 2.7.1.1) (PLK-1).
GN PLK
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 111
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Amstrup C., Hansen J.A., Haxliss Nielsen C.;
RL Submitted (MAY-1994) to the EMBL/GenBank/CDR databases.
RE !- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE (BY SIMILARITY).
CC !- SUBCELLULAR LOCATION: Nuclear (by similarity).
CC !- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC !- CDOS/POLO SUBFAMILY. CONTAINS 2 POLO BOX DOMAINS.
CC !- SIMILARITY: CONTAINS 2 POLO BOX DOMAINS.
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; U01882; AAA18885.1;
CC InterPro: IPR000959; POLO BOX.
CC InterPro: IPR000719; Prot_Kinase.
CC InterPro: IPR022290; Ser_thr_kinase.
CC Pfam: PF00069; kinase; 1.
CC Pfam: PF00659; POLO box; 2.
CC ProDom: PD000001; Prot_Kinase; 1.
CC SMART; SM00220; 5 TKc; 1.
CC PROSITE; PS50078; POLO BOX; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DCG; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC Transferrase: Serine/threonine-protein kinase, ATP-binding; Repeat;
KW Nuclear protein.
FT DOMAIN 53 105 PROTEIN_KINASE
FT NP_BIND 59 67 ATP (BY SIMILARITY)
FT BINDING 82 82 ATP (BY SIMILARITY)
FT ACT_SITE 176 176 BY SIMILARITY.

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FT DOMAIN 417 480 POLO BOX 1.
FT DOMAIN 515 584 POLO BOX 2.
SQ SEQUENCE 603 AA; 68313 MW; 107AFFB3B7EDC002 CRC64;

Query Match 86.4%; Score 38; DB 1; Length 603;
Best Local Similarity 75.0%; Pred. NO. 6.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
DB 244 LLVGKPPF 251

RESULT 13
KPC1 DROME
ID KPC1 DROME STANDARD; PRT; 679 AA.
AC PG5130; Q9V7V6; Q9V7V7.
DT 13-AUG-1987 (Rel. 25; Created)
DT 28-FEB-2003 (Rel. 41; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Protein kinase C, brain isozyme (EC 2.7.1.1) (PKC) (dPKC53E(BR)).
GN PKC53E OR PKC1 OR CG6622.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
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RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC STRAIN=Canton-S, and Oregon-R;
RX MEDLINE=87218499; PubMed=3107983;
RA Rosenthal A., Rhee L., Yadegari R., Paro R., Ullrich A., Goeddel D.V.;
RT "Structure and nucleotide sequence of a Drosophila melanogaster
RL protein kinase C gene.";
RL EMBO J. 6:433-441 (1987).
RN 121
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Saxe E.G., Helt G., Nelson C.R., Miklos G.D.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

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RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*;"
 RA Science 287:2185-2195(2000).
 RA [3]
 RA SEQUENCE FROM N.A. (ISOFORM LONG).
 RA STRAIN=Berkley; TISSUE=ovary;
 RA Scapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,
 RA Chapeton M., Chavez C., Dorsett V., Dresnok D., Farfan D., Frise E.,
 RA George R.A., Gonzalez M., Guarin H., Krommiller B., Li P.W., Liac G.,
 RA Miranda A., Mungall C.J., Nuroo J., Pacleb J.V., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
 RA Ceolnik S.E.;
 RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
 CC - ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Names=Long;
 CC IsoId=P05130-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=P05130-2; Sequence=VSP_004743;
 CC Note=No experimental confirmation available;
 CC TISSUE SPECIFICITY: HEAD NEURAL TISSUE
 CC MISCELLANEOUS: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-
 CC DEPENDENT, SERINE- AND THREONINE-SPECIFIC ENZYME.
 CC - MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF GREGON R.
 CC - SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC - SIMILARITY: Contains 1 C2 domain.
 CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. PKC
 CC SUBFAMILY.

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 EMBL: X03695; CAA28890.2; JOINED

DR GC: GO:0005634; C:nucleus; IDA.
 DR GC: GO:0005196; P:MAPKK cascade (cell wall biogenesis); IGI.
 DR GC: GO:0006468; P:protein amino acid phosphorylation; IDA.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR Pfam: PFC0069; Pkinase_I.
 DR ProDom: PDC00001; Prot_kinase; 1.
 DR SMART: SM0220; S_TK; 1.
 DR PROSITE: PSC0107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PSC0108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PSC011; PROTEIN_KINASE_DCM; 1.
 KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
 KW ATP-binding.
 FT DOVAIN 179 443 PROTEIN_KINASE.
 FT NP_BIND 185 193 ATP (BY SIMILARITY).
 FT BINDING 208 208 ATP (BY SIMILARITY).
 FT ACT_SITE 303 303 BY SIMILARITY.
 SQ SEQUENCE 1081 AA; 121660 MW; BE0DD9D49AC2BEC3 CRC64;

Query Match 84.1%; Score 37; DB 1; Length 1081;
 Best Local Similarity 75.0%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
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 DB 135 MLAGMPFF 142

RESULT 16
 STK6_HUMAN STANDARD; PRT; 403 AA.
 AC O14965; O60445; O75873; Q9BQD6; G9UPG5;
 DT 28-FEB-2003 (Rel. 4); Created;
 DT 28-FEB-2003 (Rel. 4); Last sequence update;
 DT 15-SEP-2003 (Rel. 42); Last annotation update;
 DE Serine/threonine kinase 6 (EC 2.7.1.37) [Serine/threonine kinase 15;
 DE (Aurora-A)] (Breast-tumor-amplified kinase 1) (Aurora-related kinase 1) (HARK1)
 GN STK6 OR STK15 OR AIK OR ARK1 OR AURA OR BTAK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=97298083; PubMed=9153231;
 RA Kinura M., Kotani S., Hattori T., Sumi N., Yoshioka T., Todokoro K.,
 RA Okano Y.;
 RT "Cell cycle-dependent expression and spindle pole localization of a
 RT novel human protein kinase, Aik, related to Aurora of Drosophila and
 RT Yeast Ipl1.";
 RT J. Biol. Chem. 272:13766-13771 (1997).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98183439; PubMed=9514916;
 RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
 RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
 RT "cDNA cloning, expression, subcellular localization, and chromosomal
 RT assignment of mammalian aurora homologues, aurora-related kinase (ARX)
 RT 1 and 2.";
 RL Biochem. Biophys. Res. Commun. 244:285-292 (1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast;
 RX MEDLINE=9842657; PubMed=9771714;
 RA Zhou H., Kuang J., Zhong L., Kuo W.-L., Gray J.W., Sahin A.,
 RA Brinkley B.R., Sen S.;
 RT "Tumour amplified kinase STK15/BTAK induces centrosome amplification,
 RT aneuploidy and transformation.";
 RT Nat. Genet. 23:189-193 (1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Wang L., Thibodeau S.N.;
 RT "Mutational analysis of the STK15 gene in human tumors.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Brown A.J.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Clee C.M.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.R.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Levaslatko M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,

DR GC: GO:0005634; C:nucleus; IDA.
 DR GC: GO:0005196; P:MAPKK cascade (cell wall biogenesis); IGI.
 DR GC: GO:0006468; P:protein amino acid phosphorylation; IDA.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR Pfam: PFC0069; Pkinase_I.
 DR ProDom: PDC00001; Prot_kinase; 1.
 DR SMART: SM0220; S_TK; 1.
 DR PROSITE: PSC0107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PSC0108; PROTEIN_KINASE_ST; 1.
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RESULT 16
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 RA Okano Y.;
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 RT novel human protein kinase, Aik, related to Aurora of Drosophila and
 RT Yeast Ipl1.";
 RT J. Biol. Chem. 272:13766-13771 (1997).
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 RX MEDLINE=98183439; PubMed=9514916;
 RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
 RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
 RT "cDNA cloning, expression, subcellular localization, and chromosomal
 RT assignment of mammalian aurora homologues, aurora-related kinase (ARX)
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 RC TISSUE=Breast;
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 RA Brinkley B.R., Sen S.;
 RT "Tumour amplified kinase STK15/BTAK induces centrosome amplification,
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 RP SEQUENCE FROM N.A.
 RA Wang L., Thibodeau S.N.;
 RT "Mutational analysis of the STK15 gene in human tumors.";
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 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Brown A.J.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Clee C.M.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.R.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Levaslatko M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,

PA Philimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
 RA Suze C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore A.C., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall Y., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Williams J., Wray P.W., Hubbard T., Lush R.M., Bentley P.R., Beck S.,
 RA Rogers J.,
 RC "The DNA sequence and comparative analysis of human chromosome 20";
 RL Nature 414:865-871(2001).
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EMBL; D84212; BAA3592.1; AUT_FRAME.
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 DR EMBL; AF011467; AAC23448.1; -
 DR EMBL; AF011468; AAC63932.1; -
 DR EMBL; AF195947; AAF29508.1; -
 DR EMBL; AF195942; AAF29508.1; JOINED.
 DR EMBL; AF195943; AAF29508.1; JOINED.
 DR EMBL; AF195944; AAF29508.1; JOINED.
 DR EMBL; AF195945; AAF29508.1; JOINED.
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 DR EMBL; AL121914; CAC12717.1; -
 DR EMBL; BC001280; AAH01280.1; -
 DR EMBL; BC002499; AAH02499.1; -
 DR EMBL; BC006423; AAH06423.1; -
 DR EMBL; BC027464; AAH27464.1; -
 DR GK; OL4965; -
 DR MIM; 602687; -
 DR MIM; 603072; -
 DR HSP; P24941; 1BUH.
 DR Genew; HGNC:11409; STK6.
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0005819; C:spindle; TAS.
 DR GO; GO:0007067; P:mitosis; TAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR01245; Tyr_kinase.
 DR Pfam; PF03069; pkinase; 1.
 DR ProDom; PDC00001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.
 FT DOWAIN 133 383 PROTEIN KINASE.
 FT NP_BIND 139 147 ATP (BY SIMILARITY).
 FT BINDING 162 162 ATP (BY SIMILARITY).
 FT ACT_SITE 256 256 BY SIMILARITY.
 FT CONFLICT 31 31 F - S 1 (IN REF. 3).
 FT CONFLICT 57 57 V - S 1 (IN REF. 2).
 SQ SEQUENCE 403 AA; 45809 MW; 125F3594834CD157 CRC64;
 Query Match 81.8%; Score 36; DB 1; Length 403;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LLGKPPF 8
 DB 323 LVCKPPF 329
 RESULT 17
 STK6 XENLA
 ID STK6 XENLA STANDARD; PRT; 407 AA.
 AC 091820;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serine/threonine protein kinase Eg2 (EC 2.7.1.37) (pEg2) (p46Eg265).
 GN EG2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodidae; Xenopus.

CELL-CYCLE REGULATION.
 MEDLINE=21895866; PubMed=1193071;
 Taraka M., Teda A., Kanarori H., Ideguchi H., Yang J., Kitajima S.,
 Shigauchi Y.,
 "Cell-cycle dependent regulation of human aurora A transcription is mediated by periodic repression of E4F1";
 C. Biol. Chem. 277:10719-10726(2002).
 [6]
 REVIEW.
 MEDLINE=21306577; PubMed=1413463;
 Nigg E.A.,
 "Mitotic kinases as regulators of cell division and its checkpoints";
 Nat. Rev. Mol. Cell Biol. 2:212-224(2001).
 [7]
 FUNCTION: May play a role in cell cycle regulation during anaphase and/or telophase, in relation to the function of the centrosome/spindle pole region during chromosome segregation. May be involved in microtubule formation and/or stabilization. May play a key role during tumor development and progression.
 CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 SUBCELLULAR LOCATION: Localizes on centrosomes in interphase cells and at each spindle pole in mitosis.
 TISSUE SPECIFICITY: Highly expressed in testis and weakly in skeletal muscle, thymus and spleen. Also highly expressed in colon, ovarian, prostate, neuroblastoma, breast and cervical cancer cell lines. Expression is cell-cycle regulated, low in G1/S, accumulates during G2/M, and decreases rapidly after.
 PTM: Phosphorylated.
 DISEASE: Defects in STK6 are responsible for numerical centrosome aberrations including aneuploidy.
 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 AURORE SUBFAMILY.
 CAUTION: Ref.1 sequence differs from that shown due to frameshifts in positions 105, 125, 129, 235 and 241.
 CAUTION: Although authors have considered STK6 and STK15 as two different proteins, it is clear that they are the same protein.
 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

to the human gastrointestinal tract.";
 RE Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
 CC 1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC 1- SIMILARITY: CONTAINS 4 PASTA DOMAINS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AE014680; AAC24413.1;
 CC InterPro: IPR005543; PASTA.
 CC InterPro: IPR000719; Prot kinase.
 CC InterPro: IPR002293; Ser/Thr kinase.
 CC InterPro: IPR001245; Tyr_kinase.
 CC Pfam: PF03793; PASTA; 2.
 CC Pfam: PF03569; pkinase; 1.
 CC ProDom: PDC00001; Prot kinase; 1.
 CC SMART: SMC0740; PASTA; 4.
 CC SMART: SMC0220; S_TKc; 1.
 CC SMART: SMC0219; TYKc; 1.
 CC PROSITE: PS03007; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS03011; PROTEIN_KINASE_DOM; 1.
 CC PROSITE: PS03008; PROTEIN_KINASE_ST; 1.
 CC KW Hypothetical protein; Transferase; Serine/threonine protein kinase;
 KW ATP-binding; Repeat; Complete proteome.
 FT DOMAIN 1 1 285 PROTEIN KINASE
 FT DOMAIN 2 286 467 PASTA 1
 FT DOMAIN 3 468 536 PASTA 2
 FT DOMAIN 4 537 601 PASTA 3
 FT DOMAIN 5 602 666 PASTA 4
 FT DOMAIN 6 667 689 GLY RICH
 FT NP_BIND 23 28 ATP (BY SIMILARITY)
 FT BINDING 43 43 ATP (BY SIMILARITY)
 FT ACT_SITE 146 146 BY SIMILARITY
 SQ SEQUENCE 690 AA; 72243 MW; 6A419EABCE5D32D CRC64;

 Query Match 91.8%; Score 36; DB 1; Length 690;
 Best Local Similarity 75.0%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

 QY : MLGKPPF 8
 D6 217 MLGKPPF 224

 RESULT 20
 ID HUPK_RHOCA STANDARD; PRT; 294 AA.
 AC F20797;
 DT 01-JUL-1993 (Rel. 26, Created;
 DT 01-JUL-1993 (Rel. 26, Last sequence update;
 DT 16-OCT-2001 (Rel. 40, Last annotation update;
 DE Hydrogenase expression/formation protein hupK
 GN HUPK.
 OS Rhodobacter capsulatus (Rhodospirillum rubrum)
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
 CC Rhodobacteraceae; Rhodobacter.
 CX NCBI_TaxID=10621;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91177833; PubMed=2007559;
 RA Xu H.W., Wall J.D.;
 RT "Clustering of genes necessary for hydrogen oxidation in Rhodobacter
 RT capsulatus.";
 RL J. Bacteriol. 173:2401-2405(1991).
 RP ERRATUM.
 RA Pepio A.M., Fan X., Sossin W.S.;
 RL J. Biol. Chem. 273:22856-22856(1998).
 CC 1- FUNCTION: THIS IS CALCIUM-DEPENDENT, PHOSPHOLIPID-DEPENDENT.

RX MEDLINE=93268090; PubMed=8497190;
 RA Colbeau A., Richaud P., Toussaint B., Caballero F.J., Elster C.,
 RA Delphin C., Smith R.L., Chabert J., Vignals P.M.;
 RT "Organization of the genes necessary for hydrogenase expression in
 RT Rhodobacter capsulatus. Sequence analysis and identification of two
 RT hyp regulatory mutants.";
 RL Mol. Microbiol. 8:15-29(1993).
 CC 1- SIMILARITY: BELONGS TO THE HUPK FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: M55089; AAA72924.1;
 CC EMBL: 215089; CAA78803.1;
 CC PIR: S32947; S32947.
 CC CONFLICT 70 70 A -> R (IN REF. 2).
 SQ SEQUENCE 294 AA; 30222 MW; 2669E8B70AF35EDA CRC64;

 Query Match 79.5%; Score 35; DB 1; Length 294;
 Best Local Similarity 85.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY : MLGKPP 7
 D6 31 LLGKPP 37

 RESULT 21
 ID KPCI_APLCA STANDARD; PRT; 649 AA.
 AC Q16974;
 DT 30-MAY-2000 (Rel. 39, Created;
 DT 30-MAY-2000 (Rel. 39, Last sequence update;
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Calcium-dependent protein kinase C (EC 2.7.11.-) (APL I).
 GN PKC1.
 OS Aplysia californica (California sea hare).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 CC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
 CC Aplysioidea; Aplysiidae; Aplysia.
 CX NCBI_TaxID=6500;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91332620; PubMed=1869917;
 RA Kruger K.E., Sossin W.S., Sacktor T.C., Bergold P.J., Beushausen S.,
 RA Schwartz J.H.;
 RT "Cloning and characterization of Ca(2+)-dependent and Ca(2+)-
 RT independent PKCs expressed in Aplysia sensory cells.";
 RL J. Neurosci. 11:2303-2313(1991).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=93194877; PubMed=8449941;
 RA Sossin W.S., Diaz-Arastia R., Schwartz J.H.;
 RT "Characterization of two isoforms of protein kinase C in the nervous
 RT system of Aplysia californica.";
 RL J. Biol. Chem. 268:5763-5768(1993).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=98334636; PubMed=9668085;
 RA Pepio A.M., Fan X., Sossin W.S.;
 RT "The role of C2 domains in Ca2+-activated and Ca2+-independent protein
 RT kinase Cs in aplysia.";
 RL J. Biol. Chem. 273:19040-19048(1998).
 RN [4]
 RP ERRATUM.
 RA Pepio A.M., Fan X., Sossin W.S.;
 RL J. Biol. Chem. 273:22856-22856(1998).
 CC 1- FUNCTION: THIS IS CALCIUM-DEPENDENT, PHOSPHOLIPID-DEPENDENT.

CC SERINE- AND THREONINE-SPECIFIC ENZYME. ACTIVATION OF PKC BY
 CC SEROTONIN RESULTS IN PRESYNAPTIC FACILITATION OF DEPRESSED
 CC SENSORY-TO-MOTOR NEURON SYNAPSES, WHICH IS THOUGHT TO UNDERLIE
 CC BEHAVIORAL DISINHIBITION.
 CC FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
 CC SIMILARITY).
 CC ENZYME REGULATION: ACTIVATED BY PHOSPHATIDYL SERINE.
 CC SUBCELLULAR LOCATION: CYTOPLASMIC; TRANSLOCATED TO NEURONAL
 CC MEMBRANES
 CC SIMILARITY: Contains 2 zinc-dependent phorbol ester and DAG
 CC binding domains.
 CC SIMILARITY: Contains: C2 domain.
 CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: N94883; AAA27770.2; --
 CC HSSP: P05697; ITEN.
 CC InterPro: IPR000008; C2.
 CC InterPro: IPR002219; DAG_PE-bind.
 CC InterPro: IPR000961; Pkinase C.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR002290; Ser_thr_pkinase.
 CC Pfam: PF00168; C2; 1.
 CC Pfam: PF00130; DAG_PE-bind; 2.
 CC Pfam: PF00069; pkinase; 1.
 CC Pfam: PF02433; pkinase; 1.
 CC PRINTS: PR00360; C2DOMAIN.
 CC PRINTS: PR00008; DAGPEDOMAIN.
 CC ProDom: PD000001; Prot_kinase; 1.
 CC SMART: SM00139; C1; 2.
 CC SMART: SM00239; C2; 1.
 CC SMART: SM00133; S_TK_X; 1.
 CC SMART: SM00220; S_TK; 1.
 CC PROSITE: PS00499; C2_DOMAIN; 1.
 CC PROSITE: PS00479; DAG_PE_BIND_DOM; 1; 2.
 CC PROSITE: PS00081; DAG_PE_BIND_DOM; 2; 2.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC ATP-binding: Transferase; Serine/threonine-protein kinase;
 CC Phorbol-ester binding; Zinc; Repeat.
 CC FT DOMAIN 22 71 PHORBOL-ESTER AND DAG BINDING 1.
 CC FT DOMAIN 96 135 PHORBOL-ESTER AND DAG BINDING 2.
 CC FT DOMAIN 157 244 C2 DOMAIN.
 CC FT DOMAIN 320 578 PROTEIN KINASE.
 CC FT NP_BIND 326 334 ATP (BY SIMILARITY).
 CC FT BINDING 349 349 ATP (BY SIMILARITY).
 CC FT ACT_SITE 444 444 BY SIMILARITY.
 CC SEQUENCE 649 AA; 74079 MW; A5125339284F310 CRC64;

Query Match 79.5%; Score 35; DB 1; Length 649;
 Best Local Similarity 75.0%; Pred. No. 29;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 DB 512 MLAGQPPF 519

RESULT 22
 K2C1_LYTP1 STANDARD; PRT; 658 AA.
 ID_KF01_LYTP1

AC 025378;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Protein kinase C (EC 2.7.1.1).
 GN PKC.
 OS Ectechinus pictus (Painted sea urchin).
 OS Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Temnopleurida; Toxopneustidae;
 OC Ectechinus.
 OC NCBI_TaxID:7653;
 RN [1]_SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RC TISSUE:Ovary;
 RA Rakow T.L., Shen S.S.;
 RT "Molecular cloning and characterization of protein kinase C from the
 RL sea urchin Ectechinus pictus".
 RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
 CC FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
 CC SERINE- AND THREONINE-SPECIFIC ENZYME (BY SIMILARITY).
 CC FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
 CC SIMILARITY).
 CC SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC SIMILARITY: Contains: C2 domain.
 CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC
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 CC
 CC EMBL: U02967; AA03447.1; --
 CC HSSP: P05697; ITEN.
 CC InterPro: IPR000008; C2.
 CC InterPro: IPR002219; DAG_PE-bind.
 CC InterPro: IPR000961; Pkinase C.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR002290; Ser_thr_pkinase.
 CC Pfam: PF00168; C2; 1.
 CC Pfam: PF00130; DAG_PE-bind; 2.
 CC Pfam: PF00069; pkinase; 1.
 CC Pfam: PF02433; pkinase; 1.
 CC PRINTS: PR00360; C2DOMAIN.
 CC PRINTS: PR00008; DAGPEDOMAIN.
 CC ProDom: PD000001; Prot_kinase; 1.
 CC SMART: SM00109; C1; 2.
 CC SMART: SM00239; C2; 1.
 CC SMART: SM00133; S_TK_X; 1.
 CC SMART: SM00220; S_TK; 1.
 CC PROSITE: PS00499; C2_DOMAIN; 1; 1.
 CC PROSITE: PS00479; DAG_PE_BIND_DOM; 1; 2.
 CC PROSITE: PS00081; DAG_PE_BIND_DOM; 2; 2.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC ATP-binding: Transferase; Serine/threonine-protein kinase;
 CC Phorbol-ester binding; Zinc; Repeat.
 CC FT DOMAIN 28 77 PHORBOL-ESTER AND DAG BINDING 1.
 CC FT DOMAIN 93 142 PHORBOL-ESTER AND DAG BINDING 2.
 CC FT DOMAIN 164 251 C2 DOMAIN.
 CC FT DOMAIN 325 583 PROTEIN KINASE.
 CC FT NP_BIND 331 339 ATP (BY SIMILARITY).
 CC FT BINDING 354 354 ATP (BY SIMILARITY).

```

FT ACT_SITE 449 449 BY SIMILARITY.
SQ SEQUENCE 658 AA; 74871 MW; 7485A27A49C835A2 CRC64;

Query Match 79.5%; Score 35; DB 1; Length 658;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MLLGKPPF 8
II :|||
DB 517 MLAGQPPF 524

RESULT 23
KPCA_BOVIN
ID KPCA_BOVIN STANDARD; PRT; 672 AA.
AC P04459;
DT 13-AUG-1987 (Rel. 05, Created)
DE 15-AUG-1987 (Rel. 05, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein Kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
GN PRKCA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9911;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96289425; PubMed=3755547;
RA Parker P.J., Gonsens L., Terry N., Rhee L., Young S., Chen Z.,
RA Sabel S., Waterfield M.D., Gillich A.;
RA "The complete primary structure of protein kinase C -- the major
RA phorbol ester receptor.";
RL Science 233:853-859(1986).
RN [2]
RP REVIEW.
RX MEDLINE=88318921; PubMed=3045562;
RA Nishizuka Y.;
RA "The molecular heterogeneity of protein kinase C and its implications
RA for cellular regulation.";
RL Nature 334:661-665(1988).
CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
CC serine and threonine-specific enzyme.
CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn
CC phosphorylates a range of cellular proteins. PKC also serves as
CC the receptor for phorbol esters, a class of tumor promoters.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated
CC protein.
CC -!- SUBUNIT: Interacts with PRKABP by stimulating
CC -!- SIMILARITY: Contains 2 zinc-dependent phospholipid ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- PKC SUBFAMILY.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; M13973; AAA30706.1;
CC PIR; A00621; KIBOC.
CC HSP; P05697; ITBN.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002219; DAG_PE-bind.
CC InterPro; IPR000961; PKinase_C.
CC InterPro; IPR000719; Prot_Kinase.
CC InterPro; IPR002290; Ser_Thr_pkinase.
CC Pfam; PF00168; C2; 1.
CC Pfam; PF00130; DAG_PE-bird; 2.

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DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; Dkinase_C; 1.
DR PRINTS; PR00160; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMC0109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S-TK_X; 1.
DR SMART; SM00220; S-TKG; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 672 AA; 76837 MW; 97BF46DB80FC21A CRC64;

Query Match 79.5%; Score 35; DB 1; Length 672;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MLLGKPPF 8
II :|||
DB 531 MLAGQPPF 538

RESULT 24
KPCA_HUMAN
ID KPCA_HUMAN STANDARD; PRT; 672 AA.
AC P17252; O15137; Q96RE4;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein Kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
GN PRKCA OR PKCA OR PRKACA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=90245676; PubMed=2336401;
RA Finkenzeller G., Warme D., Hug H.;
RA "Sequence of human protein kinase C alpha.";
RL Nucleic Acids Res. 18:2183-2183(1990).
RN [2]
RP SEQUENCE OF 15-445 FROM N.A.
RX MEDLINE=91332033; PubMed=1714454;
RA McSwine-Kennick R.L., McKeegan E.M., Johnson M.D., Morin M.J.;
RA "Phorbol diester-induced alterations in the expression of protein
RA kinase C isozymes and their mRNAs. Analysis in wild-type and phorbol
RA diester-resistant HL-60 cell clones.";
RL J. Biol. Chem. 266:15135-15143(1991).
RN [3]
RP SEQUENCE OF 1-57 FROM N.A.
RA Haridas V., Hackenbruck J., Glaser R.I.;
RA "Homo sapiens protein kinase C alpha 5'-flanking sequence.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,

```



```

DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00130; DAG_PE_BIND_2.
DR Pfam: PF00369; pkinase; 1.
DR Pfam: PF00433; pkinase; C; 1.
DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR PRODOM: PD00000; Prot_kinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SM00239; C2; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK_X; 1.
DR PROSITE: PS00499; C2_DOMAIN_1; 1.
DR PROSITE: PS00004; C2_DOMAIN_2; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 C2 DOMAIN.
FT DOMAIN 172 260 C2 DOMAIN.
FT NP_BIND 339 597 PROTEIN KINASE.
FT BINDING 345 353 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT VARIANT 106 106 L -> V (IN MUTANT FORM JVD5).
FT VARIANT 111 111 S -> G (IN MUTANT FORM JVD5).
FT VARIANT 240 240 L -> Q (IN MUTANT FORM JVD5).
FT VARIANT 339 339 F -> L (IN MUTANT FORM JVD5).
FT CONFLICT 147 147 D -> V (IN REF. 2).
FT CONFLICT 218 218 N -> T (IN REF. 2).
FT CONFLICT 277 278 AH -> L (IN REF. 2).
FT CONFLICT 313 313 V -> A (IN REF. 2).
FT CONFLICT 467 467 N -> D (IN REF. 2).
FT CONFLICT 472 472 N -> D (IN REF. 2).
FT CONFLICT 576 576 Q -> H (IN REF. 2).
SQ SEQUENCE 672 AA; 76852 MW; 3348483522B9D50 CRC64.

Query Match: 79.58; Score 35; DB 1; Length 672;
Best Local Similarity 75.08; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY I MLACKPPF 8
DB 531 MLACQPPF 538

RESULT 26
KPCA_RABIT
ID KPCA_RABIT STANDARD; PRT; 672 AA.
AC P10102;
DT 01-MAR-1999 (Rel. 10, Created:
DT 01-MAR-1999 (Rel. 10, Last sequence update:
DT 15-SEP-2003 (Rel. 42, Last annotation update:
DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC alpha) (PKC-A).
GN PRKCA.
OS Eukaryotae; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Cuniculidae.
CX NCBI_TaxID=9996;
RV [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
PA MEDLINE=97115893; PubMed=3808073;
RA Chao S., Kawasaki H., Imajob S., Suzuki K., Inagaki M., Yokokura H.,
RA Sakoh T., Hidaka H.;
RT "Tissue-specific expression of three distinct types of rabbit protein
kinase C.";
Nature 325:161-166(1987).
[2]
RP REVIEW
RX MEDLINE=88318921; PubMed=3045562;
RA Nishizuka Y.;
RT "The molecular heterogeneity of protein kinase C and its implications
for cellular regulation.";
Nature 334:661-665(1988).
CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
serine- and threonine-specific enzyme.
CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn
phosphorylates a range of cellular proteins. PKC also serves as
the receptor for phorbol esters, a class of tumor promoters.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts with PRKCAPB (By similarity).
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.

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EMBL: X04796; CAA28483.1;
PIR: C26037; KIRBC.
HSP: P04410; IAZ5.
InterPro: IPR000008; C2.
InterPro: IPR002219; DAG_PE_BIND.
InterPro: IPR000961; pkinase; C.
InterPro: IPR000719; Prot_kinase.
InterPro: IPR002290; Ser_thr_pkinase.
Pfam: PF00168; C2; 1.
Pfam: PF00130; DAG_PE_BIND_2.
Pfam: PF00069; pkinase; 1.
Pfam: PF00433; pkinase; C; 1.
PRINTS: PR00360; C2DOMAIN.
PRODOM: PD00000; Prot_kinase; 1.
SMART: SM00109; C1; 2.
SMART: SM00239; C2; 1.
SMART: SM00133; S_TK_X; 1.
SMART: SM00220; S_TK_X; 1.
PROSITE: PS00499; C2_DOMAIN_1; 1.
PROSITE: PS00004; C2_DOMAIN_2; 1.
PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 C2 DOMAIN.
FT DOMAIN 172 260 C2 DOMAIN.
FT NP_BIND 339 597 PROTEIN KINASE.
FT BINDING 345 353 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 672 AA; 76782 MW; 3D311367D3577A77 CRC64;

```

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QY      1 MLJGKPPF 8
DB      531 MLAGQPPF 538

RESULT 27
KPCA_RAT
ID KPCA_RAT STANDARD; PRT: 672 AA.
AC P05656;
DT 01-NOV-1988 (Rel. 09, Created);
DT 01-NOV-1988 (Rel. 09, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update);
DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A);
GN PKCA OR PKCA;
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98262515; PubMed=3387228;
RA Cno Y., Fujii T., Igarashi K., Kikkawa U., Ogita K., Nishizuka Y.;
RT "Nucleotide sequences of cDNAs for alpha and gamma subtypes of rat
  brain protein kinase C";
RL Nucleic Acids Res. 16:5199-5200(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98330055; PubMed=3666147;
RA Kikkawa U., Ogita K., Cno Y., Asaka Y., Shearman M.S., Fujii T.,
  Ase K., Sekiguchi K., Igarashi K., Nishizuka Y.;
RT "The common structure and activities of four subtypes of rat brain
  protein kinase C family";
RL FEBS Lett. 223:212-216(1987).
RN [3]
RP REVIEW.
RX MEDLINE=88318921; PubMed=3045562;
RA Nishizuka Y.;
RT "The molecular heterogeneity of protein kinase C and its implications
  for cellular regulation.";
RL Nature 334:661-665(1988).
CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
  serine- and threonine-specific enzyme.
CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn
  phosphorylates a range of cellular proteins. PKC also serves as
  the receptor for phorbol esters, a class of tumor promoters.
CC -!- CATALYTIC ACTIVITY: ATP + a protein + H2O = a phosphoprotein.
CC -!- SUBUNIT: Interacts with PKCdelta by similarity.
CC -!- SIMILARITY: Contains 2 zinc dependent phorbol ester and DAG
  binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THP FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (see http://www.isb.ch/announce/
  or send an email to license@isb-sib.ch).
CC
CC EMBL: X07286; CAA30266.1;
CC PIR: S02248; MRTC.
CC PDB: 1DSY; 26-CAN-00.
CC InterPro: IPR000308; C2.
CC InterPro: IPR002219; DAG_PE-bind.
CC InterPro: IPR000961; Pkinase_C.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR022490; Ser_thr_kinase.
CC Pfam: PF00168; C2; 1.

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DR Pfam: PF00130; DAG_PE-bind; 2.
DR Pfam: PF00669; pkinase; 1.
DR Pfam: PF00433; pkinase_C; 1.
DR PRINTS: PRO0360; C2DOMAIN.
DR PRINTS: PRO0338; DAGFODOMAIN.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SM00239; C2; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00499; C2_DOMAIN_1; 1.
DR PROSITE: PS00044; C2_DOMAIN_2; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PS00307; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; Atp-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KM Phosphorylation; 3D-structure
FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT DOMAIN 339 597 PROTEIN KINASE.
FT NP_BIND 345 353 ATP (BY SIMILARITY).
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 672 AA; 76732 MW; 94889E7339C17719 CRC64;

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Query Match 79.5%; Score 35; DB 1; Length 672;

Best Local Similarity 75.0%; Pred No: 30;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      1 MLJGKPPF 8
      |||||
DB      531 MLAGQPPF 538

```

RESULT 28

```

KPCG_BOVIN
ID KPCG_BOVIN STANDARD; PRT: 682 AA.
AC P05128;
DT 13-AUG-1987 (Rel. 05, Created);
DT 13-AUG-1987 (Rel. 05, Last sequence update);
DT 15-JUL-1999 (Rel. 38, Last annotation update);
DE Protein kinase C, gamma type (EC 2.7.1.37) (PKC-gamma) (Fragment).
GN PRKCG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86289426; PubMed=3755548;
RA Coussens L., Parker P.J., Rhee L., Yang-Feng T.L., Chen E.,
  Waterfield M.D., Francke U., Ullrich A.;
RT "Multiple, distinct forms of bovine and human protein kinase C
  suggest diversity in cellular signaling pathways.";
RL Science 233:859-866(1986).
RN [2]
RP REVIEW.
RX MEDLINE=88318921; PubMed=3045562;
RA Nishizuka Y.;
RT "The molecular heterogeneity of protein kinase C and its implications
  for cellular regulation.";
RL Nature 334:661-665(1988).
CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
  SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
  PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS

```



```

DR MIM: 176980;
DR GC: GO:0034697; F-protein kinase C activity; TAS
DR GO: GO:0034668; P-protein amino acid phosphorylation; TAS
DR InterPro: IPR000008; C2
DR InterPro: IPR002219; DAG_PE-BIND
DR InterPro: IPR000961; PKINASE_C
DR InterPro: IPR000719; Prot_kinase
DR InterPro: IPR022290; Ser_thr_kinase
DR InterPro: IPR001245; Tyr_kinase
DR Pfam: PF00668; C2_1
DR Pfam: PF00130; DAG_PE-BIND; 2
DR Pfam: PF00069; pk_kinase; 1
DR Pfam: PF00433; pk_kinase_C; 1
DR PRINTS: PR00160; C2DOMAIN
DR PRINTS: PR00008; DAGPEDOMAIN
DR PRINTS: PR00139; TYRKINASE
DR ProDom: PDC00061; Prot_kinase; 1
DR SMART: SMC0109; C2; 2
DR SMART: SMC0133; S_TK_X; 1
DR SMART: SMC0220; S_TKC; 1
DR PROSITE: PS00499; C2_DOMAIN_1; 1
DR PROSITE: PS00004; C2_DOMAIN_2; 1
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1
DR PROSITE: PS00188; PROTEIN_KINASE_ST; 1
DR Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation; Polymorphism
FT DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1;
FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2;
FT DOMAIN 170 260 C2 DOMAIN;
FT DOMAIN 351 614 PROTEIN KINASE;
FT NP_BIND 357 365 ATP (BY SIMILARITY);
FT BINDING 380 380 ATP (BY SIMILARITY);
FT ACT_SITE 480 480 BY SIMILARITY;
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL);
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL);
FT VARIANT 141 141 R -> C;
FT VARIANT 415 415 H -> Q;
FT VARIANT 523 523 A -> D;
FT VARIANT 659 659 P -> S;
FT SEQUENCE 697 AA; 78447 MW; 1F511BAEEF135418164;
Query Match 79.5% Score 35; DR 1; Length 697;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGKPPF 8
DB 548 MLAGQPPF 555
ID -KPCG MOUSE STANDARD; PRT: 657 AA.
AC P05697;
DR 01-NOV-1988 (Rel. 09, Created);
DR 01-NOV-1988 (Rel. 09, Last sequence update);
DR 15-SEP-2003 (Rel. 42, Last annotation update);
DE Protein kinase C, gamma type (EC 2.7.1.37) (PKC-gamma);
GN PKCG OR PKCG OR PKCC OR PKCK.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat);
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CC NCBI_TaxID:10090, 10116;

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RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=rat; TISSUE=Brain;
RX MEDLINE=88262515; PubMed=3387228;
RA Ono Y., Fujii T., Igarashi K., Kikkawa U., Ogita K., Nishizuka Y.;
RT "Nucleotide sequences of cDNAs for alpha and gamma subtypes of rat
RL brain protein kinase C.";
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=rat;
RX MEDLINE=86272097; PubMed=3755379;
RA Knopf J.L., Lee M.-H., Sultzman L.A., Kriz R.W., Loomis C.R.,
RW Hewick R.M., Bell R.M.;
RT "Cloning and expression of multiple protein kinase C cDNAs.";
RN [3]
RP SEQUENCE OF 1-56 FROM N.A.
RC SPECIES=rat;
RX MEDLINE=91060619; PubMed=2246272;
RA Chen K.H., Widen S.G., Wilson S.H., Huang K.P.;
RT "Characterization of the 5'-flanking region of the rat protein kinase
RL C gamma gene.";
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=mouse; TISSUE=Brain;
RX MEDLINE=93154595; PubMed=8428669;
RA Bowers B.J., Parham C.L., Sikeia J.M., Wehner J.M.;
RT "Isolation and sequence of a mouse brain cDNA coding for protein
RL kinase C-gamma isozyme.";
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=mouse; STRAIN=BALB/c; TISSUE=Brain;
RA Tseng C.P., Verma A.;
RT Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
RN [6]
RP STRUCTURE BY NMR OF 91-172.
RC SPECIES=rat;
RX MEDLINE=97419134; PubMed=9271501;
RA Xu R.X., Pawelczyk T., Xia T.-H., Brown S.C.;
RT "NMR structure of a protein kinase C-gamma phorbol-binding domain and
RL study of protein-lipid micelle interactions.";
RN [7]
RP BIOCHEMISTRY 36:10709-10717(1997).
CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07287; CAA30267.1; -
DR EMBL; M13707; AAA41874.1; -
DR EMBL; M55417; AAA41873.1; -
DR EMBL; X67129; CAA47608.1; -
DR EMBL; L28035; AAA39939.1; -
DR PIR; A05105; K1RTGC.
DR PIR; JN0548; JN0548.
DR PDB; 1TBN; 29-APR-98.

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DR PDB; 1TBO; 29-APR-98.
DR MGD; MG; 97597; PKCC.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-BIND.
DR InterPro; IPR000961; PKINASE_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-BIND; 2.
DR Pfam; PF0069; pkinase; 1.
DR Pfam; PF0433; pkinase; 1.
DR PRINTS; PR00160; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000003; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK_X; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation; 3D-structure.
FT DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 170 260 C2 DOMAIN.
FT NP_BIND 351 614 ATP (BY SIMILARITY).
FT BINDING 380 380 ATP (BY SIMILARITY).
FT ACT_SITE 480 480 BY SIMILARITY.
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT STRAND 103 105
FT STRAND 113 113
FT STRAND 120 120
FT TURN 123 124
FT STRAND 129 131
FT TURN 132 134
FT STRAND 137 138
FT TURN 140 145
SQ SEQUENCE 697 AA; 78357 MW; 548 MLAGQPPF 555

Query Match 79.5%; Score 35; DB 1; Length 697;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAGQPPF B
DB 548 MLAGQPPF 555

RESULT 31
KPGC RABIT STANDARD; PRT; 697 AA.
AC PIC829;
DT 31-JUL-1989 (Rel. 11, Created);
DT 01-JUL-1989 (Rel. 11, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Protein kinase C, gamma type (EC 2.7.1.37); (PKC-gamma); (PKC-delta).
GN PKCG
OS Crystallagus cuniculus (Rabbit);
OC Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Cricetologus.
OX NCBI_TaxID=9986;
RN 1;
RP SEQUENCE FROM N.A.

MEDLINE-88241036; PubMed-2837282;
Ohno S., Kawasaki H., Konno Y., Inagaki M., Hidaka H., Suzuki K.;
Biochemistry 27:2883-2087(1988).
-1- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
SERINE- AND THREONINE-SPECIFIC ENZYME.
-2- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
-3- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated
protein.
-4- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
binding domains.
-5- SIMILARITY: Contains 1 C2 domain.
-6- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-7- PKC SUBFAMILY.

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or send an email to licenses@isb-sib.ch).

EMBL; M19338; AAA31449.1;
PIR; A28708; KIRBGC.
HSP; P05697; IIBN.
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE-BIND.
DR InterPro; IPR000961; PKINASE_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-BIND; 2.
DR Pfam; PF0069; pkinase; 1.
DR Pfam; PF0433; pkinase; 1.
DR PRINTS; PR00160; C2DOMAIN.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000003; Prot_kinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK_X; 1.
DR PROSITE; PS00499; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation.
FT DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 170 260 C2 DOMAIN.
FT NP_BIND 351 614 ATP (BY SIMILARITY).
FT BINDING 380 380 ATP (BY SIMILARITY).
FT ACT_SITE 480 480 BY SIMILARITY.
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT STRAND 103 105
FT STRAND 113 113
FT STRAND 120 120
FT TURN 123 124
FT STRAND 129 131
FT TURN 132 134
FT STRAND 137 138
FT TURN 140 145
SQ SEQUENCE 697 AA; 78357 MW; 548 MLAGQPPF 555

Query Match 79.5%; Score 35; DB 1; Length 697;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAGQPPF B
DB 548 MLAGQPPF 555

```


CC 1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC S6 KINASE SUBFAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an e-mail to license@isb-sib.ch.
CC
DR EMBL: AB016869; BAA34422.1; AUT, INIT.
DR EMBL: AB019245; BAA37145.1;
DR EMBL: AF076931; AAD46063.1;
DR EMBL: AF099739; AAD20930.1;
DR EMBL: BC000294; AAH00094.1;
DR PIR: JE0377; JE0377.
DR HSSP: Q63450; 1A06.
DR Genew; HGNC:10437; RPS6KB2.
DR GO: GO:0094674; P:protein serine/threonine kinase activity; TAS.
DR GO: GO:0006412; P:protein biosynthesis; TAS.
DR GO: GO:0000074; P:regulation of cell cycle; TAS.
DR GO: GO:0037165; P:signal transduction; TAS.
DR InterPro: IPR000561; Pkinase_C.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR002290; Ser_Thr_Pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR Pfam: PF00433; Pkinase_C; 1.
DR ProDom: PDC00001; Prot_Kinase; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Serine/threonine protein kinase; Phosphorylation;
KW ATP-binding.
FT DOMAIN 67 328 PROTEIN KINASE.
FT DOMAIN 411 485 PRO-RICH.
FT NP_BIND 73 81 ATP (BY SIMILARITY).
FT BINDING 99 99 ATP (BY SIMILARITY).
FT ACT_SITE 194 194 BY SIMILARITY.
FT CONFLICT 90 90 MISSING (IN REF. 2).
FT CONFLICT 409 409 R -> C (IN REF. 2).
FT CONFLICT 420 420 V -> A (IN REF. 2).
SQ SEQUENCE 482 AA; 53493 MW; 502C631F44VDG9 NC(64).
Query March 77.3%; Score 34; DB 1; Length 485;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;
CY 1 MLTKGPPF 8
DB 262 MLTKGPPF 269
RESULT 34
ID K6B2_MOUSE STANDARD; PRT; 485 AA.
AC Q621M4
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Ribosomal protein S6 kinase beta 2 (p70-S6K2) (p70 ribosomal S6 kinase
DE beta 2) (p70-S6K2).
GN RPS6KB2
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=99043870; PubMed=9822628;

RA Shima H., Pende M., Chen Y., Fumagalli S., Thomas G., Kozma S.C.;
RT "Disruption of the p70(s6k)/p85(s6k) gene reveals a small mouse
RL EMBO J. 17:6649-6659(1998).
CC 1- FUNCTION: PHOSPHORYLATES SPECIFICALLY RIBOSOMAL PROTEIN S6.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC S6 KINASE SUBFAMILY.
CC
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CC
DR EMBL: AJ007938; CAA07774.1;
DR HSSP: Q63450; 1A06.
DR MGD; MG1:1927343; Rps6kb2.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR002290; Ser_Thr_Pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR Pfam: PF00433; Pkinase_C; 1.
DR ProDom: PDC00001; Prot_Kinase; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Serine/threonine protein kinase; Phosphorylation;
KW ATP-binding.
FT DOMAIN 67 328 PROTEIN KINASE.
FT DOMAIN 411 485 PRO-RICH.
FT NP_BIND 73 81 ATP (BY SIMILARITY).
FT BINDING 99 99 ATP (BY SIMILARITY).
FT ACT_SITE 194 194 BY SIMILARITY.
SQ SEQUENCE 485 AA; 53538 MW; 396929ADAB0F6CB6 CRC64;
Query March 77.3%; Score 34; DB 1; Length 485;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY 1 MLTKGPPF 8
DB 262 MLTKGPPF 269
RESULT 35
ID KDC2_DROME STANDARD; PRT; 502 AA.
AC P16912;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase DC2 (EC 2.7.1.-).
GN PKA-C3 OR DC2
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN=Canton-S;
RX MEDLINE=89107990; PubMed=3215511;
RA Kalderon D., Rubin G.M.;
RC "Isolation and characterization of Drosophila cAMP-dependent protein
RT kinase genes".
RJ Genes Dev. 2:1539-1556(1988).
CC 1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC 1- TISSUE SPECIFICITY: MORE ABUNDANT IN ADULT HEAD THAN ADULT BODY.
CC 1- DEVELOPMENTAL STAGE: IN EMBRYONS, PUPAE AND ADULTS.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMP SUBFAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X16961; CAA34835.1; -
 CC HSSP: P05132; IATP.
 CC FLYBase: FBgn000489; Pka-C3
 CC GO: GO:0038602; F-AMP-dependent protein kinase, catalyze act. ; IDA.
 CC GO: GO:0036468; P-protein amino acid phosphorylation; IDA.
 CC InterPro: IPR000961; Pkinase_C.
 CC InterPro: IPR000719; Prot Kinase.
 CC InterPro: IPR002293; Ser/Thr kinase.
 CC InterPro: IPR001245; Tyr_kinase.
 CC Pfam: PF00369; Pkinase; 1.
 CC PRINTS: PF00433; Pkinase_C; 1.
 CC PROSITE: PRO109; TYRKINASE.
 CC ProDom: PD003001; Prot kinase; 1.
 CC SMART: SY00133; S TK_X; 1.
 CC SMART: SY00220; S_TKc; 1.
 CC PROSITE: PS0107; PROTEIN KINASE ATP; 1.
 CC PROSITE: PS0108; PROTEIN KINASE ST; 1.
 CC PROSITE: PS0311; PROTEIN KINASE DOM; 1.
 CC KX Transferase; Serine/threonine-protein kinase; ATP-binding.
 CC FT DOMAIN 193 447 PROTEIN KINASE
 CC FT NP_BIND 193 207 ATP [BY SIMILARITY]
 CC FT BINDING 222 222 ATP [BY SIMILARITY]
 CC FT ACT_SITE 316 316 BY SIMILARITY
 CC SQ SEQUENCE 502 AA; 56960 MW; CAA674A5A40191D CRC64;
 CC
 CC Query Match 77.3%; Score 14; DB 1; Length 502;
 CC Best local Similarity 75.3%; Pred. No. 35;
 CC Matches 6; Conservative 1; Mismatches 0; Gaps 0;
 CC
 CC QY : MLVGYGFF A
 CC II : I I
 CC QK 38: MLVGYGFF 388
 CC
 CC RESULT 16
 CC PERP_HUMAN
 CC ID PERP_HUMAN STANDARD; PRT; 388 AA.
 CC AC P14222
 CC DT 01-JAN-1993 (Ref. 13, Created:
 CC DT 01-APR-1993 (Ref. 14, Last sequence update)
 CC DT 28-FEB-2003 (Ref. 41, Last annotation update)
 CC DE Perforin, precursor (P1) (Lymphocyte pore forming protein) (PFP)
 CC DE (Cytolysin)
 CC DE PRT; CR PFP.
 CC OS Homo sapiens (Human)
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CC CX NCBI TaxID:9606;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RA MEDLINE=9007533; PubMed=2592021;
 CC RA Lichterfeld M.G., Podack E.R.;
 CC RT "Structure of the human perforin gene. A simple gene organization
 CC with interesting potential regulatory sequences.";
 CC J. Immunol. 143:4267-4274 (1989).
 CC (2).
 CC RP SEQUENCE FROM N.A.
 CC RA MEDLINE=88334729; PubMed=3419519;
 CC RA Lichterfeld M.G., Olsen K.J., Lu P., Liang D.M., Karsenti A.,
 CC Hegerl R., Podack E.R.;
 CC RT "Structure and function of human perforin".
 CC Nature 335:448-451 (1988).
 CC

RP SEQUENCE FROM N.A.
 RX MEDLINE=9007533; PubMed=2592021;
 RA Shinkai Y., Yoshida K.M., Maeda K., Kobata T., Maruyama K.,
 RA Yodoi J., Yagita H., Okumura K.;
 RT "Molecular cloning and chromosomal assignment of a human perforin
 RT (PFP) gene.";
 RL Immunogenetics 30:452-457 (1989).
 RN [4]
 RP SEQUENCE OF 520-555 FROM N.A., AND INDUCTION.
 RC TISSUE=Natural killer cells;
 RX MEDLINE=96265183; PubMed=8676885;
 RA Goebel W.S., Schloemer R.H., Brahmi Z.;
 RT "Target cell-induced perforin mRNA turnover in NK3.3 cells is mediated
 RT by multiple elements within the mRNA coding region.";
 RL Mol. Immunol. 33:341-349 (1996).
 RN [5]
 RP 3D-STRUCTURE MODELING OF MEMBRANE-SPANNING DOMAIN (MSD).
 RX MEDLINE=90370039; PubMed=2395434;
 RA Peitsch M.C., Amiguet P., Guy R., Brunner J., Maizel J.V. Jr.,
 RA Tschopp J.;
 RT "Localization and molecular modelling of the membrane-inserted domain
 RT of the ninth component of human complement and perforin.";
 RL Mol. Immunol. 27:589-602 (1990).
 RN [6]
 RP VARIANTS HPLH2 GLY-183; TRP-225; SER-252; TYR-279; LEU-345 AND
 RP GLU-429.
 RX MEDLINE=20050957; PubMed=10581959;
 RA Stepp S.E., Dufourcq-Lageouse R., Le Deist F., Bhawan S., Certain S.,
 RA Mathew P.A., Henter J.-I., Bennett M., Fischer A., de Saint Basile G.,
 RA Kumar V.;
 RT "Perforin gene defects in familial hemophagocytic
 RT lymphohistiocytosis.";
 RL Science 286:1957-1959 (1999).
 RN [7]
 RP VARIANTS HPLH2 MET-50; ASP-224 AND LYS-285 DEL.
 RX MEDLINE=21090530; PubMed=11179037;
 RA Goerandotter Ericsson K., Fadel B., Nilsson-Ardnor S., Gueguy A.,
 RA Soederhaell C., Samuelsson A., Janka G., Schneider M., Gueguy A.,
 RA Yaman N., Revesz T., Egeler R., Jahnukainen K., Storm-Mathisen I.,
 RA Haraldsson A., Poole J., de Saint Basile G., Nordenskjöld M.,
 RA Henter J.-I.;
 RT "Spectrum of perforin gene mutations in familial hemophagocytic
 RT lymphohistiocytosis.";
 RL Am. J. Hum. Genet. 68:590-597 (2001).
 CC -!- FUNCTION: IN THE PRESENCE OF CALCIUM, PERFORIN POLYMERIZES INTO
 CC TRANSMEMBRANE TUBULES AND IS CAPABLE OF LYSING NON-SPECIFICALLY
 CC A VARIETY OF TARGET CELLS.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC GRANULES OF CYTOLYTIC
 CC T-LYMPHOCYTES.
 CC -!- INDUCTION: Repressed by contact with target cells.
 CC -!- DISEASE: Defects in PFI are a cause of familial hemophagocytic
 CC lymphohistiocytosis type 2 (HPLH2) [MIM:603553], also known as
 CC FHL. HPLH2 is a rare and lethal autosomal recessive disorder of
 CC early childhood characterized by excessive immune activation.
 CC Patients have a nonmalignant accumulation and multivisceral
 CC infiltration of activated T lymphocytes and histiocytes
 CC (macrophages).
 CC -!- SIMILARITY: TO COMPLEMENT FACTORS C6, C7, C8, AND C9.
 CC -!- SIMILARITY: Contains 1 C2 domain.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC
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 CC
 CC EMBL: M31951; AAA60167.1; -
 CC EMBL: X13224; CAA31612.1; -
 CC EMBL: M28193; AAA60065.1; -
 CC DR
 CC DR


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DR PIR: S22127.
DR HSP: Q63450; IAO6.
DR FlyBase: F5gn003124; polo.
DR GO: GO:00035813; C:centrosome; IDA.
DR GO: GO:0005819; C:spindle; IDA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR GO: GO:0007140; F:female meiosis; IMP.
DR GO: GO:0007671; P:mitosis; IMP.
DR InterPro: IPR000959; POLO_box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PFC0659; pkinase; 1.
DR Pfam: PFC0659; POLO_box; 2.
DR PrcDom: PC002001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS50078; POLO_BOX; 2.
DR PROSITE: PS0137; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00311; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS0108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
FT DOMAIN 25 277
FT NP_BIND 31 39
FT BINDING 54 54
FT ACT_SITE 148 148
FT DOMAIN 398 461
FT DOMAIN 496 564
FT CONFLICT 187 187
FT SEQUENCE 576 AA; 66973 MW; 5C2B89AC0E886FAD CRC64;

Query Match 77.3%; Score 34; DB 1; Length 576;
Best Local Similarity 62.5%; Pred.No. 4;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MJLCKPPF 8
Ch 216 LKVGQPPF 223

RESULT 39
MPS1_YEAST STANDARD; PRT: 764 AA.
AC P54153;
CT 01-OCT-1996 (Rel. 34, Created);
CT 01-OCT-1996 (Rel. 34, Last sequence update);
CT 16-OCT-2001 (Rel. 40, Last annotation update);
DE Serine/threonine protein kinase MPS1 (EC 2.7.11); Regulatory cell
DE Proliferation kinase 1;
GN MPS1 OR RPK1 OR YUL028C OR YJ2785.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetidae; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae;
OC KCB1_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ELL00;
RX MEDLINE=94301294; PubMed=8028580;
RA Poch C., Schwob E., de Fraipont F., Camasses A., Bordonne R.,
RA Martin R.P.;
RT "RpK1, an essential yeast protein kinase involved in the regulation
RT of the onset of mitosis, shows homology to mammalian dual-specificity
RT kinases.";
RL Mol. Gen. Genet. 243:641-653 (1994);
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=9719792; PubMed=9046088;
RA Saren A.M., Lamaren P., Lejarcegui J.B., Paulin L.;
RT "The sequence of a 36.7 kb segment on the left arm of chromosome IV
RT from Saccharomyces cerevisiae reveals 20 non-overlapping open reading
RT frames (ORFs) including S1T4, FAD1, NAV1, RN11, S1R2, NAT1, PRP9,
RT ACT2 and MPS1 and 11 new ORFs.";
RL Yeast 13:65-72 (1997);
RN [3]

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RP CHARACTERIZATION AND MUTAGENESIS OF ASP-580.
RX MEDLINE=95255223; PubMed=7737118;
RA Lauze E., Stoelcker B., Luca F.C., Weiss E., Schutz A.R., Winey M.;
RT "Yeast spindle pole body duplication gene MPS1 encodes an essential
RT dual specificity protein kinase.";
RL EMBO J. 14:1655-1663 (1995).
CC 1- FUNCTION: INVOLVED IN THE REGULATION OF THE ONSET OF MITOSIS.
CC INVOLVED IN A PATHWAY THAT COORDINATES CELL PROLIFERATION AND
CC DIFFERENTIATION. IMPLICATED IN SPINDLE POLE BODY (SPB)
CC DUPLICATION. DUAL SPECIFICITY KINASE THAT CAN PHOSPHORYLATE
CC SERINE, THREONINE AND TYROSINE RESIDUES.
CC 1- PTM: AUTOPHOSPHORYLATED.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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CC
CC EMBL: L08909; AAA88731.1;
CC EMBL: Z71781; CAA96461.1;
CC EMBL: Z74076; CAA98587.1;
CC PIR: S67561; S67561.
CC SGD: S0002186; MPS1.
CC GO: GO:0005599; C:kinetochore; IDA.
CC GO: GO:0005816; C:spindle pole body; IDA.
CC GO: GO:0004712; F:protein threonine/tyrosine kinase activity; IDA.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC Pfam: PFC0659; pkinase; 1.
CC ProDom: PD030001; Prot_kinase; 1.
CC SMART: SM00220; S_TKC; 1.
CC PROSITE: PS0107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS0108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 273 282
FT DOMAIN 309 315
FT DOMAIN 440 720
FT NP_BIND 446 454
FT BINDING 468 468
FT ACT_SITE 563 563
FT MUTAGEN 580 580
FT CONFLICT 146 146
FT CONFLICT 211 213
FT SEQUENCE 764 AA; 86827 MW; 26B17CDF8B8EB4D CRC64;

Query Match 77.3%; Score 34; DB 1; Length 764;
Best Local Similarity 62.5%; Pred.No. 54;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MJLCKPPF 8
DB 647 MIYKPPY 654

RESULT 39
PUR4_VIBCH STANDARD; PRT: 1297 AA.
AC Q9KTN2;
DT 16-OCT-2001 (Rel. 40, Created);
DT 16-OCT-2001 (Rel. 40, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Phosphoribosylformylglycinamide synthase (EC 6.3.5.3) (FGAM
DE synthase) (FGAMS) (formylglycinamide ribotide amidotransferase)
DE (FGARAT) (formylglycinamide ribotide synthetase).
GN PURL OR VCC869.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

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OC Vibrionaceae; Vibrio.
CX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E1 Tor N16961 / Serotype O1;
RC MEDLINE=20406233; PubMed=10952307;
RX Wedelberg J.F., Eisen J.A., Nelson W.C., Clayton P.A., Gwinn M.L.,
RA Dodson R., Haft D.H., Hickey E.K., Peterson C.D., Mayam J.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson E.,
RA Emolaeve M.D., Vamathevan S., Bass S., Qin H., Dragoi T., Sellers P.,
RA McDonald L., Butlerback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae";
RJ Nature 406:477-483(2000).
CC -1- CATALYTIC ACTIVITY: ATP + N(2)-formyl-N(1)-(5-phospho-D-
CC ribosyl)glycinamide + L-glutamine + H(2)O = ADP + phosphate + 2-
CC (formamido)-N(1)-(5-phospho-D-ribose)acetamide + L-glutamate.
CC -1- PATHWAY: De novo purine biosynthesis; fourth step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE FGAMS
CC FAMILY.
CC -1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
CC
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CC
CC -----
CC EMBL; AE004171; AAF94031.1; -
CC FIRM; AB2272; AB2272.
CC TIGR; VC0969; -
CC HAVAP; MF 00419; -
CC InterPro; IPR000728; AIRS-related.
CC Pfam; PF00586; AIRS; 1.
CC Pfam; PF02763; AIRS; 2.
CC Purine biosynthesis; Ligase; ATP-binding; Glutamine amidotransferase;
CC Complete proteome.
CC NP BIND 307 318 ATP (POTENTIAL).
CC AC SITE 1327 1337 GATASE (BY SIMILARITY).
CC SEQUENCE 1297 AA; 141420 MW; 02AF4F5D74269C3764.
CC
CC Query Match 77.3%; Score 34; DB 1; Length 1320;
CC Best Local Similarity 85.7%; Pred. No. 95;
CC Matches 6; Conservative 1; Mismatches 3; Indels 3; Gaps 0;
CC
CC QY 1 MLLGKPP 7
CC
CC DB 604 VLLGKPP 610
CC
CC RESULT 43
CC PUR4_NEIMA
CC AC PUR4_NEIMA STANDARD; PRT; 1320 AA.
CC Q9-WC5;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16 OCT-2001 (Rel. 40, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Phosphoribosylformylglycinamide synthase (EC 6.3.5.3) (FGAM
CC synthase) (FGAMS) (Formylglycinamide ribotide amidotransferase)
CC (FGARAT) (Formylglycinamide ribotide synthetase).
CC PURL OR NMA0445.
CC OS Neisseria meningitidis (serogroup A).
CC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
CC Neisseriaceae; Neisseria.
CC NCBI_TaxID=65699;
CC RN 1;
CC RP SEQUENCE FROM N.A.

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RC STRAIN=z2491 / Serogroup A / Serotype 4A;
RC MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltham T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajadream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis z2491";
RJ Nature 404:502-506(2000).
CC -1- CATALYTIC ACTIVITY: ATP + N(2)-formyl-N(1)-(5-phospho-D-
CC ribosyl)glycinamide + L-glutamine + H(2)O = ADP + phosphate + 2-
CC (formamido)-N(1)-(5-phospho-D-ribose)acetamide + L-glutamate.
CC -1- PATHWAY: De novo purine biosynthesis; fourth step.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE FGAMS
CC FAMILY.
CC -1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
CC
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CC
CC -----
CC EMBL; AL162753; CAB83743.1; -
CC PIR; G81961; G81961.
CC HAMAP; MF 00419; -
CC InterPro; IPR000728; AIRS-related.
CC Pfam; PF00586; AIRS; 1.
CC Pfam; PF02763; AIRS; 2.
CC Purine biosynthesis; Ligase; ATP-binding; Glutamine amidotransferase;
CC Complete proteome.
CC NP BIND 311 322 ATP (POTENTIAL).
CC AC SITE 1162 1162 GATASE (BY SIMILARITY).
CC SEQUENCE 1320 AA; 143790 MW; FEB32DC315CEDD50 CRC64;
CC
CC Query Match 77.3%; Score 34; DB 1; Length 1320;
CC Best Local Similarity 85.7%; Pred. No. 95;
CC Matches 6; Conservative 1; Mismatches 0; Indels 3; Gaps 0;
CC
CC QY 1 MLLGKPP 7
CC
CC DB 604 VLLGKPP 610
CC
CC Search completed: November 14, 2003, 13:25:58
CC Job time : 6.94286 secs

```

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OX protein : protein search, using sw model

Run on: November 14, 2003, 13:18:40 : Search time 24 seconds

(without alignment)
86.0:8 Million cell updates/sec

Title: US-09-736-076-16

Perfect score: 44

Sequence: MLLGRPF 8

Scoring table: BLCSM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258352604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 3

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp.archaea:
- 2: sp.bacteria:
- 3: sp.fungi:
- 4: sp.human:
- 5: sp.invertebrate:
- 6: sp.mammal:
- 7: sp.mic:
- 8: sp.organella:
- 9: sp.phage:
- 10: sp.plant:
- 11: sp.podent:
- 12: sp.virus:
- 13: sp.vertbrate:
- 14: sp.unclassified:
- 15: sp.virus:
- 16: sp.bacteriap:
- 17: sp.archaea:

Pred. No. is the number of results (including those to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	93.2	316	Q9BDK4	Q9BDK4 sus scrofa
2	41	93.2	372	Q8NTM6	Q8NTM6 homo sapien
3	41	93.2	666	Q9CXS4	Q9CXS4 xenopus lae
4	41	93.2	692	Q8K226	Q8K226 mus musculus
5	40	90.9	456	Q8MYE1	Q8MYE1 dictyosteli
6	39	88.6	270	Q95Z72	Q95Z72 caenorhabdi
7	39	88.6	325	Q8MG39	Q8MG39 caenorhabdi
8	39	88.6	371	Q20541	Q20541 caenorhabdi
9	39	88.6	454	Q8M3V7	Q8M3V7 asparagus o
10	39	88.6	465	Q8LFC1	Q8LFC1 arabidopsis
11	39	88.6	480	Q43380	Q43380 avena sativ
12	39	88.6	592	Q12721	Q12721 schizosacch
13	39	88.6	766	Q034C7	Q034C7 saccharomyc
14	38	86.4	526	Q9BDP8	Q9BDP8 sus scrofa
15	38	86.4	582	Q9G8B7	Q9G8B7 nematocent
16	38	86.4	598	P00032	P00032 xenopus lae

17	38	86.4	623	5	Q8IU35	Q8IU35 asterina pe
18	38	86.4	673	5	Q82567	Q82567 suberites d
19	38	86.4	677	5	Q96997	Q96997 geodia cydo
20	38	86.4	2883	16	Q8PEX7	Q8PEX7 xanthomonas
21	37	94.1	388	2	Q9KX10	Q9KX10 staphylococ
22	37	94.1	664	16	Q9UP8	Q9UP8 staphylococ
23	37	94.1	664	16	Q8NX14	Q8NX14 staphylococ
24	37	94.1	667	16	Q8CSV9	Q8CSV9 staphylococ
25	37	84.1	962	11	Q9Z0W4	Q9Z0W4 mus musculu
26	37	84.1	1012	5	Q17874	Q17874 caenorhabdi
27	37	84.1	1042	11	Q9JM13	Q9JM13 mus musculu
28	37	84.1	1046	4	Q9P2X1	Q9P2X1 homo sapien
29	37	84.1	1047	11	Q8CDJ4	Q8CDJ4 mus musculu
30	37	84.1	1088	4	Q3NRW7	Q3NRW7 homo sapien
31	37	84.1	1099	5	Q40936	Q40936 drosophila
32	37	84.1	1099	5	Q45590	Q45590 drosophila
33	37	84.1	1105	5	Q9VA38	Q9VA38 drosophila
34	37	84.1	1130	4	Q95835	Q95835 homo sapien
35	37	84.1	2483	16	Q8XOB2	Q8XOB2 ralstonia s
36	37	84.1	2497	16	Q8XYB9	Q8XYB9 ralstonia s
37	36	81.8	90	13	Q91891	Q91891 xenopus lae
38	36	81.8	305	5	Q01427	Q01427 caenorhabdi
39	36	81.8	315	8	Q9TD68	Q9TD68 mytilus cal
40	36	81.8	324	11	Q9CVR6	Q9CVR6 mus musculu
41	36	81.8	568	5	Q8MXG6	Q8MXG6 caenorhabdi
42	36	81.8	690	16	Q8GSP9	Q8GSP9 bifidobacte
43	36	81.8	749	5	Q8MXG7	Q8MXG7 caenorhabdi
44	36	81.9	790	5	Q76360	Q76360 caenorhabdi
45	36	81.8	830	3	Q9Y7T4	Q9Y7T4 schizosacch

ALIGNMENTS

RESULT 1

Q9BDK4	PRELIMINARY;	PRT;	316 AA.
ID Q9BDK4			
AC Q9BDK4			
DT C1-JUN-2001 (TrEMBLrel. 17, Created)			
DT C1-JUN-2001 (TrEMBLrel. 17, Last sequence update)			
DT C1-MAR-2003 (TrEMBLrel. 23, Last annotation update)			
DE Serum-inducible kinase (Frag-ent):			
OS Sus scrofa (pig)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX NCBI_TaxID=9823;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Anger M., Kuss W.A., Klima J., Mollik J., Carnwath J.W., Niemann H.;			
RT "Purified serum-inducible kinase";			
RL Submitted (FEB-2001) to the EMBL/GenBank/DBAJ databases.			
DR EMBL; AF348424; AAK27154.1; 1.			
DR InterPro; IPR000959; POLO box.			
DR InterPro; IPR000719; Prot_kinase.			
DR Pfam; PF00659; pkinase; 1.			
DR Pfam; PF00659; POLO box; 1.			
DR ProDom; PD000001; Prot_kinase; 1.			
DR PROSITE; PS00078; POLO_BOX; 1.			
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.			
KW ATP-binding; Kinase; Transferase.			
FT NON_TER 1			
FT NON_TER 316			
SQ SEQUENCE 316 AA; 35330 MW; F63BBE4A2691D62F CRC64;			

Query Match Similarity 93.2%; Score 41; DB 6; Length 316;

Best Local Similarity 87.5%; Pred.No. 3.1;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPF 8

DB 25 MLLGRPF 32


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RESULT 2
Q8N7M6 PRELIMINARY: PRT; 372 AA.
AC Q8N7M6:
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLN42844.
CS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Trachea;
RA Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,
RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
RA Matsumura Y., Moriya S., Chiba E., Moriyama H., Chogawa S.,
RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,
RA Kuga N., Kuroda A., Satoh T., Kanata K., Takami S., Terashima Y.,
RA Matsumoto K., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T.,
RA Wakamatsu A., Ishii S., Yamamoto S., Isono Y., Kawai-Hio Y., Saito K.,
RA Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y.,
RA Sekine M., Kikuchi H., Kanda K., Wagatsuma Y., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RA "NEO" human cDNA sequencing project;
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK98163; BAC05247;
DR InterPro: IPR000719; Prot_kinase
DR InterPro: IPR002290; Ser_thr_kinase
DR Pfam: PF00659; Tyr_kinase
DR Pfam: PF00659; pkinase; 1
DR ProDom: PD000001; Prot_kinase; 1
DR SMART: SM00220; S_TKc; 1
DR SMART: SM00219; TyrKc; 1
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1
KW Hypothetical protein; ATP-binding; Transferase.
SQ SEQUENCE 372 AA; 42632 MW; 7E3033F45C26A0C4 CRC64;

Query Match 93.2%; Score 41; DB 4; Length 372;
Best Local Similarity 87.5%; Pred. No. 3.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 266 MLLGPPPF 273

RESULT 3
Q9X5X4 PRELIMINARY: PRT; 666 AA.
AC Q9X5X4:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Polo like kinase 2.
CS Xenopus laevis (African clawed frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
CX Xeropodinae; Xenopus.
CX NCBI_TaxID=8155;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=21487843; PubMed=11597129;
RA Duran P.L., Pollet N., Niehs C., Ng S.E.
RA "Cloning and Characterization of Plx2 and Plx3, Two Additional Polo-
R like Kinases from Xenopus laevis."
RA Exp. Cell Res. 270:78-87(2001).
KW SIMILARITY: BELONGS TO THE SER. THR FAMILY OF PROTEIN KINASES.

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DR EMBL: AF357840; BAI30175.1;
DR InterPro: IPR000959; POLO_box.
DR InterPro: IPR000719; Prot_kinase.
DR Pfam: PF00069; pkinase; 1
DR Pfam: PF00659; POLO_box; 2
DR ProDom: PD000001; Prot_kinase; 1
DR SMART: SM00220; S_TKc; 1
DR PROSITE: PS00078; POLO_BOX; 2
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 666 AA; 76322 MW; A3D9F8BF85D4FC CRC64;

Query Match 93.2%; Score 41; DB 11; Length 682;
Best Local Similarity 87.5%; Pred. No. 6.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 254 MLLGPPPF 261

RESULT 4
Q8K226 PRELIMINARY: PRT; 682 AA.
AC Q8K226:
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serum-inducible kinase.
GS SNK.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC034513; AAH34513.1;
DR MGI: MGI:109790; Snk.
DR InterPro: IPR000959; POLO_box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF001245; Tyr_kinase.
DR Pfam: PF00659; pkinase; 1
DR ProDom: PD000001; Prot_kinase; 1
DR SMART: SM00220; S_TKc; 1
DR SMART: SM00219; TyrKc; 1
DR PROSITE: PS00078; POLO_BOX; 2
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 682 AA; 77777 MW; 89BA65C8DFAFFD95 CRC64;

Query Match 93.2%; Score 41; DB 11; Length 682;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 270 MLLGPPPF 277

RESULT 5
Q8MYF1 PRELIMINARY: PRT; 456 AA.
AC Q8MYF1:
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

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DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE RAC-family serine/threonine kinase homolog.
 OS Dictyostellium discoideum (Slime mold).
 CC Eukaryota; Mycetozoa; Dictyostelidia; Dictyostelium.
 ON NCBI_TaxID=44689;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA G. Cecckner G., Eschinger L., Szatranski K., Pachbat J., Dear P.,
 RA Lehmann R., Baurgart C., Parra G., Apr. J.F., Guigo R., Kumpf K.,
 RA Tungga B., Cox E., Quail M.A., Platzer M., Rosenthal A., Kegel A.A.;
 RT "Sequence and Analysis of Chromosome 2 of Dictyostelium";
 RL Submitted (WAY-2002) to the EMBL/GenBank/DBJ databases
 DR EMBL; AC117081; AAM43765.1;
 DR InterPro; IPR000961; Pkinase.C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase.C.1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase.1.
 DR SMART; SM00220; S_TKc.1.
 DR SMART; SM00133; S_TKc.1.
 DR SMART; SM00219; TYKc.1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE; PS00031; PROTEIN_KINASE_DOM.1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST.1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 456 AA; 51154 MW; EB8749EC64C894C9 CRC64;

 Query Match 92.9%; Score 40; DB 5; Length 456;
 Best Local Similarity 75.0%; Pred. No. 7.2;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MLLGKPPF 8
 Db 319 MMLGKPPF 326

 RESULT 6
 Q95ZT2 PRELIMINARY; PRT; 270 AA.
 AC Q95ZT2;
 DT 01-DEC-2001 (TrEMBLrel. 12, Created)
 DT 01-DEC-2001 (TrEMBLrel. 13, Last sequence update)
 DE Hypothetical protein F47F2.1a.
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Peoderinae; Caenorhabditis.
 ON NCBI_TaxID=6239;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Bentley D.;
 RT "The sequence of C. elegans cosmid F47F2.1";
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U40943; AAM69117.1;
 DR WormPep; F47F2.1c; CB31171.
 DR InterPro; IPR000961; Pkinase.C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase.1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase.1.
 DR SMART; SM00220; S_TKc.1.
 DR SMART; SM00133; S_TKc.1.
 DR SMART; SM00219; TYKc.1.

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; U40943; AAK39236.1;
 DR WormPep; F47F2.1a; CE27166.
 DR InterPro; IPR000961; Pkinase.C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase.C.1.
 DR Pfam; PF00433; pkinase.C.1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase.1.
 DR SMART; SM00220; S_TKc.1.
 DR SMART; SM00133; S_TKc.1.
 DR PROSITE; PS00107; PROTEIN_KINASE_DOM.1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST.1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 270 AA; 31346 MW; CEFFB41BC895B6A5 CRC64;

 Query Match 88.6%; Score 39; DB 5; Length 270;
 Best Local Similarity 75.0%; Pred. No. 6.8;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MLLGKPPF 8
 Db 150 MMVGKPPF 157

 RESULT 7
 Q8MQ39 PRELIMINARY; PRT; 325 AA.
 AC Q8MQ39;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein F47F2.1c.
 GN F47F2.1.
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Peoderinae; Caenorhabditis.
 ON NCBI_TaxID=6239;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Bentley D.;
 RT "The sequence of C. elegans cosmid F47F2.1";
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U40943; AAM69117.1;
 DR WormPep; F47F2.1c; CB31171.
 DR InterPro; IPR000961; Pkinase.C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00433; pkinase.C.1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase.1.
 DR SMART; SM00220; S_TKc.1.
 DR SMART; SM00133; S_TKc.1.
 DR SMART; SM00219; TYKc.1.

DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE_ST; 1.
 KW Hypothetical protein; ATP-binding; Transferase.
 SQ SEQUENCE 325 AA; 37528 MW; 210DFB8A13FC18D7 CRC64;

Query Match 88.6%; Score 39; DB 5; Length 325;
 Best Local Similarity 75.0%; Pred. No. 9.2;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 |::|||
 DB 205 MMVGKPPF 212

RESULT 8
 Q20541 PRELIMINARY; PRT; 371 AA.
 AC Q20541;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cyclic AMP-dependent protein kinase, catalytic subunit (EC 2.7.1.37)
 DE (Hypothetical protein F47F2.1b).
 GN F47F2.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodidae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2
 RA MEDLINE=99187059; PubMed=1009246;
 RA Tabish M., Clegg R.A., Rees H.R., Fisher M.J.
 RT "Organization and alternative splicing of the Caenorhabditis elegans
 RT cyclic AMP-dependent protein kinase (PKA) catalytic subunit gene
 RT (kin-1)."
 RJ Biochem. J. 339:209-216(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium";
 RL Science 282:2212-2218(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Benley D.;
 RT "The sequence of C. elegans cosmid F47F2.";
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RT "Direct Submission";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AJ012357; CAB41352.1;
 DR EMBL: J40943; AAK72061.1;
 DR HSSP: P05132; ATP;
 DR WormPep: F47F2.1b; CE04603.
 DR InterPro: IPR000961; Pkinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR01245; Tyr_pkinase.
 DR Pfam: PF0069; Pkinase; 1.
 DR Pfam: PF00433; Pkinase_C; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc;
 DR SMART: SM00133; S_TK_X; 1.

DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 371 AA; 42486 MW; 0C4873B5F3A45661 CRC64;

Query Match 88.6%; Score 39; DB 5; Length 371;
 Best Local Similarity 75.0%; Pred. No. 9.4;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 |::|||
 DB 251 MMVGKPPF 258

RESULT 9
 Q9M3V7 PRELIMINARY; PRT; 454 AA.
 AC Q9M3V7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE S6 ribosomal protein kinase.
 GN PK1.
 OS Asparagus officinalis (Garden asparagus).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asparagaceae;
 OC Asparagus.
 OC NCBI_TaxID=4686;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Conovers Colossal;
 RA Deacon K., Warner S.A.J., Draper J.;
 RT "Characterisation of an Asparagus S6 ribosomal protein cDNA and an S6
 RT ribosomal protein kinase homologue";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AJ277534; CAB89082.1;
 DR HSSP: Q63450; 1AC6.
 DR InterPro: IPR000961; Pkinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF0069; Pkinase; 1.
 DR Pfam: PF00433; Pkinase_C; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00133; S_TK_X; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE_ST; 1.
 KW ATP-binding; Kinase; Ribosomal protein;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 454 AA; 50467 MW; 0E4DEC52509997C5 CRC64;

Query Match 88.6%; Score 39; DB 10; Length 454;
 Best Local Similarity 87.5%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 |::|||
 DB 315 MLTGKPPF 322

RESULT 10
 Q8LFC1 PRELIMINARY; PRT; 465 AA.
 AC Q8LFC1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative ribosomal-protein S6 kinase ATPK6.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN (1)
 R2 SEQUENCE FROM N.A.
 RA Haas B.J., Volfovsky N., Town C.D., Troupkhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; genome
 RI "Full-length messenger RNA sequences greatly improve genome
 RI annotation."
 RL Genome Biol. 3:0-0(2002).
 RN (2)
 RN SEQUENCE FROM N.A.
 RP Broeyer V., Troupkhan M., Alexandrov N., Lu Y.-P., Flavell S.,
 RA Feldmann K.
 RT "Full-length cDNA from Arabidopsis thaliana."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY084935; AAM61496.1;
 DR InterPro: IPR000961; Pkinase C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00433; pkinase C; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SV002220; S_TKc; 1.
 DR SMART: SM00133; S_TKc; 1.
 DR SMART: SM00219; TYRKc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 KW ATP binding; Kinase; Transferase.
 SQ SEQUENCE 465 AA; 52587 MW; D81EA58F159E923 CRC64;
 Query Match 88.6%; Score 39; DB 10; Length 465;
 Best Local Similarity 87.5%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLCKPPF 8
 DB 324 MLCKPPF 331
 ID Q43380 PRELIMINARY; PRT; 480 AA.
 AC Q43380;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created;
 FT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update;
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update;
 DE Putative pp70 ribosomal protein S6 kinase.
 GN ASPK1.
 OS Avena sativa (Oat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Aveneae; Avena.
 OX NCBI_TaxID=4498;
 RN (1)
 RN SEQUENCE FROM N.A.
 RP STRAIN=ecv. Rhamnon; TISSUE=Aleurone;
 RX MEDLINE=95284341; PubMed=7766974;
 RA Huttly A.K., Phillips A.L.;
 RT "gibberellin regulated expression in oat aleurone cells of two kinases
 RI that show homology to nap kinase and a ribosomal protein kinase."
 RL Plant Mol. Biol. 27:1043-1052(1995).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: X79992; CAA56313.1;
 DR HSSP: P05132; ICTP.
 DR InterPro: IPR000961; Pkinase C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00433; pkinase C; 1.
 DR ProDom: PD000001; Prot_kinase; 1.

DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00133; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Ribosomal protein;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 480 AA; 53532 MW; 33596A10DBB077D CRC64;
 Query Match 88.6%; Score 39; DB 10; Length 480;
 Best Local Similarity 87.5%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLCKPPF 8
 DB 341 MLCKPPF 348
 ID Q12701 PRELIMINARY; PRT; 592 AA.
 AC Q12701;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created;
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Protein kinase (EC 2.7.1.37).
 GN KSG1 OR SPCC576.15C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN (1)
 RN SEQUENCE FROM N.A.
 RP STRAIN=H90;
 RC Niederberger C.;
 RA Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RN SEQUENCE FROM N.A.
 RP STRAIN=972H;
 RA Wood V., Rajadream M.A., Barrell B.G., Murphy L., Harris D.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: X99280; CAA67672.1;
 DR EMBL: AL031798; CAA21194.1;
 DR GeneDB: Spombe; SPCC576.15C;
 DR InterPro: IPR001849; PH.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00233; PH; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 592 AA; 65661 MW; B9A857D1989F2C61 CRC64;
 Query Match 88.6%; Score 39; DB 3; Length 592;
 Best Local Similarity 87.5%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLCKPPF 8
 DB 305 MLCKPPF 312
 ID Q03407 PRELIMINARY; PRT; 766 AA.
 AC Q03407;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created;

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE D8035.33P.
 GN PKH1 OR D8035.33 CR YDR490C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
 OC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dietrich F.S., Mulligan J., Allen E., Azais R., Aviles E., Berne A.,
 RA Carpenter J., Chen B., Cherry J.M., Chung E., Duncan M.,
 RA Hunkeler-Smith S., Hyman R., Kemp G., Laskari D., Lew H., Lin D.,
 RA Mosedale D., Nakahara K., Namath A., Ochner P., Ch C., Petel F.X.,
 RA Roberts D., Schramm S., Schroeder M., Shogren P., Shroff N.,
 RA Winant A., Yelton M., Botstein D., Davis R.W.
 RL Submitted (AJG-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Dietrich F.S.,
 RL Submitted (AJG-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Jia Y., Cherry J.M.,
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DE EMBL: J133057; AAB64917.1; ...
 DR HSP: P28523; ILR4.
 DR SGP: S602898; PKH1.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Prot_Kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS0108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 766 AA; 86252 MW; 7F9C2E9B5B9C367 CRC64;
 Query Match 88.6%; Score 191; DB 3; Length 766;
 Best Local Similarity 87.5%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 1; Gaps 0;
 QY 1 MLIGKPPF 8
 DB 330 LVLGKPPF 337
 RESULT 14
 ID Q9BDF9 PRELIMINARY; PRT: 506 AA.
 AC Q9BDF9
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Polo-like protein kinase (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sui.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Arget V., Kues W.A., Klira J., Mielenz M., Mettlak J., Garnswath J.W.,
 RA Niermann H.,
 RL "Expression Of Polo-like Kinase In Cell Cycle Synchronized Porcine
 Fetal Fibroblasts".
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DE EMBL: AF339021; AAK28550.1; ...
 DR HSP: Q61452; IAO6
 DR InterPro: IPR000959; Polo_box.
 DR InterPro: IPR000719; Prot_kinase.

DR InterPro: IPR002290; Ser_Thr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00659; Polo_box; 2.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00078; POLO_BOX; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS0108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON_TER 526 526
 FT NON_TER 526 526
 SQ SEQUENCE 526 AA; 60399 MW; 1AFA1E5E09B2CB83 CRC64;
 Query Match 86.4%; Score 38; DB 6; Length 526;
 Best Local Similarity 75.0%; Pred. No. 21;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLIGKPPF 8
 DB 199 LVLGKPPF 206
 RESULT 15
 ID Q9GRB7 PRELIMINARY; PRT: 582 AA.
 AC Q9GRB7
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Polo-like kinase.
 GN UPJK.
 OS Hemiecentrotus pulcherrimus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinoroza;
 OC Echinozoa; Euechinozoa; Echinacea; Echinoida; Strongylocentrotidae;
 OC Hemiecentrotus.
 OC NCBI_TaxID=7650;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yonemura I., Fujimoto H., Mabuchi I.,
 RL "Cloning of sea urchin pik.".
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yonemura I., Fujimoto H., Mabuchi I.,
 RL "Cloning of sea urchin polo-like kinase".
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DE EMBL: AB043897; BAB18588.1; ...
 DR InterPro: IPR001395; Aldo/ket_red.
 DR InterPro: IPR000959; Polo_box.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR Pfam: PF00659; pkinase; 1.
 DR Pfam: PF00659; Polo_box; 2.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00063; ALDO-KETO_REDUCTASE_3; 1.
 DR PROSITE: PS00078; POLO_BOX; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS0108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 582 AA; 66429 MW; A3774A0CAACFDE5D CRC64;
 Query Match 86.4%; Score 38; DB 5; Length 582;
 Best Local Similarity 75.0%; Pred. No. 24;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLIGKPPF 8
 DB 218 LVLGKPPF 225

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RESULT 16
ID P70032 PRELIMINARY; PRT; 596 AA.
AC P70032;
DT 01-FEB-1997 (TReMBLrel. 02, Created);
DI 01-FEB-1997 (TReMBLrel. 02, Last sequence update);
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update);
DE PIX1.
OS Xenopus laevis (African clawed frog);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.
CX NCBI_TaxID=8355;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=96355660; PubMed=8703070;
RA Kumaga, A., Dunphy W.G.;
RT "Purification and molecular cloning of Pix1, a Cdc25-regulatory kinase
from Xenopus egg extracts";
RL Science 273:1377-1380 (1996);
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U58205; AAC60017.1;
DR HSSP; Q63450; 1A36.
DR InterPro; IPR000959; POLO box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00659; POLO box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00076; POLO BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 596 AA; 68211 MW; 2467195911P22556 CRC64.

Query Match 86.48; Score 38; DB 13; Length 598;
Best Local Similarity 75.04; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLGKPPF 8
DB 235 LLVGKPPF 242
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RESULT 17
ID Q81U35 PRELIMINARY; PRT; 623 AA.
AC Q81U35;
DT 01-MAR-2003 (TReMBLrel. 23, Created);
DI 01-MAR-2003 (TReMBLrel. 23, Last sequence update);
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update);
DE Polo-like kinase.
OS Asterina pectinifera (Starfish);
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
CX NCBI_TaxID=7594;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=96355660; PubMed=8703070;
RA Uchida T.O., Tachibana K., Kishimoto T.;
RT "Starfish p.k.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB084465; BAC22692.1;
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 623 AA; 70929 MW; CFC019080C0D734A CRC64;

Query Match 86.48; Score 38; DB 5; Length 623;
Best Local Similarity 75.04; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MLGKPPF 8
DB 220 LLVGKPPF 227
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RESULT 18
ID Q62567 PRELIMINARY; PRT; 673 AA.
AC Q62567;
DT 01-AUG-1998 (TReMBLrel. 07, Created);
DI 01-AUG-1998 (TReMBLrel. 07, Last sequence update);
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update);
DE Serine/threonine protein kinase.
OS Suberites domuncula (Sponge);
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Hadromerida; Suberitidae; Suberites.
CX NCBI_TaxID=55567;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=96394688; PubMed=8798342;
RA Kruse M., Gamulin V., Cetkovic H., Pancer Z., Mueller I.M.,
RA Mueller W.E.G.;
RT "Molecular evolution of the Metazoan protein kinase C multigene
family";
RL J. Mol. Evol. 43:374-383 (1996).
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC 1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL; Y13099; CAA73553.1;
DR HSSP; P28867; 1PTQ.
DR InterPro; IPR003008; C2.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR000961; pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE-bind; 2.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00008; DAGPECDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; C2; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR PROSITE; PS04999; C2_DOMAIN_1; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 673 AA; 77344 MW; 86D24E55497C293 CRC64;

Query Match 86.48; Score 38; DB 5; Length 673;
Best Local Similarity 75.04; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLGKPPF 8
DB 535 MLVGKPPF 542
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RESULT 19
ID Q96997 PRELIMINARY; PRT; 677 AA.

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AC Q86997.
CT 01-MAY-1999 (TrEMBLrel. 10, Created;
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DI 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein kinase C.
GN PKC2.
OS Geodia cydonium (Sponge).
CC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
CC Astrophorida; Geodiidae; Geodia.
CX NCBI_TaxID=6047;
RN [1].
RP SEQUENCE FROM N.A.
RX MEDLINE=99147939; PubMed=10623072;
RA Seack J., Kruse J., Mueller I.M., Mueller W.E.G.;
RT "Promoter and exon-intron structure of the protein kinase C gene from
RT the marine sponge Geodia cydonium: Evolutionary considerations and
RT promoter activity.";
RL Biochim. Biophys. Acta 1444:241-253(1999).
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC 1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR EMBL: Y17882; CAA7691.1; -.
DR HSSP: P28867; IPTO.
DR InterPro: IPR000608; C2.
DR InterPro: IPR001564; Crystallin.
DR InterPro: IPR002219; DAG PE bind.
DR InterPro: IPR000861; Kinase_C.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00169; C2_1.
DR Pfam: PF00130; DAG PE-bind; 2.
DR Pfam: PF00069; Kinase; 1.
DR Pfam: PF00433; Kinase_C; 1.
DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR00004; DAGPEDOMAIN.
DR ProDom: PD00001; Prot_Kinase; 1.
DR SMART: SM00103; C2; 2.
DR SMART: SM00239; C2; 1.
DR SMART: SM00220; S_TK; 1.
DR SMART: SM00133; S_TK_X; 1.
DR PROSITE: PS00499; C2_DOMAIN; 1.
DR PROSITE: PS00304; C2_DOMAIN; 1.
DR PROSITE: PS00425; CRYSTALLIN_PETAGAWAY; 1.
DR PROSITE: PS00479; DAG PE BIND DOM; 1.
DR PROSITE: PS00081; DAG PE BIND DOM; 2.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine protein kinase; Transferase.
SQ SEQUENCE 607 AA; 76787 MW; 8800A5A3A3A3A3A3 64.

Query Match 86.4%; Score 38; DB 5; Length 477;
Best Local Similarity 75.0%; Pred. No. 2;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
DQ 533 MLVGSPFF 546
|||

RESULT 20
Q8P6X7 PRELIMINARY; PRT: 2883 AA
AC Q8P6X7;
CT 01-OCT-2002 (TrEMBLrel. 22, Created;
DI 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Shikimate Kinase.
GN XAC4213.
OS Xanthomonas axonopodis (pv. citri).
CC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
CC Xanthomonadaceae; Xanthomonas.
CX NCBI_TaxID=92529;
RN [1].

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RP SEQUENCE FROM N.A.
RX STRAIN=306 / ATCC 1392C / XV 101;
RX MEDLINE=2022145; PubMed=12024217;
RA da Silva A.C.R., Ferro C.A., Reinach F.C., Fatah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Chiapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria C.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.N., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.A., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima C.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL: AEC12073; AAM39048.1; -.
DR InterPro: IPR003439; ABC transporter.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW Kinase; Complete proteome.
SQ SEQUENCE 2883 AA; 313973 MW; 6AE23D657B45773D CRC64;

Query Match 86.4%; Score 39; DB 16; Length 2883;
Best Local Similarity 75.0%; Pred. No. 1; 2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
DQ 1966 LLLGPPY 1973
|||

RESULT 21
Q9KX10 PRELIMINARY; PRT: 388 AA.
AC Q9KX10;
CT 01-OCT-2000 (TrEMBLrel. 15, Created;
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein kinase.
GN PKNB_GRF388.
OS Staphylococcus aureus.
CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=1210;
RN [1].
RP SEQUENCE FROM N.A.
RX STRAIN=COL;
RX MEDLINE=20031141; PubMed=10568865;
RA de Lencastre H., Wu S.W., Pinho M.G., Ludovice A.M., Filipe S.,
RA Gardete S., Sobral R., Gill S., Chung M., Tomasz A.;
RT "Antibiotic resistance as a stress response: complete sequencing of a
RT large number of chromosomal loci in Staphylococcus aureus strain COL
RT that impact on the expression of resistance to methicillin.";
RL Microb. Drug Resist. 5:163-175(1999).
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: Y13639; CAA73979.1; -.
DR HSSP: Q63450; 1A06.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; Kinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_Kinase; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00104; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 388 AA; 43764 MW; C582839E06379580 CRC64;

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Query Match      84.1%; Score 37; DB 2; Length 388;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
Db 202 MLVGEPPF 209

RESULT 22
Q93UP8 PRELIMINARY; PRT; 664 AA.
AC Q93UP8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created);
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Protein kinase.
GN SAV1220 OR SA1063.
OS Staphylococcus aureus (strain Mu50 / ATCC 700695), and
Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN [1];
RP SEQUENCE FROM N.A.
RC SPECIES: S. aureus (strain Mu50), and S. aureus (strain N315);
EX MEDLINE=2311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Naga Y., Iiat S.-O., Ito T.,
Kusumoto Y., Matsumaru H., Maruyama A., Murakami H., Hasegawa A.,
Nakatani U. Y., Takahashi N. K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Horiuchi K., Ishino K., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hirakawa K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RL Lancet 357:1225-1240(2001).
CC -1; SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EXBL: APC03361; BAB57382.1;
DR EXBL: APC03133; BAB42315.1;
DR HSPF: Q63450, 1AC6.
DR InterPro: IPR005543; PASTA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF03793; PASTA; 3.
DR Pfam: PF03069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00740; PASTA; 3.
DR SMART: SM00220; STK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00168; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine; protein kinase; Transferase;
Complete proteome.
SQ SEQUENCE 664 AA; 74377 MW; 3461386C5DB61828 CRC64;

Query Match      84.1%; Score 37; DB 16; Length 664;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
Db 202 MLVGEPPF 209

RESULT 23
CBNX14 PRELIMINARY; PRT; 664 AA.
AC CBNX14;
DT 01-OCT-2002 (TrEMBLrel. 22, Created);
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE MW1103; protein.

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GN MW1103.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1];
RP SEQUENCE FROM N.A.
RC MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA."
RL Lancet 359:1819-1827(2002).
DR EMBL: AP004826; BAB94968.1;
DR InterPro: IPR005543; PASTA.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF03793; PASTA; 3.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00168; PROTEIN_KINASE_ST; 1.
KW Complete proteome.
SQ SEQUENCE 664 AA; 74363 MW; 26F1386C5DB61828 CRC64;

Query Match      84.1%; Score 37; DB 16; Length 664;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
Db 202 MLVGEPPF 209

RESULT 24
O8CSV9 PRELIMINARY; PRT; 667 AA.
AC O8CSV9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created);
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Protein kinase.
GN SE0895.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
Chen Z., Wen Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EXBL: AE016746; AAC04492.1;
KW Kinase; Complete proteome.
SQ SEQUENCE 667 AA; 75411 MW; 479877B4531CDD97 CRC64;

Query Match      84.1%; Score 37; DB 16; Length 667;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
Db 202 MLVGEPPF 209

RESULT 25
Q9Z0W4 PRELIMINARY; PRT; 962 AA.
AC Q9Z0W4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created);
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);

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DE Large tumor suppressor 1 (Fragment);
 GN LATS1.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RX MEDLINE=95362551; PubMed=7743921;
 RA Xu W., Wang W., Zhang S., Stewart R.A., Yu W.;
 RT "Identifying tumor suppressors in genetic mosaics: the Drosophila lats
 RT gene encodes a putative protein kinase.";
 RL Development 121:1053-1063(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99140768; PubMed=9988269;
 RA St John M.A., Tao W., Pei X., Fukumoto R., Carcangiu M.D.,
 RA Brownstein D.G., Parlow A.F., McGrath J., Xu T.;
 RT "Wic deficient of Lats1 develop soft-tissue sarcomas, ovarian tumours
 RT and pituitary dysfunction.";
 RL Nat. Genet. 21:182-186(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99140767; PubMed=9988268;
 RA Tao W., Zhang S., Trenchalk G.S., Stewart R.A., St John M.A.,
 RA Chen W., Xu T.;
 RT "Human homologue of the Drosophila melanogaster lats tumour suppressor
 RT modulates CDC2 activity.";
 RL Nat. Genet. 21:177-181(1999).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 UR EXBL: AF04414; AAD16883.1;
 CR HSSP; P05132; ICTP.
 CR MGD; MGI:1331893; Lats1.
 DR InterPro: IPR000961; Kinase_C.
 DR InterPro: IPR000729; Prot_kinase.
 DR InterPro: IPR022965; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 CR Pfam; PF00069; pkinase; 1.
 CR PRINTS; PR01217; PRICHEXTEN.
 CR Pfam; PF00433; pkinase_C; 1.
 CR ProDom; PD000001; Prot_kinase; 2.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00133; S_TKc; 1.
 DR PROSITE; PS00636; DNAD; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NCM TER
 SQ SEQUENCE 962 AA; 107312 MW; 166CF002A6C59E5 CAA64;
 Query Match 84.1%; Score 37; DB 11; Length 962;
 Best Local Similarity 75.0%; Pred. No. 64;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLLGKPPF 8
 DB 775 MLVGQPPF 782
 RESULT 26
 ID 017874 PRELIMINARY; PRT; 1012 AA.
 AC 017874; Q20475.
 DT 01-JAN-1999 (TrEMBLrel. 05, Created)
 DT 05-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE F46F6.2 protein.
 GN F46F6.2.
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Statiditida; Phabditidae.
 CC Rhabditidae; Pezodermidae; Caenothabitis.

OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Collage A.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2312-2318(1998).
 DR EMBL; Z50028; CAA90339.4;
 DR EMBL; Z50029; CAA90339.4; JOINED.
 DR EMBL; Z50029; CAA90345.4;
 DR EMBL; Z50028; CAA90345.4; JOINED.
 DR HSSP; P05132; LATP.
 DR WormPep; F46F6.2; CB31703.
 DR InterPro: IPR001623; DNAD_N.
 DR InterPro: IPR000961; Kinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR000861; REM_repeat.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 CR Pfam; PF02185; HRI; 1.
 CR Pfam; PF00069; pkinase; 1.
 CR Pfam; PF00433; pkinase_C; 1.
 CR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00074; HRI; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00133; S_TKc; 1.
 DR SMART; SM00219; TyrK; 1.
 DR PROSITE; PS00636; DNAD; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Transferase.
 SQ SEQUENCE 1012 AA; 113792 MW; D2F1930254536169 CRC64;
 Query Match 84.1%; Score 37; DB 5; Length 1012;
 Best Local Similarity 75.0%; Pred. No. 67;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGKPPF 8
 DB 877 MLVGQPPF 894
 RESULT 27
 ID 09JMI3 PRELIMINARY; PRT; 1042 AA.
 AC 09JMI3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Warts/lats-like kinase.
 GN LATS2 OR WMLATS2.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20139436; PubMed=10673337;
 RA Yabuta N., Fujii T., Copeland N.G., Gilbert D.J., Jenkins N.A.,
 RA Nishiguchi H., Endo Y., Toji S., Tanaka H., Nishimune Y., Nofima H.;
 RT "Structure, expression, and chromosome mapping of LATS2, a mammalian
 RT homologue of the Drosophila tumor suppressor gene lats/warts.";
 RL Genomics 63:263-270(2000).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AB021958; BAA92380.1;
 DR HSSP; P05132; ICTP.
 DR MGD; MGI:1354386; Lats2.

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DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR000449; UBA_domain.
DR Pfam: PF000269; pkinase_1.
DR Pfam: PF00433; pkinase_C_1.
DR ProDom: PDC00001; Prot_kinase_2.
DR SMART: SM00220; S_TKc_1.
DR SMART: SM00133; S_TK_X_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1046 AA; 11531 MW; 590E2D1740C3A2FA CRC64;

Query Match      84.1%  Score 37; DB 4; Length 1046;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
   |||:|
Db 864 MLVGQPPF 871

RESULT 29
Q9P2X1 PRELIMINARY; PRT; 1046 AA.
AC Q9P2X1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created);
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Large tumor suppressor 2 (Fragment);
DE HsJARS2;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1];
RP SEQUENCE FROM N.A.
RC MEDLINE=20139436; PubMed=10673337;
RA Yabuta N., Fujii T., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Nishiguchi H., Endo Y., Toji S., Tanaka H., Nishimune Y., Ogima H.;
RT "Structure, expression, and chromosome mapping of LATS2, a mammalian
RT homologue of the Drosophila tumor suppressor gene lats, warts."
RL Genomics 63:263-270(2000);
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB028219; BAA92381.1; .
DR HSP; P05132; ICTP.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR000449; UBA_domain.
DR Pfam: PF000269; pkinase_1.
DR Pfam: PF00433; pkinase_C_1.
DR ProDom: PDC00001; Prot_kinase_2.
DR SMART: SM00220; S_TKc_1.
DR SMART: SM00133; S_TK_X_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON TER 1
SQ SEQUENCE 1046 AA; 11531 MW; 590E2D1740C3A2FA CRC64;

Query Match      84.1%  Score 37; DB 4; Length 1046;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
   |||:|
Db 864 MLVGQPPF 871

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RESULT 29
Q8CDJ4 PRELIMINARY; PRT; 1047 AA.
AC Q8CDJ4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created);
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Large tumor suppressor 2.
DE Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002);
DR EMBL: AK029966; BAC26704.1; .
SQ SEQUENCE 1047 AA; 115282 MW; E80216A3C6E478CD CRC64;

Query Match      84.1%  Score 37; DB 11; Length 1047;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
   |||:|
Db 864 MLVGQPPF 871

RESULT 30
Q9NRW7 PRELIMINARY; PRT; 1088 AA.
AC Q9NRW7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created);
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Serine/threonine kinase KPM.
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Myeloid;
RX MEDLINE=20332247; PubMed=10871863;
RA Hori T., Takaoi-Kondo A., Kamikubo Y., Uchiyama T.;
RT "Molecular cloning of a novel human protein kinase, kpm, that is
RT homologous to warts/lats, a Drosophila tumor suppressor."
RL Oncogene 19:301-309(2000);
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF207547; AAF8C561.1; .
DR HSP; P05132; ICTP.
DR Genew: HGNC:6515; LATS2.
DR InterPro: IPR003961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR000449; UBA_domain.
DR Pfam: PF000269; pkinase_1.
DR Pfam: PF00433; pkinase_C_1.
DR ProDom: PDC000001; Prot_kinase_2.
DR SMART: SM00220; S_TKc_1.
DR SMART: SM00133; S_TK_X_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1088 AA; 12019 MW; 32C7580B6871FA63 CRC64;

Query Match      84.1%  Score 37; DB 4; Length 1088;

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Best Local Similarity 75.0%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
DB 906 MLVGQPPF 955

RESULT 32:
Q24590 PRELIMINARY; PRT; 1099 AA.
AC Q24096
DT 01-NOV-1996 (TrEMBLrel. 01, Created;
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update;
DI 01-MAR-2003 (TrEMBLrel. 23, Last annotation update;
DE LATS.
GN WTS OR CG12072.
OS Drosophila melanogaster (Fruit fly);
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota.
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1.
RP SEQUENCE FROM N.A. PubMed=7743821;
RX MEDLINE=95262551; PubMed=7743821;
RA Xu T., Wang W., Zhang S., Stewart R.A., Yu W.;
RT "Identifying tumor suppressors in genetic mosaics the Drosophila lats
RT gene encodes a putative protein kinase.";
RC Development 121:1053-1063(1995);
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; J29608; AAA70336.1; -.
DR HSSP; P05132; IAPM.
DR FlyBase; FBgn001739; wts.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1099 AA; 12718 MW; A12680948.45; P164;

Query Match 84.1%; Score 37; DB 5; Length 1099;
Best Local Similarity 75.0%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
DB 948 MLVGQPPF 955

RESULT 33:
Q9VA38 PRELIMINARY; PRT; 1105 AA.
AC Q9VA38
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE WTS protein.
GN WTS OR CG12072.
OS Drosophila melanogaster (Fruit fly);
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1.
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196036; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Aramatzides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Champ C., Pfeiffer G.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson X.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup J.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gortzel L.H., Gu Z., Guan P., Harris M.,
RA Hartis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kalai M., Kalish J., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.B., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lee Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matte B., McIntosh T.C., McLeod M.P., McPherson D.,

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Justice R.W., Zilian O., Woods D.F., Noll M., Bryant P.J.;
RT "The Drosophila tumor suppressor gene warts encodes a homolog of human
RT myctonic dysatroph kinase and is required for the control of cell
RT shape and proliferation";
RL Genes Dev. 9:534-546(1995);
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; L39837; AAA73959.1; -.
DR HSSP; P05132; IAPM.
DR FlyBase; FBgn001739; wts.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1099 AA; 12633 MW; E835192A1C470805 CRC64;

Query Match 84.1%; Score 37; DB 5; Length 1099;
Best Local Similarity 75.0%; Pred. No. 73;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
DB 948 MLVGQPPF 955

RESULT 33:
Q9VA38 PRELIMINARY; PRT; 1105 AA.
AC Q9VA38
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE WTS protein.
GN WTS OR CG12072.
OS Drosophila melanogaster (Fruit fly);
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 1.
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196036; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Aramatzides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champ C., Pfeiffer G.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson X.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup J.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gortzel L.H., Gu Z., Guan P., Harris M.,
RA Hartis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kalai M., Kalish J., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.B., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lee Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matte B., McIntosh T.C., McLeod M.P., McPherson D.,

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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy X., Murphy B., Murphy C., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.V.,
 RA Palazzolo V., Pittman G.S., Pan S., Pollard C., Puri V., Reese M.G.,
 RA Reibert K., Remington K., Saunders K.D.C., Scheeler P., Shen H.,
 RA Shue B.C., Sideri-Kianos T., Simpson M., Skurski K.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong K., Sun E.,
 RA Swikasz R., Tector C., Turner R., Venier E., Wang A.H., Wang X.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri N.S., Zhao X., Zhang G., Zhao O., Zheng J.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.C.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:12-25-2195(2003).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF003775; AAF57085.1; --
 DR HSSP: P05132; LAPM.
 DR FlyBase: FBgn0011739; wts.
 DR InterPro: IPR000961; Pkinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00433; pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 2.
 DR SMART: SM00220; S_TKc_1.
 DR SMART: SM00333; S_TKc_X; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATF; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00128; PROTEIN_KINASE_SF; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 1105 AA; 122488 MW; 7DC9D7A95BA1A656 RC064;

Query Match 84.1%; Score 377.055; Length 1105;
 Best Local Similarity 75.0%; Pred. No. 73;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGCKPPF 9
 |||
 DB 954 MLVGQPPF 96;

RESULT 34
 Q95835 PRELIMINARY; PROT: 100 AA;
 AC Q95835
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Large tumor suppressor 1.
 GN LATS1 OR WARTS
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99140767; PubMed=9988268;
 RA Xu T., Wang W., Zhang S., Stewart P.A., Yu W.,
 RA "Identifying tumor suppressors in genetic mosaics: the *Drosophila* lats
 RT gene encodes a putative protein kinase."
 RL Development 121:1053-1063(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99140767; PubMed=9988268;
 RA Tao W., Zhang S., Turenchalk G.S., Stewart P.A., St. John M.A.,
 RA Chen W., Xu T.,
 RA "Human homolog of the *Drosophila* melanogaster lats tumor suppressor
 RT modulates G2c activity."
 RL Nature 415:497-502(2002).
 RN [3]
 DR EMBL: AL646084; CAD18525.1; --

RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99140768; PubMed=9988269;
 RA St. John M.A., Tao W., Fei X., Fukumoto R., Carcangiu M.L.,
 RA Brownstein D.G., Parlow A.F., McGrath J., Xu T.,
 RA "Mice deficient of Lats1 develop soft-tissue sarcomas, ovarian tumours
 RT and pituitary dysfunction."
 RL Nat. Genet. 21:182-186(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99476136; PubMed=10518011;
 RA Nishiyama Y., Hirota T., Morisaki T., Hara T., Marumoto T., Iida S.,
 RA Makino K., Yamamoto H., Hirooka T., Kitamura N., Saya H.,
 RA "A human homolog of *Drosophila* warts tumor suppressor, h-warts,
 RT localized to mitotic apparatus and specifically phosphorylated during
 RT mitosis."
 RL FEBS Lett. 459:159-165(1999).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF164443; AAD16882.1; --
 DR EMBL: AF164041; AAD50272.1; --
 DR HSSP: P05132; ICTP.
 DR GENE: HGNC:6514; LATS1.
 DR InterPro: IPR000961; Pkinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR000449; JBA_domain.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00433; pkinase; 1.
 DR Pfam: PF00627; JBA; 1.
 DR ProDom: PD000001; Prot_kinase; 2.
 DR SMART: SM00220; S_TKc_1.
 DR SMART: SM00333; S_TKc_X; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00128; PROTEIN_KINASE_SF; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 1130 AA; 126569 MW; 11CF8CD9F87DCD8 CRC64;

Query Match 84.1%; Score 377.055; Length 1130;
 Best Local Similarity 75.0%; Pred. No. 75;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGCKPPF 8
 |||
 DB 943 MLVGQPPF 950

RESULT 35
 Q8XQB2 PRELIMINARY; PROT: 2483 AA;
 AC Q8XQB2
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE SKWP protein 2.
 GN RSP1374 OR RSC2084.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OG Plasmid megaplasmid.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Ralstoniaceae; Ralstonia.
 OX NCBI_TaxID:305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GMI1000;
 RX MEDLINE=21681879; PubMed=1823852;
 RA Salanoubat M., Genin S., Arriaguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choisme N., Claudel-Renard C., Cunha S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 RA Signer P., Thibault P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.,
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*."
 RL Nature 415:497-502(2002).
 RN [2]
 DR EMBL: AL646084; CAD18525.1; --

KW Pfam: Complete proteome.
SQ SEQUENCE 2483 AA; 272286 MW; 21E5F0A4EBA93614 (RC64;
Query Match 84.1%; Score 37; DB 16; Length 2483;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY : MLGKPPF 8
:|||||
DB :521 VLLGKPPY 1528

RESULT 36
O8XYB9 PRELIMINARY; PRT: 2497 AA.
AC Q8XYB9
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE SKWP protein 4.
GN RSC1939 OR R504276.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
CX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21621879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Goley J., Vandecast S.,
PA Ariat M., Billault A., Brothier P., Camus J.C., Cattolico L.,
RA Chandler M., Chaine N., Claudel-Ronard C., Cunac S., Denange N.,
RA Gaspin C., Lave M., Moisan A., Robert C., Saurin W., Schirix T.,
RA Sguier P., Thebaud P., Whalen M., Winkler P., Levy M.,
PA Weissbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
RJ Nature 415:497-502(2002).
DR EMBL: AL646067; CADI5541.1;
KW Complete proteome.
SQ SEQUENCE 2497 AA; 270604 MW; 12EF20A75D3C5F99 (RC64;
Query Match 84.1%; Score 37; DB 16; Length 2497;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY : MLGKPPF 8
:|||||
DB :545 VLLGKPPY 1552

RESULT 37
O91891 PRELIMINARY; PRT: 60 AA.
AC Q91891
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 9.4 kDa protein (fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Bouvet P., Onilli F., ARLOT-BONNEMAIN Y., Legagneux V., Roghi C.,
RA Bassez T., OSBORNE H.;
RT "adenylation conferred by the 3' untranslated region of a
RT developmentally controlled mRNA in xenopus embryos is switched to
RT polyadenylation by deletion of a short sequence element";
PL Mol. Cell. Biol. 14:1893-1900(1995).
LR EMBL: Z24453; CAA80826.1;
DR InterPro: IPR000719; Prot_kinase.

DR Pfam: PK00069; pkinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
KW Hypothetical protein: ATP-binding; Transferase.
FT NON_TER 1
SQ SEQUENCE 80 AA; 9388 MW; 8DFCEBA14BE14FB (RC64;
Query Match 81.8%; Score 36; DB 13; Length 80;
Best Local Similarity 85.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPF 8
:|||||
DB 3 LVGKPPF 9

RESULT 38
O01427 PRELIMINARY; PRT: 305 AA.
AC O01427
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE C. ELEGANS AURORA/1PL1-related protein KINASE 2 (AIR-2) (GB:AF071207).
OC ELEGANS AURORA/1PL1-related protein KINASE 2 (AIR-2) (GB:AF071207).
DE CONTAINS SIMILARITY TO PFAM domain PF00069 (PKINASE), SCORE=295.1.
DE E-VALUE=2.8E-85, N=1 (AIR-2) (PKINASE).
GN AIR-2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
CX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=93069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Henkhaus J., Wohldmann P.;
RT "The sequence of C. elegans cosmid B0207.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=N2 BRISTOL;
RA Schuracher J.M., Golden A., Donovan P.J.;
RT "AIR-2: An auroa/pll-related protein kinase associated with
RT chromosomes and midbody microtubules is required for polar body
RT extrusion and cytokinesis in C. elegans embryos";
RL J. Cell Biol. 0:0-0(1998).

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CC 1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U97136; AAB52459.2; ...
DR EMBL: AF071207; AAC70945.1; ...
DR HSP: P24947; IAK1.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase
DR Pfam: PF00369; PKinase; Thr_kinase
DR ProDom: PD020001; Prot_kinase; 1.
DR SMART: SMC0202; S_TKc; 1.
DR PROSITE: PS00137; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00311; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_S; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 305 AA; 34749 MW; 1635E560D2E140.1 CR64;

Query Match      81.8%; Score 36; DB 5; Length 305;
Best Local Similarity 85.7%; Pred.No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MLGKPPF 8
Db 220 LVGKPPF 226

RESULT 39
C9CD68
AC Q9CD68 PRELIMINARY; FRT; 315 AA.
DI Q9CD68;
DI 01-MAY-2000 (TrEMBLrel. 13, Created;
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update);
DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update);
DI NADH dehydrogenase subunit 2.
GN ND2.
OS Mytilus californianus (California mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytilida;
OC Mytiloidea; Mytilidae; Mytilus.
OX MCB; TaxID=6549;
WK 1.
RP SEQUENCE FROM N.A.
RX MEDLINE:99282504; PubMed:10353906;
RA Beagley C.T., Okimoto R., Wolstenholme D.R.;
RT "Mytilus mitochondrial DNA contains a functional gene for a
RT TRNAser1(UCN) with a dihydrouridine at replacement loop and a pseudo-
RT TRNAser1(UCN) gene.";
RL GenBank:1521641-65211999;
CR EMBL: AF090531; AAF02291.1;
CR InterPro: IPR001750; Oxidored_1;
CR Pfam: PF00161; Oxidored_q; 1.
KW NAD; Oxidoreductase; Ubiquinone; Mitochondrion.
SQ SEQUENCE 315 AA; 34339 MW; 839ED72637CC397 CR64;

Query Match      81.8%; Score 36; DB 6; Length 315;
Best Local Similarity 75.0%; Pred.No. 33;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
Db 233 MLGKPPF 240

RESULT 40
C9CVR6
AC Q9CVR6 PRELIMINARY; FRT; 324 AA.
DI Q9CVR6;
DI 01-JUN-2001 (TrEMBLrel. 17, Created;
DI 01-JUN-2001 (TrEMBLrel. 17, Last sequence update);
DI 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DI Serine/threonine kinase 18 (Fragment).
GN SK18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

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OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE:21085660; PubMed:11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peele G., Quackenbush J.,
RA Schriml L.M., Srauli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aoro H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK006827; BAS24759.1; ...
DR HSP: Q08534; IB18.
DR MGD: MGI:101783; Stk18.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Transferase.
FT NON_TER 324 324
SQ SEQUENCE 324 AA; 36568 MW; 04247065DFB198CC CR64;

Query Match      81.8%; Score 36; DB 11; Length 324;
Best Local Similarity 62.5%; Pred.No. 34;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
Db 204 LLGKPPF 211

Search completed: November 14, 2003, 13:27:57
Job time : 25 secs

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GenCore version 5.2.6
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CM protein: Protein search, using sw mode:

Run on: November 14, 2003, 12:54:54 ; Search time 34.714: Seconds
(without alignments:
41.151 Million cell updates/sec

Title: US-09-736-076-17
Perfect score: 49
Sequence: 1 MLLGKPPPE 9

Scoring table: BLOSUM62
Gapop 13.0 , Gapext 3.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DP seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 24
Maximum Match 100%
Listing first 45 summaries

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3: /SIDSI/gcgdata/geneseq/geneseq-emb./AA1982.DAT:
4: /SIDSI/gcgdata/geneseq/geneseq-emb./AA1983.DAT:
5: /SIDSI/gcgdata/geneseq/geneseq-emb./AA1984.DAT:
6: /SIDSI/gcgdata/geneseq/geneseq-emb./AA1985.DAT:
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8: /SIDSI/gcgdata/geneseq/geneseq-emb./AA1987.DAT:
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14: /SIDSI/gcgdata/geneseq/geneseq-emb./AA1993.DAT:
15: /SIDSI/gcgdata/geneseq/geneseq-emb./AA1994.DAT:
16: /SIDSI/gcgdata/geneseq/geneseq-emb./AA1995.DAT:
17: /SIDSI/gcgdata/geneseq/geneseq-emb./AA1996.DAT:
18: /SIDSI/gcgdata/geneseq/geneseq-emb./AA1997.DAT:
19: /SIDSI/gcgdata/geneseq/geneseq-emb./AA1998.DAT:
20: /SIDSI/gcgdata/geneseq/geneseq-emb./AA1999.DAT:
21: /SIDSI/gcgdata/geneseq/geneseq-emb./AA2000.DAT:
22: /SIDSI/gcgdata/geneseq/geneseq-emb./AA2001.DAT:
23: /SIDSI/gcgdata/geneseq/geneseq-emb./AA2002.DAT:
24: /SIDSI/gcgdata/geneseq/geneseq-emb./AA2003.DAT:

Fred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	9	AAW74161	HJ loop peptide J-
2	49	100.0	9	AAJ93117	Polo kinase serine
3	46	93.9	9	AAW74150	HJ loop peptide C-
4	46	93.9	9	AAJ93115	Polo kinase serine
5	46	93.9	10	AAW74213	HJ loop peptide KC
6	46	93.9	10	AAJ93157	Polo kinase SNX se
7	46	93.9	11	AAW74154	HJ loop peptide J
8	46	93.9	12	AAJ93119	Polo kinase serine
9	46	93.9	469	AA59471	Human protein requ

10	46	93.9	469	22	AAW74161	Amino acid sequenc
11	46	93.9	685	20	AAJ93115	Human serum induci
12	46	93.9	685	20	AAW88432	Disease associated
13	46	93.9	685	23	ABP61474	Human NF-kB activa
14	46	93.9	753	23	ABP41992	Human ovarian anti
15	44	89.8	8	20	AAW74160	HJ loop peptide J-
16	44	89.8	8	23	AAJ93116	Polo kinase serine
17	43	87.8	20	20	AAW74173	HJ loop peptide PO
18	43	87.8	20	23	AAJ93106	Peptide sequence o
19	43	87.8	329	21	AAW56690	Human prostate can
20	43	87.8	528	23	ABP73734	Candida albicans e
21	43	87.8	531	23	AAU74656	Mammalian polo-lik
22	43	87.8	603	16	AAW74620	Human lung tumour
23	43	87.8	603	23	AAU79306	Mouse polo-like ki
24	43	87.8	603	23	AAU79308	Mouse polo-like ki
25	43	87.8	603	23	AAU79309	Mouse polo-like ki
26	43	87.8	603	23	AAU79310	Mouse polo-like ki
27	43	87.8	603	23	AAU79311	Mouse polo-like ki
28	43	87.8	603	23	AAU79312	Mouse polo-like ki
29	43	87.8	603	23	AAU79313	Mouse polo-like ki
30	43	87.8	603	23	AAU79314	Mouse polo-like ki
31	43	87.8	603	23	AAU79315	Mouse polo-like ki
32	43	87.8	603	23	AAU79316	Mouse polo-like ki
33	43	87.8	603	23	AAU79317	Mouse polo-like ki
34	43	87.8	603	23	AAU79318	Mouse polo-like ki
35	43	87.8	603	23	AAU79319	Mouse polo-like ki
36	43	87.8	603	23	AAU79320	Mouse polo-like ki
37	43	87.8	603	24	ABR48196	Human bladder canc
38	41	83.7	403	18	AAW18084	Human Aurora-2. H
39	41	83.7	403	20	AAJ22476	Human AUR2 protein
40	41	83.7	403	22	AAW67435	Amino acid sequenc
41	41	83.7	403	22	AAW67435	Amino acid sequenc
42	41	83.7	403	23	AAW67435	Human NOV4 protein
43	41	83.7	403	24	ABR48160	Human bladder canc
44	41	83.7	403	24	ABP93366	Human serine/threo
45	41	83.7	403	24	ABP93367	Human serine/threo

ALIGNMENTS

RESULT 1
AAW74161
ID AAW74161 standard; peptide; 9 AA.

XX	AC	AAW74161:			
XX	DT	05-MAY-1999	(first entry)		
XX	DE	HJ loop peptide J-43.1.			
XX	XX	HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;			
XX	KW	haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;			
XX	KW	inflammatory disorder; central nervous system disease; septic shock;			
XX	KW	Parkinson's disease; hypertension.			
XX	OS	Synthetic.			
XX	XX	Key	Location/Qualifiers		
FT	FT	Modified-site	1	/note= "acetylated"	
FT	FT	Modified-site	9	/note= "amidated"	
XX	XX	W09853050-A2.			
XX	XX	26-NOV-1998.			
XX	XX	20-MAY-1998;	98NO-US10319.		
XX	XX	21-MAY-1997;	97JUS-0861336.		
XX	XX	(CHIL-) CHILDRENS MEDICAL CENT.			

PA (YISS) YISSUM RES & DEV CO.
 XX Pen-Sasson SA;
 XX WPI: 1993-070142/36.
 XX
 XX New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders
 XX
 XX Claim 14: Fig 4; 70pp; English.
 XX
 CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 49; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGKPPFE 9
 LB 1 MLLGKPPFE 9
 RESULT 2
 ID AAW98317 standard; Peptide: 9 AA
 AC AAW98317;
 DT 11-AUG-2002 (first entry)
 XX
 XX Polo kinase serine-threonine kinase HJ loop peptide J-43.1.
 KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; anti-diabetic; anorectic; neurological;
 KW anti-inflammatory; immunosuppressive; cardiac; haemostatic;
 KW modulating STK activity; polo kinase; J-43.1.
 XX
 OS Unidentified.
 CS Synthetic.
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 9
 FT Modified-site 9 /note= "Benzyl ester of Glutamic acid, C-terminal amide"
 FT
 XX US2002049301-A1
 XX 25-APR-2003.
 XX
 XX 13 DEC-2000; 2000US-0736076.
 XX

PR 21-MAY-1997; 97US-0861338.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX Ben-Sasson SA;
 XX WPI: 2002-462787/49.
 XX New peptide from the HJ loop of serine-threonine kinase, useful for
 PT treating e.g. cancer and for producing diagnostic antibodies -
 XX
 XX Disclosure; Fig 4; 41pp; English.
 XX
 CC The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase
 CC serine-threonine kinase HJ loop peptide J-43.1. This sequence is one of
 CC the short peptides of the invention that selectively modulate the
 CC activity of STK.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 49; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGKPPFE 9
 DB 1 MLLGKPPFE 9
 RESULT 3
 ID AAW74159 standard; peptide: 9 AA.
 XX AAW74159;
 AC AAW74159;
 DT 05-MAY-1999 (first entry)
 XX
 XX HJ loop peptide J-42.
 DE
 KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "acetylated"
 FT Modified-site 9
 FT Modified-site 9 /note= "amidated"
 FT Modified-site 9 /note= "benzyl ester of Glu"
 FT
 XX WO9853050-A2.
 PN
 XX 26-NOV-1998.
 PD
 XX 20-MAY-1998; 98WO-US10319.
 PF
 XX 21-MAY 1997; 97US-0861338
 PR (CHIL-) CHILDRENS MEDICAL CENT.
 PA (YISS) YISSUM RES & DEV CO.

XX PI Ben-Sasson SA;
 XX DR WPI: 1999-070142/06.
 XX PT New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders
 XX PS Claim 14: Fig 4: 70pp: English.
 XX CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.
 XX SQ Sequence 9 AA:
 Query Match 93.9% Score 46: DB 23: Length 9;
 Best Local Similarity 88.9% Pred. NO. 9.3e+05;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY : MLLGKPPPE 9
 DB |||:||||
 : 1 MLLGKPPPE 9
 RESULT 4
 AAU98315
 AC AAU98315 standard; Peptide: 9 AA.
 AC AAU98315.
 XX DT 13-AUG-2002 (first entry)
 XX DE Polio kinase serine-threonine kinase HJ loop peptide J-42.
 KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 KW anti-inflammatory; immunosuppressive; cardiac; haemostatic;
 KW modulating STK activity; polo kinase; J-42.
 XX OS Unidentified.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 9 /note= "Benzyl ester of Glutamic acid"
 FT Modified-site 9 /note= "C-terminal amide"
 XX XX US2002049301-A1.
 XX PO 25-APR-2002.
 XX PF 13-DEC-2000; 2000US-0736376.
 XX PI

PR 21-MAY-1997; 97US-0861338.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX PI Ben-Sasson SA;
 XX DR WPI: 2002-462787/49.
 XX PT New peptide from the HJ loop of serine-threonine kinase, useful for
 PT treating e.g. cancer and for producing diagnostic antibodies -
 XX PS Disclosure: Fig 4: 41pp: English.
 XX CC The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase
 CC serine-threonine kinase HJ loop peptide J-42. This sequence is one of
 CC the short peptides of the invention that selectively modulate the
 CC activity of STK.
 XX SQ Sequence 9 AA:
 Query Match 93.9% Score 46: DB 23: Length 9;
 Best Local Similarity 88.9% Pred. NO. 9.3e+05;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY : MLLGKPPPE 9
 DB |||:||||
 : 1 MLLGKPPPE 9
 RESULT 5
 AAW74213
 ID AAW74213 standard; peptide: 10 AA.
 XX AC AAW74213.
 XX DT 05-MAY-1999 (first entry)
 XX DE HJ loop peptide K038H101.
 KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "myristylated"
 FT Modified-site 10 /note= "amidated"
 XX XX WO9853050-A2.
 XX XX 26-NOV-1998.
 XX PF 20-MAY-1998; 98WO-US10319.
 XX PR 21-MAY-1997; 97US-0861338.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX PA (YISS) YISSUM RES & DEV CO.
 XX PI Ben-Sasson SA;

XX WP1; 1999-070142/06.
 XX
 XX New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders
 XX
 PS Disclosure; Fig 6; 70pp; English.
 XX
 XX This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.
 XX
 SQ Sequence 10 AA;
 Query Match 93.9%; Score 46; DB 20; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.061;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGKPPPE 9
 DB 1 1:1:1:1:
 2 MLLGRPPPE 10
 RESULT 6
 AAU98357
 ID AAU98357 standard; Peptide, 10 AA.
 XX
 XX AAU98357;
 XX
 DE 13-AUG-2002 (first entry)
 XX
 XX Polo kinase SNK serine-threonine kinase HJ loop peptide K036H01.
 XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; anti-diabetic; anorectic; neurological;
 KW anti-inflammatory; immunosuppressive; cardiac; haemostatic;
 KW modulating STK activity; polo kinase; SNK; K036H01.
 XX
 OS Unidentified.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal myristyl"
 FT Modified-site 10
 FT /note= "Benzyl Ester of Glutamic Acid, C-terminal amide"
 XX
 PN US2002049301-A1.
 XX
 XX 25-APR-2002.
 XX
 XX 13-DEC-2000; 2000US-0736076.
 XX
 XX 21-MAY-1997; 97US-0861338.
 XX
 XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Ben-Sasson SA;
 XX
 XX WP1; 2002-462787/49.
 XX
 XX New peptide from the HJ loop of serine-threonine kinase, useful for
 PT treating e.g. cancer and for producing diagnostic antibodies -
 PT
 XX
 PS Disclosure; Fig 6; 41pp; English.
 XX
 XX The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantitate ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase SNK
 CC serine-threonine kinase HJ loop peptide K036H01. This sequence is one
 CC of the short peptides of the invention that selectively modulate the
 CC activity of STK.
 XX
 SQ Sequence 10 AA;
 Query Match 93.9%; Score 46; DB 23; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.061;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGKPPPE 9
 DB 1 1:1:1:1:
 2 MLLGRPPPE 10
 RESULT 7
 AAU74163
 ID AAU74163 standard; peptide, 11 AA.
 XX
 XX AAU74163;
 XX
 XX 05-MAY-1999 (first entry)
 XX
 DE HJ loop peptide J-46.
 XX
 XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site ;
 FT /note= "acetylated"
 FT Modified-site 11
 FT /note= "amidated"
 XX
 PN WO9853050-A2.
 XX
 XX 26-NOV-1998.
 XX
 XX 20-MAY-1998; 98WO-US-0319.
 XX
 XX 21-MAY-1997; 97US-0861338.
 XX
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX (YISS) YISSUM RES & DEV CO.
 XX
 XX Ben-Sasson SA;
 XX
 XX WP1; 1999-070142/06.
 XX

PT New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders
 XX
 PS Claim 14; Fig 4; 70pp; English.

CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC hyperostosis, cardiac hypertrophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.

XX Sequence 11 AA;

Query Match 93.9%; Score 46; DB 20; Length 11;
 Best Local Similarity 88.9%; Pred. No. 0.067;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
 : : : : :
 DB 1 MLLGKPPPE 9

RESULT 8

AAJ98319
 ID AAJ98319 standard; Peptide; 11 AA.

AC AAJ98319;

DT 13-AUG-2002 (first entry)

DE Polo kinase serine-threonine kinase HJ loop peptide J-46.

XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 XX central nervous system disorder; inflammatory disorder;
 XX autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; antineoplastic; neurologica;
 KW antiinflammatory; immunosuppressive; cardiac; haematologic;
 XX modulating STK activity; polo kinase, J-46.

OS Unidentified.
 OS Synthetic.

FT Key Location/Qualifiers

FT Modified-site 1

FT Misc-difference 9 /note= "N-terminal acetyl"

FT Modified-site 11 /note= "Benzyl ester of Glutamic acid"

FT Modified-site 11 /note= "C-terminal amide"

XX US2002049301-A1.

XX 25-APR-2002.

XX 13-DEC-2000; 2000US-0736076.

XX 21-MAY-1997; 97US-0861338.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX

PI Ben-Sasson SA;

DR WPI; 2002-462787/49.

PT New peptide from the HJ loop of serine-threonine kinase, useful for
 PT treating e.g. cancer and for producing diagnostic antibodies -

XX Disclosure; Fig 4; 41pp; English.

CC The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase
 CC serine-threonine kinase HJ loop peptide J-46. This sequence is one of
 CC the short peptides of the invention that selectively modulate the
 CC activity of STK.

XX Sequence 11 AA;

Query Match 93.9%; Score 46; DB 23; Length 11;
 Best Local Similarity 88.9%; Pred. No. 0.067;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
 : : : : :
 DB 1 MLLGKPPPE 9

RESULT 9

AAJ94717

ID AAB94717 standard; Protein; 469 AA.

AC AAB94717;

DT 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:15726.

DE Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.

PN EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-0116126.

XX 29-JUL-1999; 99JP-0248036.

XX 27-AUG-1999; 99JP-0300253.

XX 11-JAN-2000; 2000JP-0118776.

XX 02-MAY-2000; 2000JP-3183767.

XX 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayaishi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -

XX Claim 8; SEQ ID 15726; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer; and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5' end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AA03166 to AAH13628 and
 CC AAH13633 to AAH19742 represent human cDNA sequences. AA09446 to
 CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 469 AA;

Query Match 93.9%; Score 46; DB 22; Length 469;
 Best Local Similarity 88.9%; Pred. No. 2.8;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : MLGKPPPE 9
 : |||||
 DB 57 MLGKPPPE 65

RESULT 10

ID AA067426
 AC AA067426 standard; Protein; 469 AA.

XX AA067426;

XX 26-NOV-2001 (first entry)

XX Amino acid sequence of a human protein kinase-affected in phosphatase.

XX Human, protein kinase; protein phosphatase; signal transduction;

XX intracellular; signalling pathway.

XX Homo sapiens.

XX W-2001C9345 A1.

XX 08-FEB-2001.

XX 28-JUL-2000; 2000WO-JP05260.

XX 29-JUL-1999; 99JP-0248036.

XX 16-OCT-1999; 99US-0159590.

XX 11-JAN-2000; 2000JP-0118776.

XX 17-FEB-2000; 2000US-0183322.

XX 02-MAY-2000; 2000JP-0183767.

XX (HELIX) HELIX RES INST.

XX Oka T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ichi S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;

XX Senoo C, Nezu J;

XX WP2; 2001-564736/63.

XX N-PSDB; AAH78069.

XX New genes encoding protein kinase and protein phosphatase, useful for
 PT identifying modulators which can be used to treat human or animal

PT disorders associated with the expression or function of these enzymes -
 XX Claim 2; Page 136-139; 336pp; Japanese.

XX The present sequence represents a human protein kinase/protein
 CC phosphatase. The polypeptides are expected to participate in signal
 CC transduction in cells. The kinase phosphatases are connected with
 CC intracellular signalling pathways. Antisense oligonucleotides and
 CC compounds identified by screening (agonists or antagonists) can be
 CC used to treat human or animal disorders associated with the expression
 CC or function of the protein. In addition, the polypeptides may be used
 CC as target molecules for drug development.

XX Sequence 469 AA;

Query Match 93.9%; Score 46; DB 22; Length 469;

Best Local Similarity 88.9%; Pred. No. 2.8;

Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : MLGKPPPE 9

DB 57 MLGKPPPE 65

RESULT 11

ID AA000915 standard; Protein; 685 AA.

XX AA000915;

XX 28-MAY-1999 (first entry)

XX Human serum inducible kinase.

XX Serum inducible kinase; SNK protein; human; proliferative disease;

XX leukaemia; solid tumour cancer; metastasis; chronic inflammatory;

XX psoriasis; rheumatoid arthritis; proliferative cardiovascular disease;

XX restenosis; ocular disorder; diabetic retinopathy; haemangioma;

XX benign hyperproliferative disease; diagnosis.

XX Homo sapiens.

XX W09909146-A1.

XX 25-FEB-1999.

XX 20-AUG-1998; 98WO-US17249.

XX 20-AUG-1997; 97US-0056112.

XX (SMK) SMITHKLINE BEECHAM CORP.

XX Anderson KM, Bouzyk M, Hansbury MJ, Jackson JR;

XX Nerurkar SS, Roshak AK;

XX WPI; 1999-181027/15.

XX N-PSDB; AAX27227.

XX New serum inducible kinase (Snk) polypeptides and polynucleotides -

XX useful for treating proliferative diseases

XX Claim 1; Page 39-40; 41pp; English.

XX This sequence is a human serum inducible kinase (SNK) of the
 CC invention. The invention relates to diagnostic assays or kits for
 CC detecting diseases associated with inappropriate SNK activity or levels.
 CC Disease states that can be diagnosed include proliferative diseases such
 CC as leukaemia, solid tumour cancers and metastases, chronic inflammatory
 CC proliferative diseases such as psoriasis and rheumatoid arthritis,
 CC proliferative cardiovascular diseases such as restenosis, proliferative
 CC ocular disorders such as diabetic retinopathy and benign
 CC hyperproliferative diseases such as haemangiomas. The polynucleotides can
 CC be used as hybridisation probes for cDNA and genomic DNA or as primers

CC This is the amino acid sequence of human disease associated protein

XX
PS
XX
CC Claim 1; Page 448-453; 841pp; Japanese.
CC The invention relates to a purified protein (I), comprising one of 90
CC fully defined sequences (ABP61424-ABP6151) or a protein based on any of
CC the sequences but with some amino acids deleted, substituted or added and
CC with a NF- κ B (nuclear factor kappa B) activating effect. The protein and
CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
CC inhibitors or promoters to control excessive activation or inhibition
CC and for treating e.g. inflammations, autoimmune diseases, cancers,
CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
CC disorders.
XX
SQ Sequence 685 AA;
Query Match 93.9%; Score 46; DB 23; Length 685;
Best Local Similarity 88.9%; Pred. No. 4.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY : MJLCKPPPE 9
Db 273 MJLGRPPPE 281
RESULT 14
ABP41992
ID ABP41992 standard; Protein: 753 AA.
XX
AC ABP41992;
XX
XX
XX 22-AUG-2002 (first entry)
XX Human ovarian antigen HAGSM33, SEQ ID NO:3124.
XX
XX Human ovarian antigen; ovary; ovarian, breast; cancer; tumour;
XX ovarian cancer; breast cancer; tumour; reproductive system disorder;
XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
XX PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
XX inflammatory condition; immune disorder; blood disorder;
XX cardiovascular disorder; respiratory disorder; neurological disorder;
XX gastrointestinal disorder; urinary system disorder; drug screening;
XX gene therapy; chromosome mapping; forensic analysis;
XX antibody preparation; cytotoxic; immunomodulatory; neuroprotective;
XX anti-inflammatory; gynaecological; reproductive; chromosome 5.
XX
XX Homo sapiens.
XX
XX W:02200677-AA.
XX
XX
XX 04-JAN-2002.
XX
XX 01-JUN-2001; 2001WO-US18569.
XX
XX 07-JUN-2000; 2000US-209467P.
XX
XX (HUNA-) HUMAN GENOME SCI INC.
XX
XX
XX Harse CE, Rosen CA;
XX
XX WPI, 2002-147879/19.
XX
XX N-PSDB; ABQ55C69.
XX
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g.
XX ovarian cancer), immune disorders, cardiovascular disorders and
XX neurological diseases.
XX
XX Claim 11; SEQ ID NO 3124; 2922pp; English.
XX
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX ABP43226) and to cDNAs encoding them (ABQ54131-ABQ54301), and also
XX encompasses polypeptides 90% identical and polynucleotides 95% identical
XX to the sequences of the invention. The invention additionally relates to

CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 753 AA;
Query Match 93.9%; Score 46; DB 23; Length 753;
Best Local Similarity 88.9%; Pred. No. 4.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY : MJLCKPPPE 9
Db 341 MJLGRPPPE 349
RESULT 15
AAW74160
ID AAW74160 standard; peptide; 8 AA.
XX
AC AAW74160;
XX
XX 05-MAY-1999 (first entry)
XX
XX HJ loop peptide J-43.
XX
XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
XX haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
XX inflammatory disorder; central nervous system disease; septic shock;
XX Parkinson's disease; hypertension.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1 /note= "acetylated"
XX Modified-site 8 /note= "amidated"
XX
XX W09853050-A2.
XX
XX
XX 26-NOV-1998.
XX
XX 20-MAY-1998; 98WO-US10319.
XX
XX 21-MAY-1997; 97US-0861338.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX (YISS) YISSUM RES & DEV CO.
XX Ben-Sasson SA;
XX

DR WP1: 1999-C70142/06.
 XX
 PT New peptides for modulating serine/threonine kinase activity -
 E1 comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers.
 XX PT inflammatory disorders or autoimmune disorders
 PS Claim 14; Fig 4; 70pp; English.
 XX
 CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.
 XX
 SQ Sequence 8 AA;
 Query Match 89.8%; Score 44; DB 20; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGKPPF 8
 DB 1 MLLGKPPF 8
 RESULT 16
 ID AAW9316
 XX AAW9316 standard; Peptide; 8 AA.
 AC AAW9316;
 DT 13-AUG-2002 (first entry)
 DE Polo kinase serine-threonine kinase HJ loop peptide J 43.
 KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 KW antiinflammatory; immunosuppressive; cardiac; haematologic;
 KW modulating STK activity; polo kinase; J 43.
 CS Unidentified.
 CS Synthetic.
 PH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 8
 FT Modified-site /note= "C-terminal amide"
 XX US2002049301-A1.
 XX
 PD 25-APR-2002.
 XX
 PF 13-DEC-2002; 2000US-0736076.
 XX
 PR 21 MAY-1997; 97US-0861338.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX

PI Ben-Sasson SA;
 XX
 DR WPI; 2002-462787/49.
 XX
 PT New peptide from the HJ loop of serine-threonine kinase, useful for
 XX treating e.g. cancer and for producing diagnostic antibodies -
 PS Disclosure; Fig 4; 41pp; English.
 XX
 CC The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase
 CC serine-threonine kinase HJ loop peptide J-43. This sequence is one of
 CC the short peptides of the invention that selectively modulate the
 CC activity of STK.
 XX
 SQ Sequence 8 AA;
 Query Match 89.8%; Score 44; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGKPPF 8
 DB 1 MLLGKPPF 8
 RESULT 17
 ID AAW74173
 XX AAW74173 standard; peptide; 20 AA.
 AC AAW74173;
 DT 05-MAY-1999 (first entry)
 DE HJ loop peptide POLO.
 KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.
 XX Synthetic.
 XX WO9853050-A2.
 XX 26-NOV-1998.
 XX 20-MAY-1998; 98WO-US10319.
 XX 21-MAY-1997; 97US-0861338.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX (YISS) YISSUM RES & DEV CO.
 XX Ben-Sasson SA;
 XX WPI; 1999-070142/06.
 XX
 PT New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders
 XX Claim 41; Fig 3b; 70pp; English.
 XX

CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis), cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HC loop of the STK
 CC from which the peptide was derived.

XX
 SQ Sequence 20 AA;

Query Match 87.8%; Score 43; DB 20; Length 20;
 Best Local Similarity 77.8%; Pred. No. 0.43;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
 :|||
 DB 3 LVGKPPPE 11

RESULT 19
 AAB56690
 ID AAB56690 standard; Peptide: 20 AA.
 XX
 AC AAB56690;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Peptide sequence of HJ loop of serine/threonine kinase polo kinase.

XX
 KW HJ loop; serine/threonine kinase, STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
 KW modulating STK activity; polo kinase.

XX
 OS Unidentified.
 XX
 PN US2002049101 A;
 XX
 PD 25-APR-2002.
 XX
 PF 13 DEC-2000; 2000US-0736076.
 XX
 PR 21-MAY-1997; 97US-0861338.
 XX
 PA (CHILDRENS MEDICAL CENT.
 XX
 PI Ben-Sasson SA;
 XX
 DR WPI: 2002-462767/49.

XX
 PT New peptide from the HJ loop of serine/threonine kinase, useful for
 PT treating e.g. cancer and for producing diagnostic antibodies -

XX Claim 33; Fig 3; 41pp; English.

XX The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for

CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the peptide sequence of the HJ
 CC loop of serine-threonine kinase polo kinase. This sequence is one of the
 CC short peptides of the invention that selectively modulate the activity
 CC of STK.

SQ Sequence 20 AA;

Query Match 97.8%; Score 43; DB 23; Length 20;
 Best Local Similarity 77.8%; Pred. No. 0.43;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
 :|||
 DB 3 LVGKPPPE 11

RESULT 19
 AAB56690
 ID AAB56690 standard; Protein: 329 AA.
 XX
 AC AAB56690;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Human prostate cancer antigen protein sequence SEQ ID NO:1268.

XX
 KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
 KW vulnery; gastrointestinal; nephrotropic; antiinfective; gynaecological;
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease.

XX Homo sapiens.

XX WO2000055174-A1.

XX 21-SEP-2000.

XX C8-MAR-2000; 2000WC-US05988.

XX 12-MAR-1999; 99US-024270.

XX (HUMA-) HUMAN GENOME SC¹ INC.
 PA :ROSE/; ROSEN C A.

XX Rosen CA, Ruben SM;

XX WPI: 2000-587513/55.

XX N-PSDB; AAF15693.

XX Prostate cancer associated gene sequences, referred to as prostate
 PT cancer antigens, useful for treatment, prevention, and diagnosis of
 PT disorders such as prostate cancer -

XX Claim 11; Page 1691-1692; 2338pp; English.

XX AAF15566 to AAF16505 encode the human prostate cancer associated
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytostatic,
 CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
 CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
 CC and can be used in gene therapy. The prostate cancer antigen
 CC polynucleotides may be used for detection of prostate cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The prostate cancer antigens may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention.


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XX (CHIL-) CHILDRENS MEDICAL CENT.
PA (YISS-) YISSUM RES & DEV CO.
XX
XX Ben-Sasson SA;
PI
XX WPI: 1999-070142/06.
XX
XX New peptides for modulating serine/threonine kinase activity -
PI comprise a sequence corresponding to the HJ loop of a
XX serine/threonine kinase, used for treating, e.g. cancers,
XX inflammatory disorders or autoimmune disorders.
XX
XX Claim 14; Fig 4; 70pp; English.
XX
XX This sequence represents a peptide of the invention, and is a derivative
XX of the HJ loop of a serine/threonine kinase (STK). The peptides can be
XX used for the treatment of disorders caused by overactivity or
XX underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
XX shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
XX arteriosclerosis, cardiachyper trophy, ischaemia, reperfusion injury and
XX hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
XX psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
XX of organ transplant rejection, multiple sclerosis, inflammatory bowel
XX disease and AIDS), central nervous system diseases (e.g. Alzheimer's
XX disease, stroke and trauma), septic shock, Parkinson's disease or
XX hyperreflexion. The peptides can also be used to produce antibodies which
XX can be used to identify cells expressing the STK and to study the
XX intracellular distribution of the STK. In addition, the peptides can be
XX used to identify and quantitate ligands which bind the HJ loop of the STK
XX from which the peptide was derived.
XX
XX Sequence 9 AA:
SQ
Query Match: 100.0%; Score 49; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
DB 1 MLLGRPPPE 9
AAW74213
RESULT 2
ID AAW74213 standard; Peptide; 9 AA
XX
XX RAJ98405;
XX
XX 13-AUG-2002 (first entry);
XX
XX Polo kinase serine-threonine kinase HJ loop peptide C 42.
XX
XX HJ loop; serine/threonine kinase; STK; Cancer; diabetes; obesity;
XX central nervous system disorder; inflammatory disorder;
XX autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
XX lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
XX antiinflammatory; immunosuppressive; cardiac; haemostatic;
XX modulating STK activity; polo kinase; C 42.
XX
XX Unidentified.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX Modified-site 9 /note= "N-terminal acetyl"
XX Modified-site 9 /note= "Benzyl ester of glutamic acid"
XX Modified-site 9 /note= "C-terminal amide"
XX
XX W5200043301-A1.
XX
XX 15-APR-2002.
XX

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XX 13-DEC-2000; 2050US-0736076.
XX
XX 21-MAY-1997; 97US 0861338.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX Ben-Sasson SA;
XX
XX WPI: 2002-462787/49.
XX
XX New peptide from the HJ loop of serine-threonine kinase, useful for
XX treating e.g. cancer and for producing diagnostic antibodies -
XX
XX Disclosure; Fig 4; 41pp; English.
XX
XX The present invention relates to new peptides derived from the HJ loop
XX of a serine/threonine kinase (STK). The peptides of the invention are
XX used to modulate STK activity, especially for treating cancer, diabetes,
XX obesity or a wide variety of central nervous system, inflammatory,
XX autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
XX regulating lipid metabolism. The peptides are also used to generate
XX antibodies that bind specifically to the parent STK, used e.g. for
XX identifying STK-expressing cells and to study intracellular distribution
XX of STK, and to identify or quantify ligands that bind to the HJ loop.
XX The present amino acid sequence represents the polo kinase
XX serine-threonine kinase HJ loop peptide J-42. This sequence is one of
XX the short peptides of the invention that selectively modulate the
XX activity of STK.
XX
XX Sequence 9 AA:
SQ
Query Match: 100.0%; Score 49; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
DB 1 MLLGRPPPE 9
AAW74213
RESULT 3
ID AAW74213 standard; peptide; 10 AA.
XX
XX AC AAW74213;
XX
XX 05 MAY-1999 (first entry);
XX
XX HJ loop peptide K038H101.
XX
XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
XX haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
XX inflammatory disorder; central nervous system disease; septic shock;
XX Parkinson's disease; hypertension.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1 /note= "myristylated"
XX Modified-site 10
XX Modified-site 10 /note= "amidated"
XX
XX W09853050-A2.
XX
XX 26 NOV-1998.
XX
XX 20-MAY-1998; 98W0-US10319.
XX
XX 21-MAY-1997; 97US-0861338.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX

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PA (YISS) YISSUM RES & DEV CO.
 XX Ben Sasson SA;
 PI WPI; 1999-070142/06.
 XX New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the H3 loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders
 XX
 XX Disclosure: Fig 6; 70pp; English.
 XX
 XX This sequence represents a peptide of the invention, and is a derivative
 CC of the H3 loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity of
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the H3 loop of the STK
 CC from which the peptide was derived.
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 100.0%; Score 43; DB 20; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPPE 9
 DB 2 MLLGRPPPE 10
 RESULT 5
 AA098357
 ID AA098357 standard; Peptide: 10 AA.
 XX
 AC AA098357;
 DT 05-MAY-1999 (first entry);
 XX H3 loop peptide J-46.
 DE
 XX H3 loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
 KW modulating STK activity; polo kinase; SNK; K038H101.
 XX
 CS Unidentified.
 CS Synthetic
 XX
 XX Key Location/Qualifiers
 FH Modified site 1 /note= "N-terminal myristyl."
 FT Modified-site 10
 FT Modified-site 10 /note= "Benzyl Ester of Glutamic Acid, C-terminal amide"
 XX
 XX US2002049301-A1.
 XX 26-APR 2002.
 XX
 XX 1--DEC-2000; 2000US-0736076.
 XX

PR 21-MAY-1997; 97US-0861338.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX Ben-Sasson SA;
 PI WPI; 2002-462787/49.
 XX
 XX New peptide from the H3 loop of serine-threonine kinase, useful for
 PT treating e.g. cancer and for producing diagnostic antibodies -
 XX
 XX Disclosure: Fig 6; 41pp; English.
 XX
 XX The present invention relates to new peptides derived from the H3 loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the H3 loop.
 CC The present amino acid sequence represents the polo kinase SNK
 CC serine-threonine kinase H3 loop peptide K038H101. This sequence is one
 CC of the short peptides of the invention that selectively modulate the
 CC activity of STK.
 XX
 XX Sequence 10 AA;
 SQ
 Query Match 100.0%; Score 49; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPPE 9
 DB 2 MLLGRPPPE 10
 RESULT 5
 AA074163
 ID AA074163 standard; peptide: 11 AA.
 XX
 AC AA074163;
 DT 05-MAY-1999 (first entry);
 XX H3 loop peptide J-46.
 DE
 XX H3 loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.
 XX
 XX Synthetic.
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "acetylated"
 FT Modified-site 11
 FT /note= "amidated"
 XX
 XX WC9853050-A2.
 XX
 XX 26-NOV-1998.
 XX
 XX 20-MAY-1998; 98WC-US10319.
 XX
 XX 21-MAY-1997; 97US-0861338.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA (YISS) YISSUM RES & DEV CO.
 XX Ben-Sasson SA;
 PI

XX WP1: 1993-070142/06.
 XX
 XX
 PT New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders
 XX
 XX Claim 14, Fig 4; 7opp; English.
 XX
 CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity of
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.
 XX
 XX
 EQ Sequence 11 AA;
 Query Match 100.0%; Score 49; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY : MLLGRPFPE 9
 DB : MLLGRPFPE 9
 : |||||
 : MLLGRPFPE 9

RESULT 6
 AAU94119
 ID AAC96319 standard; Peptide: 11 AA.
 XX
 AC AAU98319;
 XX
 DT 13 AUG 2002 (first entry)
 XX
 DE Polo kinase serine-threonine kinase HJ loop peptide J-46.
 KW HJ loop; serine/threonine kinase; cytokinesis; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; antineoplastic; neurological;
 KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
 KW modulating STK activity; polo kinase; J-46.
 XX
 XX Unidentified.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl"
 FT Misc-difference 9
 FT /note= "Benzyl ester of Glutamic acid"
 FT Modified-site 11
 FT /note= "C-terminal amide"
 FT
 XX US2002049301-A1.
 XX
 XX 25 APR-2002.
 XX
 XX 13-DEC-2000; 2000US-0736076.
 XX
 XX 21-MAY-1997; 97US-0861338.

XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 XX Ben-Sasson SA;
 XX
 XX WP1: 2002-462787/49.
 XX
 XX New peptide from the HJ loop of serine-threonine kinase, useful for
 XX treating e.g. cancer and for producing diagnostic antibodies -
 XX
 XX Disclosure: Fig 4; 4opp; English.
 XX
 CC The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase
 CC serine-threonine kinase HJ loop peptide J-46. This sequence is one of
 CC the short peptides of the invention that selectively modulate the
 CC activity of STK.
 XX
 XX Sequence 11 AA;
 EQ
 Query Match 100.0%; Score 49; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY : MLLGRPFPE 9
 DB : MLLGRPFPE 9
 : |||||
 : MLLGRPFPE 9

RESULT 7
 AAB94717
 ID AAB94717 standard; Protein: 469 AA.
 XX
 AC AAB94717;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human protein sequence SEQ ID NO:15726.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN EP-074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 XX 28-JUL-2000; 2000EP-0116126.
 XX
 XX 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-030253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 XX (HELI-) HELIX RES INST.
 XX
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 XX WP1: 2001-318749/34.
 XX
 XX Primer sets for synthesizing polynucleotides, particularly the 56C2
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the

ocular disorders such as diabetic retinopathy and benign hyperproliferative diseases such as haemangiomas. The polynucleotides can be used as hybridisation probes for cDNA and genomic DNA or as primers for a nucleic acid amplification (PCR) reaction, to isolate full-length cDNAs and genomic clones encoding polypeptides of this invention and to isolate cDNA and genomic clones of other genes which have a high sequence similarity to the SNK coding sequence. The differences between cDNA and genomic sequences can be observed and therefore mutations detected. Any mutations may then be attributed to likely causative agents of disease. The nucleotide sequences are also useful for chromosome identification.

Sequence 685 AA;
Query Match 100.0%; Score 49; DB 20; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9

Db 273 MLLGRPPPE 281

RESULT 10

AAW88432

ID AAW88432 standard; Protein: 685 AA.

XX AC AAW88432;

XX XX

XX 26 APR-1999 (first entry)

DE Disease associated protein kinase DAPK-1.

XX DAPK-1; disease associated protein kinase; human; diagnosis; therapy; adult respiratory distress syndrome; allergy; asthma; arteriosclerosis; bronchitis; emphysema; hyperosmophilia; myocardial inflammation; pericardial inflammation; anaemia; rheumatoid arthritis; Addison's disease; AIDS; arteriosclerosis; atopic dermatitis; dermatomyositis; diabetes mellitus; glomerulonephritis; gout; Grave's disease; lupus erythematosus; multiple sclerosis; myasthenia gravis; osteoarthritis; osteoporosis; pancreatitis; polycystic kidney disease; polymyositis; scleroderma; Sjorgren's syndrome; autoimmune thyroiditis; cancer; infection; trauma; cell proliferation.

XX Homo sapiens.

XX Key Location/Qualifiers

PH Binding site 89..96

FT /note= "potential ATP binding site"

FT Peptide 506..511

FT /note= "presumed regulatory sequence common to polc family protein kinases"

XX WC9858052-A2.

XX PN

XX 23-DEC-1998.

XX 19-JUN-1998; 98WO-US12813.

XX 19-JUN-1997; 97US-0878989.

XX (INCYTE PHARM INC.

PA Bandman O, Corley NC, Goli SK, Guejter KU, Hillman JL;

XX Lai P, Shah P;

PI WPI; 1999-080952/07.

CR N-PSDB; AAX06831.

XX New disease associated protein kinases - used to stimulate cell proliferation and to treat the immune response and cancer

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

PS Claim 1; Page 54-56; 93pp; English.

XX This is the amino acid sequence of human disease associated protein kinase DAPK-1, as deduced from a consensus sequence (see AAX06831; of overlapping cDNA clones from libraries which are immortalised or cancerous and show inflammatory or immune responses. DAPK-1 shows 53% homology to human proliferation-related protein kinase PRK (GI 1488263). The invention provides DAPK-1 to DAPK-7 polypeptides (see AAW88432-38) and cDNA clones encoding them (see AAX06831-36 and AAX06882), as well as expression vectors, host cells, agonists, antagonists and antibodies. The invention further provides uses of such products in the diagnosis, prevention and treatment of diseases associated with cell proliferation, especially cancer or an immune response (claimed). Conditions that may be treated include adult respiratory distress syndrome, allergies, asthma, arteriosclerosis, bronchitis, emphysema, hyperosmophilia, myocardial or pericardial inflammation, rheumatoid arthritis, Addison's disease, AIDS, anaemia, arteriosclerosis, various diseases of the digestive system, atopic dermatitis, dermatomyositis, diabetes mellitus, glomerulonephritis, gout, Grave's disease, lupus erythematosus, multiple sclerosis, myasthenia gravis, osteoarthritis, osteoporosis, pancreatitis, polycystic kidney disease, polymyositis, scleroderma, Sjorgren's syndrome, autoimmune thyroiditis, complications of cancer, extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal and helminthic infections, and trauma (disclosed).

XX Sequence 685 AA;

Query Match 100.0%; Score 49; DB 20; Length 685;

Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9

Db 273 MLLGRPPPE 281

RESULT 11

ABP61474

ID ABP61474 standard; Protein: 685 AA.

XX AC ABP61474;

XX XX

XX 30-SEP-2002 (first entry)

XX Human NF-kB activating protein; SEQ ID NO 101.

XX DE

XX Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;

XX immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;

XX neuroprotective; anti-HIV; autoimmune disease; cancer; infection;

XX bone disease; AIDS; neurodegenerative disease; ischaemic disorder.

XX OS

XX Homo sapiens.

XX XX

XX WO200253737-A1.

XX PN

XX 11-JUL-2002.

XX 25-DEC-2001; 2001WO-JP11389.

XX 28-DEC-2000; 2000JP-0402288.

XX 26-MAR-2001; 2001JP-0088912.

XX 24-AUG-2001; 2001JP-0254018.

XX (ASAH) ASAH1 KASEI KOGYO KK.

XX Matsuda A, Honda G, Muramatsu S, Nagano Y;

XX WPI; 2002-583617/62.

XX N-PSDB; ABQ91962.

XX NF-approximate,ykB activating gene and expressed protein, applicable in

XX PI Ben-Sasson SA;
XX WP; 1999-070142/06.
XX
XX New peptides for modulating serine/threonine kinase activity -
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g., cancers,
PT inflammatory disorders or autoimmune disorders
XX
XX Claim 14; Fig 4; 70pp; English.
XX
XX This sequence represents a peptide of the invention, and is a derivative
CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
CC used for the treatment of disorders caused by overactivity or
CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
CC arteriosclerosis), cardiac hypertrophy, ischaemia, reperfusion injury and
CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
CC psoriasis), systemic lupus erythematosus, diabetes mellitus, suppression
CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
CC disease, stroke and trauma), septic shock, Parkinson's disease or
CC hypertension. The peptides can also be used to produce antibodies which
CC can be used to identify cells expressing the STK and to study the
CC intracellular distribution of the STK. In addition, the peptides can be
CC used to identify and quantitate ligands which bind the HJ loop of the STK
CC from which the peptide was derived.
XX
XX Sequence 9 AA;

Query Match 93.9%; Score 46; DB 20; Length 9;
Best Local Similarity 88.9%; Pred. No. 9,3e+05;
Matches 9; Conservative 1; Mismatches 0; Idels 0; Gaps 0

QY : MLGGRPFPE 9
DE : |||||
E : 1 MLGGRPFPE 9

RESULT 14
RAU98317
ID AU98317 standard; Peptide; 9 AA.

AC AAU98317;
ET 13-AUG-2002 (first entry)
EE Polio kinase serine threonine kinase (HJ loop) protein J 43.1.
XX HJ loop; serine/threonine kinase; STK; cancer, diabetes; obesity;
XX central nervous system disorder; inflammatory disorder;
XX autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
XX lipid metabolism; cytostatic; antidiabetic; anti-infective; neurologic;
XX anti-inflammatory; immunosuppressive; cardiac; haematologic;
XX modulating STK activity; polo kinase; J 43.1.
XX
CS Unidentified.
CS Synthetic.

FH Key Location/Qualifiers
FT Modified site 1 /note= "N-terminal acetyl"
FT Modified site 9 /note= "Benzyl ester of Glutamic acid, C-terminal amide"

PB US2002049301-A1.
PD 25-APR-2002.
PP 13-OCT-2000; 2000US-0716076.
XX
XX 21-MAY-1997; 97US-0861138.

XX Polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -
 CC AAB35806 which are involved in regulating the cell cycle. The protein and
 CC DNA sequences have been isolated from Zea mays (corn), and the invention
 CC also includes oligonucleotides AAC83114 - AAC83119 which are related to
 CC the cell cycle polynucleotides. The cell cycle polynucleotide sequences
 CC are useful for producing transgenic plants such as maize, soybean,
 CC sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and
 CC millet with increased levels of cell cycle gene activity, such as
 CC activity of cyclin and cyclin-dependent kinases. The DNA sequences are
 CC also useful as probes for detecting deficiencies in the level of mRNA in
 CC screening for desired transgenic plants, for detecting mutations in the
 CC gene, for monitoring upregulation of expression or changes in enzyme
 CC activity in screening assays of compounds, for detecting any number of
 CC allelic variants, orthologs or paralogues of the gene, and site-directed
 CC mutagenesis in eukaryotic cells. The DNA sequences are also useful for
 CC recombinant expression of the encoded polypeptides and as immunogens for
 CC preparing and screening antibodies. A transgenic plant comprising an
 CC expression cassette including a cell cycle regulatory gene is useful for
 CC assaying enzyme agonists and antagonists, and as immunogens or antigens
 CC to obtain antibodies. The antibodies are useful in assaying expression
 CC levels of cell cycle regulatory proteins, for identifying and isolating
 CC nucleic acids from expression libraries, for identifying homologues of
 CC polypeptides from other species, and for purification of the proteins.
 CC
 CC Sequence 626 AA;
 CC
 CC Query Match 97.8%; Score 43; DB 21; Length 626;
 CC Best Local Similarity 77.8%; Pred. No. 12;
 CC Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 MLGCRPPE 9
 CC :|||:
 CC 228 LLVGRPPE 236
 CC
 CC RESULT 16
 CC ABB61067
 CC ID ABB61067 standard; Protein; 769 AA.
 CC AC ABB61067;
 CC XX
 CC DT 26-MAR-2002 (first entry)
 CC YV
 CC DE Drosophila melanogaster polypeptide SEQ ID NO 1599
 CC KW Drosophila: developmental biology; cell signalling; insecticide;
 CC KW pharmaceutical.
 CC XX
 CC QS Drosophila melanogaster.
 CC PN W0200171342-A2.
 CC XX
 CC PD 27-SEP-2001.
 CC XX
 CC PF 23-MAR-2001; 200.WO-US09231.
 CC XX
 CC PP 23-MAR-2000; 2000US-191637P.
 CC FR 11-JUL-2000; 2000US-061415O.
 CC XX
 CC PA (PEKE) PE CORP NY.
 CC XX
 CC PI Venter JC, Adams M, Li PWD, Myers EW.
 CC XX
 CC DR WPI; 2001-656960/75.
 CC DR N-PSDB; A620717C.
 CC XX
 CC PT New isolated nucleic acid detection reagent for detecting 1000 or more
 CC PT genes from Drosophila and for elucidating cell signalling and cell-cell
 CC PT interactions -
 CC XX
 CC PS Disclosure; SEQ ID NO 1599; 21bp + Sequence Listing; English.
 CC XX

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.
 CC
 CC SQ Sequence 769 AA;
 CC
 CC Query Match 87.8%; Score 43; DB 22; Length 769;
 CC Best Local Similarity 77.8%; Pred. No. 14;
 CC Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 MLGCRPPE 9
 CC :|||:
 CC 206 LLVGRPPE 214
 CC
 CC RESULT 17
 CC AAW74160
 CC ID AAW74160 standard; peptide; 8 AA.
 CC XX
 CC AC AAW74160;
 CC XX
 CC DT 05-MAY-1999 (first entry)
 CC XX
 CC DE HJ loop peptide J-43.
 CC XX
 CC KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 CC KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 CC KW inflammatory disorder; central nervous system disease; septic shock;
 CC KW Parkinson's disease; hypertension.
 CC XX
 CC OS Synthetic.
 CC XX
 CC FH Key Location/Qualifiers
 CC FT Modified-site 1 /note= "acetylated"
 CC FT Modified-site 8 /note= "amidated"
 CC FT
 CC XX WC9853350-A2.
 CC PN
 CC XX 26-NOV-1998.
 CC PD
 CC XX 20-MAY-1998; 98WO-US10319.
 CC PF
 CC XX 21-MAY-1997; 97US-0861338.
 CC PR
 CC XX (CHIL-) CHILDRENS MEDICAL CENT.
 CC PA (VISS) VISSUM RES & DEV CO.
 CC XX
 CC PI Ben-Sasson SA;
 CC XX
 CC DR WPI; 1999-070142/06.
 CC XX
 CC PT New peptides for modulating serine/threonine kinase activity -
 CC PT comprise a sequence corresponding to the HJ loop of a
 CC PT serine/threonine kinase, used for treating, e.g. cancers,
 CC PT inflammatory disorders or autoimmune disorders
 CC XX
 CC PS Claim 14, Fig 4; 70pp; English.
 CC XX
 CC CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,

CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.

XX Sequence 8 AA;
 SQ Query Match 83.7%; Score 41; DB 20; Length 8;
 Best Local Similarity 87.5%; Pred. No. 9.3e+05;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 |||:||||
 DB 1 MLGKPPF 8

RESULT 18
 AAU98316
 ID AAC98316 standard; Peptide; 8 AA.

XX AC AAU98316;
 XX DT 13-AUG-2002 (first entry)

XX DE Polo kinase serine-threonine kinase HJ loop peptide J-43.

XX KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
 KW modulating STK activity; polo kinase; J-43.

XX CS Unidentified.
 XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal: acetyl"
 FT Modified-site 8 /note= "C-terminal: amide"

XX PN US2002049301 A1.
 XX PD 25-APR-2002.
 XX EF 13-DEC-2000; 2000US-0736076.
 XX FR 21-MAY-1997; 97US-086338.
 XX PA (CHILDREN) CHILDRENS MEDICAL CENT.
 XX PI Ben-Sasson SA;
 XX CR WPI; 2002-462787/49.

XX PT New peptide from the HJ loop of serine-threonine kinase, useful for
 PT treating e.g. cancer and for producing diagnostic antibodies -
 XX PS Disclosure; Fig 4; 41pp; English.

XX CC The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for

CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase
 CC serine-threonine kinase HJ loop peptide J-43. This sequence is one of
 CC the short peptides of the invention that selectively modulate the
 CC activity of STK.

XX Sequence 8 AA;

Query Match 83.7%; Score 41; DB 23; Length 8;
 Best Local Similarity 87.5%; Pred. No. 9.3e+05;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 |||:||||
 DB 1 MLGKPPF 8

RESULT 19
 AAR92176
 ID AAR92176 standard; Protein; 416 AA.

XX AC AAR92176;
 XX DT 25-MAY-1996 (first entry)

XX DE Sak serine-threonine kinase N-terminus.

XX KW Sak; serine-threonine kinase; STK; agonist; antagonist;
 KW proliferative disease; cancer; tumour; antitense; transgenic animal;
 KW therapy.

XX OS Mus musculus.

XX PN CA2150789-A.

XX PD 03-DEC-1995.

XX PF 01-JUN-1995; 95CA-2150789.

XX PR 02-JUN-1994; 94US-0252995.

XX PA (MOUN) MOUNT SINAI HOSPITAL CORP.

XX PI Dennis JW, Fode C, Hefferman M;

XX DR WPI; 1996-129817/14.

XX DR N-PSDB; AAT08710.

XX PT Nucleic acid encoding Sak serine-threonine kinase - useful for
 PT identifying modulators potentially useful in treatment or prevention
 PT of proliferative disease.

XX PS Claim 3; Page 46-48; 73pp; English.

XX CC 2 isoforms, sak-a and sak-b, of a novel serine/threonine kinase
 CC have an identical N-terminal sequence (AAR92176) that contains the
 CC kinase domain and that shows significant homology to the polo
 CC subfamily. The C-terminal sequences (each contg. 3 PEST regions)
 CC of the 2 isoforms differ (see AAR92177 and AAR92214). Sak-a and Sak-b
 CC are associated with mitotic and meiotic cell division, and may be
 CC involved in cell proliferation. They can be obtd. in recombinant
 CC form by expression of encoding sequences (see AAT08710-12) and used
 CC to test for inhibitory or stimulatory cpds. that may be useful
 CC in the treatment/diagnosis of proliferative disorders, such as
 CC cancer and viral (esp. HIV) infection.

XX Sequence 416 AA;

Query Match 83.7%; Score 41; DB 17; Length 416;
 Best Local Similarity 66.7%; Pred. No. 18;

```

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 204 LLIGRPPFD 212

RESULT 20
AAR92214
ID AAR92214 standard; Protein; 464 AA.
AC AAR92214;
XX
XX
DT 25-MAY-1996 (first entry)
XX
DE SAK-b serine-threonine kinase.
XX
XX SAK-b; serine-threonine kinase; STK; agonist; antagonist;
XX proliferative disease; cancer; tumour; antisense; transgenic animal;
XX therapy.
XX
OS Mus musculus.
XX
XX Key Location/Qualifiers
FH Key 1..416
FT Domain /label= N-terminal domain
FT /note= "contains the kinase domain"
FT 417..464
FT Domain /label= C-terminal domain
FT /note= "contains 3 PEST regions"
XX
XX CA2150789-A.
XX
XX 03-DEC-1995.
XX
XX 01-JUN-1995; 95CA-2150789.
XX
XX 02-JUN-1994; 94US-0252995.
XX
XX (MOUN) MOUNT SINAI HOSPITAL CORP.
XX
XX Dennis JW, Fode C, Heffernan M;
XX
XX WPI; 1996-129817/14.
XX N-PSDB; AAT08711.
XX
XX Nucleic acid encoding Sak serine-threonine kinase - useful for
XX identifying modulators potentially useful in treatment or prevention
XX of proliferative disease.
XX
XX Claim 6; Page 58-61; 73pp; English.
XX
XX 2 Isoforms, SAK-a (AAR92177) and SAK-b (AAR92214), of a novel
XX serine/threonine kinase are associated with mitotic and meiotic cell
XX division and are characterized by having a kinase domain at the
XX N-terminus and 3 PEST sequences (rich in Pro, Ser, Thr, Asp, Glu) at
XX the C-terminus. The N-terminal regions of the 2 isoforms are
XX identical (see AAR92176). SAK-a and SAK-b can be covalently modified in recombinant
XX form by expression of encoding sequences (see AAT08711-12), and used
XX to test for inhibitory or stimulatory cpds. useful in the
XX treatment/diagnosis of proliferative disorders such as cancer and
XX and viral (esp. HIV) infection, or used to raise antibodies.
XX
XX Sequence 464 AA;

Query Match 83.7%; Score 41; DB 17; Length 464;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 204 LLIGRPPFD 212

RESULT 21
AAR92177
ID AAR92177 standard; Protein; 925 AA.
AC AAR92177;
XX
XX
DT 25-MAY-1996 (first entry)
XX
DE SAK-a serine-threonine kinase.
XX
XX SAK-a; serine-threonine kinase; STK; agonist; antagonist;
XX proliferative disease; cancer; tumour; antisense; transgenic animal;
XX therapy.
XX
OS Mus musculus.
XX
XX Key Location/Qualifiers
FH Key 1..416
FT Domain /label= N-terminal domain
FT /note= "contains the kinase domain"
FT 417..925
FT Domain /label= C-terminal domain
FT /note= "contains 3 PEST regions"
XX
XX CA2150789-A.
XX
XX 03-DEC-1995.
XX
XX 01-JUN-1995; 95CA-2150789.
XX
XX 02-JUN-1994; 94US-0252995.
XX
XX (MOUN) MOUNT SINAI HOSPITAL CORP.
XX
XX Dennis JW, Fode C, Heffernan M;
XX
XX WPI; 1996-129817/14.
XX N-PSDB; AAT08711.
XX
XX Nucleic acid encoding Sak serine-threonine kinase - useful for
XX identifying modulators potentially useful in treatment or prevention
XX of proliferative disease.
XX
XX Claim 5; Page 50-55; 73pp; English.
XX
XX 2 Isoforms, SAK-a (AAR92177) and SAK-b (AAR92214), of a novel
XX serine/threonine kinase are associated with mitotic and meiotic cell
XX division and are characterized by having a kinase domain at the
XX N-terminus and 3 PEST sequences (rich in Pro, Ser, Thr, Asp, Glu) at
XX the C-terminus. The N-terminal regions of the 2 isoforms are
XX identical (see AAR92176). SAK-a and SAK-b can be covalently modified in recombinant
XX form by expression of encoding sequences (see AAT08711-12), and used
XX to test for inhibitory or stimulatory cpds. useful in the
XX treatment/diagnosis of proliferative disorders such as cancer and
XX and viral (esp. HIV) infection, or used to raise antibodies.
XX
XX Sequence 925 AA;

Query Match 83.7%; Score 41; DB 17; Length 925;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
DB 204 LLIGRPPFD 212

RESULT 22
ABB57273
ID ABB57273 standard; Protein; 925 AA.
XX
XX ABB57273;

```

```

XX 07-MAR-2002 (first entry)
XX
XX Mouse ischaemic condition related protein sequence SEQ ID NO:766.
XX
XX Mouse, ischaemia; compressive ischaemia; occlusive ischaemia;
XX vasospastic ischaemia; ischaemic condition; ischaemic disease.
XX
XX M.1s musculus.
XX
XX WO2001088-88-A2.
XX
XX 22-NOV-2001.
XX
XX 18-MAY-2001; 2001WO-0904192.
XX
XX 18-MAY-2000; 2000JP-0145977.
XX
XX (JUNIOR) UNIV NIHOON SCHOOL JURIDICAL PERSON.
XX
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y.
XX
XX WPI; 2002-034733/04.
XX
XX N-PSDB; AB199713.
XX
XX Examining the ischemic condition (e.g. occlusive ischaemia) by measuring
XX expression levels of particular genes defined in the specification or
XX by determining the expression profile of a gene group comprising these
XX genes.
XX
XX Claim 2; Page 1893-1897; 2690pp; English.
XX
XX The present invention describes a method for examining ischaemic
XX conditions, comprising measuring the expression levels of particular
XX genes in a test sample or determining the expression profile of a
XX gene group in the sample comprising genes selected from (i). The method
XX is useful for examining the ischaemic condition (e.g. compressive
XX ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
XX expression levels of particular genes (AB199202 to AB199912, encoding
XX the protein sequences in AB85702 to AB85734) or by determining the
XX expression profile of a gene group comprising these genes. The
XX expression levels or expression profiles produced by these genes are
XX used as an indicator when screening for ischaemic condition-improving
XX drugs or therapeutics for ischaemic diseases. AB19913 and AB199914
XX represent PCR primers for a mouse ischaemic condition-related sequence,
XX which are used in the exemplification of the present invention.
XX
XX Sequence 925 AA;
XX
XX Query Match 83.7%; Score 41; DB 23; Length 925;
XX Best Local Similarity 66.7%; Pred. No. 43;
XX Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX : MLGRRPPE 9
XX :|:|:|:|:
XX 204 LLIGRRPFD 212
XX
XX RESULT 23
XX AAM78813
XX ID AAM78813 standard; Protein; 970 AA.
XX
XX AC AAM78813;
XX
XX 26-NOV-2001 (first entry)
XX
XX Human protein SEQ ID NO 1495.
XX
XX Human; cytochrome; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation.
XX

```

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OS Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US04098.
XX
XX 03-FEB-2000; 2000US-0496914.
XX
XX 27-APR-2000; 2000US-0560975.
XX
XX 20-JUN-2000; 2000US-0598075.
XX
XX 19-JUL-2000; 2000US-0620125.
XX
XX 01-SEP-2000; 2000US-0654936.
XX
XX 15-SEP-2000; 2000US-0663561.
XX
XX 20-OCT-2000; 2000US-0693125.
XX
XX 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y,
XX Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW,
XX Xue AJ, Yang Y, Wehrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
XX
XX N-PSDB; AAK51966.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX useful in diagnosis and gene therapy.
XX
XX Claim 20; Page 3782-3784; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK5:456-AAK5:3435) and the
XX encoded polypeptides (AAM78123-AAK80302) that exhibit activity relating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX (AAM80020) are omitted as the relevant pages from the sequence listing
XX were missing at the time of publication.
XX
XX Sequence 970 AA;
XX
XX Query Match 83.7%; Score 41; DB 22; Length 970;
XX Best Local Similarity 66.7%; Pred. No. 43;
XX Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX : MLGRRPPE 9
XX :|:|:|:|:
XX 204 LLIGRRPFD 212
XX
XX RESULT 24
XX AAM39244
XX ID AAM39244 standard; Protein; 970 AA.
XX
XX AC AAM39244;
XX
XX 22-OCT-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 2389.
XX
XX Human; neutropenic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX atrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX

```


KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

OS Homo sapiens.

PN WC20C153112-A1.

PD 26-JUL-2001.

FF 26-DEC-2000; 2000WC-US34263.

XX 21-JAN-2000; 2000US-0498725.

PR 05-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0538042.

PR 19-JUL-2000; 2000US-0623322.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693236.

PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen P, Ma Y, Qian XB, Ren F, Wang D,

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AC, Yang Y, Zhang C,

PI Zhao QA, Zhou P, Goodrich R, Diranac RT,

XX WPI: 2001-442253/47.

DR N-PSDB; AA:EC186.

XX Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries.

XX Example 2; SEQ ID NO 5961; 10278pp; English.

PS The invention relates to human nucleic acids (AA159798 AA161369) and

XX the encoded polypeptides (AA159642-AA162213) with neurotropic,

CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as immune system regulation,

CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, anti-sclerosis,

CC assays for receptor activity, arthritis and inflammatory leukemias and

CC C.R.S disorders.

CC Note: The sequence data for this patent did not form part of the printed

CC specification.

XX SQ Sequence 980 AA;

Query Match 83.7%; Score 41; DB 22; Length 980;

Best Local Similarity 66.7%; Pred. No. 44;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XLGGPPPE 9

PD 214 LGGPPPE 222

RESULT 27

AAU98319

ID AAU98319 standard; peptide: 9 AA

XX AC

XX AC

DT 05-MAY-1993 (first entry)

XX HC loop peptide J-45.

XX HC loop; serine/threonine kinase; cancer; diabetes; obesity;

XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity;

XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity;

XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity;

XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity;

XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity;

XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity;

XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity;

KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.

OS Synthetic.

XX Key

XX Location/Qualifiers

PH Modified-site 1

FT Modified-site 9

FT Modified-site 9

FT Modified-site 9

FT Modified-site 9

FT Modified-site 9

FT Modified-site 9

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FT Modified-site 9

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KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cyclostatic; antidiabetic; anorectic; neurological;
 KW antiinflammatory; immunosuppressive; cardiant; haemostatic;
 KW modulating STK activity; polo kinase; J-45.
 OS Unidentified.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Misc-difference 7
 FT Modified-site 9 /note= "Benzyl ester of Glutamic acid"
 FT Modified-site /note= "C-terminal amide"
 XX US2002049301-A1.
 XX 25-APR 2002.
 XX 13 DEC 2000; 2000US-0736076.
 XX 21 MAY 1997; 97US-0861338.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX Ben Sasson SA;
 XX WPI; 2002-462787/49.
 XX New peptide from the HJ loop of serine-threonine kinase, useful for
 XX treating e.g. cancer and for producing diagnostic antibodies.
 XX Disclosure; Fig 4; 4:pp; English.
 CC The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase
 CC serine-threonine kinase HJ loop peptide J 45. This sequence is one of
 CC the short peptides of the invention that selectively modulate the
 CC activity of STK
 XX Sequence 9 AA:
 SQ
 Query Match 81.6%; Score 40; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9 3e-05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LGPPPE 9
 DB 1 LGPPPE 7
 RESULT 29
 AAW74173
 ID AAW74173 standard; peptide; 20 AA.
 XX AC
 XX AC AAW74173;
 XX AC
 DT 05-MAY-1999 (first entry)
 XX HJ loop peptide POLC.
 XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;

KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.
 XX Synthetic.
 OS
 PN WO9853050-A2.
 XX 26-NOV-1998.
 XX 20-MAY-1998; 98WO-US10319.
 XX 21-MAY-1997; 97US-0861338.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX (Y'SS) VISSUM RES & DEV CO.
 XX Ben-Sasson SA;
 XX WPI; 1999-070142/06.
 XX New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders
 XX Claim 41; Fig 3b; 70pp; English.
 CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.
 XX Sequence 20 AA:
 SQ
 Query Match 81.6%; Score 40; DB 20; Length 20;
 Best Local Similarity 66.7%; Pred. No. 1.3;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGRRPPE 9
 DB 3 LLVGKPPPE 11
 RESULT 30
 AAU98306
 ID AAU98306 standard; Peptide; 20 AA.
 XX AC
 XX AC AAU98306;
 XX 13-AUG-2002 (first entry)
 XX Peptide sequence of HJ loop of serine-threonine kinase polo kinase.
 DE HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cyclostatic; antidiabetic; anorectic; neurological;
 KW antiinflammatory; immunosuppressive; cardiant; haemostatic;
 KW modulating STK activity; polo kinase.
 XX Unidentified.
 OS

XX US2002049301-A1.
 XX 25-APR-2002.
 XX 13-DEC-2000; 2000US-0736076.
 XX 21-MAY-1997; 97US-0961339.
 XX (CHILDREN) CHILDRENS MEDICAL CENT.
 XX Ben-Sasson SA;
 XX WPI; 2002-462787/49.
 XX New peptide from the HJ loop of serine-threonine kinase, useful for
 PT treating e.g. cancer and for producing diagnostic antibodies.
 XX Claim 33; Fig 3; 41pp; English.
 XX The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the peptide sequence of the HJ
 CC loop of serine-threonine kinase polo kinase. This sequence is one of the
 CC short peptides of the invention that selectively modulate the activity
 CC of STK.
 XX
 SQ Sequence 20 AA;
 Query Match 81.6%; Score 40; DB 23; Length 20;
 Best Local Similarity 66.7%; Pred. No. 1.33;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGRRPPE 9
 Db 3 LLVGKPPPE 11
 RESULT 11
 AAB56690
 ID AAB56690 standard; Protein; 329 AA.
 XX AAB56690;
 XX 13-MAR-2001 (first entry)
 XX Human prostate cancer antigen protein sequence SE, ID NC:1263.
 XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroproliferative; cystostatic; cardiac; immunomodulatory; muscular;
 KW vulnary; gastrointestinal; nephrotropic; antineoplastic; gynaecological;
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease.
 XX Homo sapiens.
 CS
 XX W020005174-A1.
 XX 21-SEP-2000.
 XX 08-MAR-2000; 2000WO-US05988.
 XX 12-MAR-1999; 99US-0124270.
 XX (HUMAN) HUMAN GENOME SCI INC.
 PT Constructing strains for identifying gene products as effective targets

PA (ROSE/) ROSEN C A.
 XX Rosen CA, Ruben SM;
 XX WPI; 2000-587513/55.
 XX N-PSDB; AAF15893.
 XX Prostate cancer associated gene sequences, referred to as prostate
 PT cancer antigens, useful for treatment, prevention, and diagnosis of
 PT disorders such as prostate cancer.
 XX Claim 11; Page 1691-1692; 238pp; English.
 XX AAF15566 to AAF16505 encode the human prostate cancer associated
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytostatic,
 CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
 CC nephrotropic, antineoplastic, gynaecological and antibacterial activities,
 CC and can be used in gene therapy. The prostate cancer antigen
 CC polynucleotides may be used for detection of prostate cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The prostate cancer antigens may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 329 AA;
 Query Match 81.6%; Score 40; DB 21; Length 329;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGRRPPE 9
 Db 260 LLVGKPPPE 268
 RESULT 32
 AAB73734
 ID AAB73734 standard; Protein; 528 AA.
 XX AAB73734;
 XX 30-JAN-2003 (first entry)
 XX Candida albicans essential protein SEQ ID NO 7571.
 XX Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
 KW signal transduction; DNA replication; cell division; growth;
 KW proliferation; Candida albicans; fungicide; antifungal.
 XX Candida albicans.
 OS
 XX W0200253728-A2.
 XX 11-JUL-2002.
 XX 26-DEC-2001; 2001WO-US49486.
 XX 29-DEC-2000; 2000US-259128P.
 XX 20-FEB-2001; 2001US-0792024.
 XX 22-AUG-2001; 2001US-314050P.
 XX (ELIT-) ELITRA PHARM INC.
 XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
 XX WPI; 2002-566694/60.
 XX N-PSDB; AB232284.
 XX Constructing strains for identifying gene products as effective targets

PT for therapeutic intervention, by inactivating in the strain one allele
PT of a gene and placing other allele of the gene under conditional
XX expression
PS Ciam 44: SEQ ID NO 7571; 167pp + Sequence Listing: English.
XX
XX The invention relates to constructing (M1) a strain of diploid fungal
XX cells in which both alleles of a gene are modified, comprising modifying
XX one allele by insertion or replacement by a cassette having an
XX expressible selectable marker and modifying other allele by
XX recombination, of a promoter replacement fragment with a heterologous
XX promoter, so that expression of the second allele is regulated by the
XX promoter. (M1) is useful for constructing a strain of diploid fungal
XX cells in which both alleles of a gene are modified. The diploid fungal
XX cells having both alleles modified are useful for identifying a gene that
XX is essential to the survival or growth of a fungus, a gene that
XX contributes to the virulence and/or pathogenicity of a fungus, a gene
XX that contributes to the resistance of a diploid fungus to an antifungal
XX agent, an antifungal agent that inhibits the growth of a diploid fungus
XX and for identifying a therapeutic agent for treatment of a mammalian
XX disease. (M1) is useful for identifying a compound which modulates the
XX activity of a gene product, preferably enzymatic activity, carbon
XX compound catabolism, biosynthesis, transporter, transcriptional,
XX translational, signal transduction, DNA replication and cell division
XX activity. The method is useful for identifying a compound having the
XX ability to inhibit growth or proliferation of C. albicans cells and for
XX treating infection by C. albicans. The present sequence is that of an
XX essential Candida albicans protein used in the method of the invention.
XX Note: The sequence data for this patent is not represented in the printed
XX specification but is based on sequence information supplied to Derwent by
XX the European Patent Office.

SC Sequence 528 AA:

Query Match 81.6% Score 407 DB 21 Length 528,
Best Local Similarity 66.7% Pred No 367
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

CV 1 MLGKPPPE 9
DE 454 LMGKPPPE 462

RESULT 11

AAU74656
ID AAU74656 standard; Protein. 131 AA.

XX AAU74656
XX
XX 09-APR 2002 (first entry)
XX
XX Mammalian polo-like kinase (Plk).
XX
XX Polo-like kinase; Plk; polo-box; cytostatic; neoplasm;
XX hyperproliferative disorder; cytokinesis; solid tumor;
XX carcinoma; sarcoma; cancer; small cell carcinoma; melanocarcinoma;
XX Mullerian tumour; squamous cell carcinoma; protein.
XX
XX Mammalia.

XX Key Location/Qualifiers
XX
XX Misc-difference 130
XX /label= Unknown
XX
XX Misc-difference 131
XX /label= Unknown
XX
XX Misc-difference 132
XX /label= Unknown
XX
XX Misc-difference 133
XX /label= Unknown
XX
XX Misc-difference 134
XX /label= Unknown
XX
XX Misc-difference 135
XX /label= Unknown

FT Misc-difference 136
FT /label= Unknown
FT Misc-difference 137
FT /label= Unknown
FT Misc-difference 138
FT /label= Unknown
FT Misc-difference 139
FT /label= Unknown
FT Misc-difference 140
FT /label= Unknown
FT Misc-difference 141
FT /label= Unknown
FT Misc-difference 147
FT /label= Unknown
FT Misc-difference 148
FT /label= Unknown
FT Misc-difference 149
FT /label= Unknown
FT Misc-difference 150
FT /label= Unknown
FT Misc-difference 151
FT /label= Unknown
FT Misc-difference 152
FT /label= Unknown
FT Misc-difference 153
FT /label= Unknown
FT Misc-difference 154
FT /label= Unknown
FT Misc-difference 155
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FT Misc-difference 156
FT /label= Unknown
FT Misc-difference 157
FT /label= Unknown
FT Misc-difference 158
FT /label= Unknown
FT Misc-difference 159
FT /label= Unknown
FT Misc-difference 160
FT /label= Unknown
FT Misc-difference 161
FT /label= Unknown
FT Misc-difference 162
FT /label= Unknown
FT Misc-difference 163
FT /label= Unknown
FT Misc-difference 164
FT /label= Unknown
FT Misc-difference 165
FT /label= Unknown
FT Region
FT 410..439
FT /label= Polo-box
FT /note= "Core polo-box consensus sequence"
XX
XX WO200190401-A2.
XX
XX 29-NOV-2001.
XX
XX 23-MAY-2001; 2001WO-US:6903.
XX
XX 23-MAY-2000; 2000US-206588P.
XX
XX (HARD) HARVARD COLLEGE.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (USSH) US NAT INST OF HEALTH.
XX
XX Lee KS, Song S, Erikson R;
XX WPI; 2002-106210/14.
XX
XX Identifying polo-like kinase modulators by contacting eukaryotic cells
XX expressing polo-box peptides with test compounds and evaluating changes
XX in dominant negative cytokinesis-defective growth patterns -

XX Example 2: Fig 5: 57pp; English.
 PS The invention describes a novel method of detecting compounds with
 CC polo-like kinase (PLK) modulating activity. This comprises contacting
 CC eukaryotic cells expressing polo-box or polo-box related peptides,
 CC binding peptides comprising 25 contiguous residues from a polo-like
 CC kinase C-terminal region, with a test compound. Ecopic expression of a
 CC polo-box in a eukaryotic cell causes a severe cytotoxic defect in the
 CC cell. These eukaryotic cells can also be tested with the test compound
 CC used in the method of the invention. The polo-box related peptides and
 CC polo-like kinase activity modulatory compounds can be used to inhibit or
 CC enhance cellular proliferation and subsequently for treating
 CC hyper-proliferative disorders including neoplasia, solid tumours,
 CC carcinomas, sarcomas and cancers e.g. small cell carcinoma,
 CC adenocarcinoma, Mullerian tumours and squamous cell carcinomas. This
 CC is the amino acid sequence of a mammalian polo-like kinase (Plk),
 CC uncontrolled expression of the Plk family is implicated in the
 CC development of human cancers, discussed in the method of the invention.

XX SQ Sequence 531 AA;
 Query Match 81.6%; Score 40; DB 23; Length 531;
 Best Local Similarity 66.7%; Pred. No. 36;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
 DB 204 LLVGKPPPE 212

RESULT 34
 AAR74620
 ID AAR74620 standard; Protein: 603 AA;
 XX AC AAR74620;
 XX DT 25-MAR-2003 (updated);
 DT 26-OCT-1995 (first entry);
 XX DE Human lung tumour Polo-like kinase.
 XX KW Polo-like kinase; PK; serine threonine kinase; human; lung tumour;
 KW autoimmune disease; lymphocyte activity
 XX CS Homo sapiens.
 XX FH Key Location/Qualifiers
 FH Binding-site 60..86
 FT Label: ATP binding motif
 FT Region 174..177
 FT /note= "motif that is highly conserved in protein
 FT kinases"
 FT Region 194..196
 FT /note= "motif that is highly conserved in protein
 FT kinases"

XX FE4329177-A1.
 XX DT 22-MAR-1995.
 XX DT 30-AUG-1993; 93DE-4329177.
 XX DT 30-AUG-1993; 93DE-4329177.
 XX (CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG
 XX Poltrich U. Rutsamen-Waigmann H. Stierwald H.
 FI Rutsamen-Waigmann H;
 FI WPI: 1995-099454/14.
 FI N-PSBB; AAR88155.
 XX

PT A polo-like serine threonine kinase-protein - isolated from
 PT proliferating human tissue, useful in the determin of lymphocyte
 PT activity, eg in auto-immune diseases
 XX Claim 1; Page 8-10; 11pp; German.
 XX A human lung tumour-derived cDNA (AAR88155) was found to have high
 CC homology with sequences from members of the serine/threonine kinase
 CC family. Due to the strong homology with the Drosophila polo gene,
 CC the protein encoded by the new cDNA (AAR74620) was designated a polo-
 CC like kinase (PLK). PLK mRNA is expressed in proliferating cells such
 CC as placenta, colon and tumours of the lung, oesophagus, gut and
 CC intestine. Resting lymphocytes do not express the PLK gene but after
 CC stimulation with phytohaemagglutinin, PLK is expressed and can be
 CC used as an indicator of lymphocyte stimulation.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 603 AA;

Query Match 81.6%; Score 40; DB 16; Length 603;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
 DB 244 LLVGKPPPE 252

RESULT 35
 AAU79306
 ID AAU79306 standard; Peptide: 603 AA;
 XX AC AAU79306;
 XX DT 02-JUL-2002 (first entry);
 DT Mouse polo-like kinase (Plk).
 DE
 XX KW Polo box; PBL; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; candida; lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk.

XX MS Musculus.
 XX US6358738-B1.
 XX DT 19-MAR-2002.
 XX DT 13-MAY-1999; 99US-031131.
 XX DT 13-MAY-1998; 98US-085296P.
 XX HARD : HARVARD COLLEGE.
 XX Erikson RL, Lee KS;
 XX WPI: 2002-314756/35.

XX Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections
 XX Example 1; Column 59-64; 47pp; English.
 XX The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer

CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of the polo-like kinase (Plk), a
 CC protein from which mitotic protein polo kinase inhibitory peptides are
 CC derived.

XX Sequence 603 AA;

Query Match 81.6%; Score 40; DB 23; Length 603;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
 :||:||||
 Db 244 LLGKPPPE 252

RESULT 36
 AAU79309
 ID AAU79309 standard; Peptide: 603 AA.

XX AC AAU79308;

XX DT 02-JUL-2002 (first entry);

XX DE Mouse polo-like kinase (Plk) T212D mutant.

XX KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; murein.

XX OS Mus musculus.
 XX OS Synthetic.

XX FH Key Location/Qualifiers
 XX FT Misc-difference 21C /note= "Wild type Thr substituted by Asp"

XX PN US6358738-B1.

XX PD 19-MAR-2002

XX PF 13-MAY-1999; 99US-031311.

XX PR 13-MAY-1998; 98US-085296P.

XX PA (HARD) HARVARD COLLEGE.

XX PI Erikson RL, Lee KS;

XX DR WPI; 2002-314756/35.

XX PT Administering polo kinase inhibitors for the treatment of cancers and
 XX PT fungal infections -
 XX PS Example 1; Page -; 47pp; English.

XX CC The invention describes a method of inhibiting growth of an isolated
 XX CC population of cells by inhibiting a cell polo kinase by administering a
 XX CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 XX CC carboxy terminal domain of the polo kinase which excludes the polo
 XX CC kinase catalytic domain. The method is used for the treatment of cancer
 XX CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 XX CC cervix, the epithelium, the brain, the retina, the prostate, and the
 XX CC throat), infection by fungi (e.g. Candida, lichen, Trichophyton,
 XX CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.

CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information
 CC given in the invention.

XX Sequence 603 AA;

Query Match 81.6%; Score 40; DB 23; Length 603;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
 :||:||||
 Db 244 LLGKPPPE 252

RESULT 37
 AAU79309
 ID AAU79309 standard; Peptide: 603 AA.

XX AC AAU79309;

XX DT 02-JUL-2002 (first entry);

XX DE Mouse polo-like kinase (Plk) T212E mutant.

XX KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; murein.

XX OS Mus musculus.
 XX OS Synthetic.

XX FH Key Location/Qualifiers
 XX FT Misc-difference 21D /note= "Wild type Thr substituted by Glu"

XX PN US6358738-B1.

XX PD 19-MAR-2002

XX PF 13-MAY-1999; 99US-031311.

XX PR 13-MAY-1998; 98US-085296P.

XX PA (HARD) HARVARD COLLEGE.

XX PI Erikson RL, Lee KS;

XX DR WPI; 2002-314756/35.

XX PT Administering polo kinase inhibitors for the treatment of cancers and
 XX PT fungal infections -
 XX PS Example 1; Page -; 47pp; English.

XX CC The invention describes a method of inhibiting growth of an isolated
 XX CC population of cells by inhibiting a cell polo kinase by administering a
 XX CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 XX CC carboxy terminal domain of the polo kinase which excludes the polo
 XX CC kinase catalytic domain. The method is used for the treatment of cancer
 XX CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 XX CC cervix, the epithelium, the brain, the retina, the prostate, and the
 XX CC throat), infection by fungi (e.g. Candida, lichen, Trichophyton,
 XX CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 XX CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 XX CC mutant, used to determine the residues required for kinase activity.

CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information
 CC given in the invention.

XX SQ Sequence 603 AA;

Query Match 81.6%; Score 40; DB 23; Length 603;
 Best Local Similarity 66.7%; Pred No. 41;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY : MLGRRPPE 9
 : : : : :
 Db 244 LLVGKPPPE 252

RESULT 38
 AAU79310
 ID AAU79310 standard; Peptide: 603 AA.
 XX
 AC AAU79310;
 XX
 DT 02-JUL-2002 (first entry);
 XX
 DE Mouse polo-like kinase (Plk) T206V mutant.
 XX
 KW Polo box; PBL; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutcin.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 210 /note= "Wild type Thr substituted by Val"
 FT
 XX US6359738 B1.
 XX
 PD 19-MAR-2002.
 XX
 PF 13-MAY-1999; 99US-0311311.
 XX
 PR 13 MAY 1998; 98US-085296P.
 XX
 PA (HARD : HARVARD COLLEGE.
 XX
 PI Erickson RL, Lee KS;
 XX
 WP1; 2002-314756/35.
 XX
 PT Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections
 XX
 PS Example 1; Page 47pp; English.
 XX
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information

CC given in the invention.
 XX SQ Sequence 603 AA;

Query Match 81.6%; Score 40; DB 23; Length 603;
 Best Local Similarity 66.7%; Pred No. 41;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY : MLGRRPPE 9
 : : : : :
 Db 244 LLVGKPPPE 252

RESULT 39
 AAU79311
 ID AAU79311 standard; Peptide: 603 AA.
 XX
 AC AAU79311;
 XX
 DT 02-JUL-2002 (first entry);
 XX
 DE Mouse polo-like kinase (Plk) E206V mutant.
 XX
 KW Polo box; PBL; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutcin.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 206 /note= "Wild type Glu substituted by Val"
 FT
 XX US6359738-B1.
 XX
 PD 19-MAR-2002.
 XX
 PF 13-MAY-1999; 99US-0311311.
 XX
 PR 13-MAY-1998; 98US-085296P.
 XX
 PA (HARD : HARVARD COLLEGE.
 XX
 PI Erickson RL, Lee KS;
 XX
 WP1; 2002-314756/35.
 XX
 PT Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections
 XX
 PS Example 1; Page 47pp; English.
 XX
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information
 CC given in the invention.

SQ Sequence 603 AA;
Query Match 81.6%; Score 40; DB 23; Length 603;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
244 LLVGKPPFE 252

Db

Search completed: November 14, 2003, 13:25:19
Job time : 34.7143 secs

SQ Sequence 603 AA;
Query Match 81.6%; Score 40; DB 23; Length 603;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFE 9
244 LLVGKPPFE 252

Db

Search completed: November 14, 2003, 13:25:19
Job time : 34.7143 secs

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OM protein - protein search, using sw model

Run on: November 14, 2003, 11:21:00 Search time 11.8246 Seconds
(without alignment)
32.193 Million cell updates/sec

Title: us-09-736-076-15

Perfect score: 49

Sequence: MLLGRPPPE 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42312858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 3

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:
1: /cgn2_6/prodata//iaa/aa/conv.pep.*
2: /cgn2_6/prodata//iaa/aa/conv.pep.*
3: /cgn2_6/prodata//iaa/aa/conv.pep.*
4: /cgn2_6/prodata//iaa/aa/conv.pep.*
5: /cgn2_6/prodata//iaa/aa/conv.pep.*
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7: /cgn2_6/prodata//iaa/aa/conv.pep.*
8: /cgn2_6/prodata//iaa/aa/conv.pep.*
9: /cgn2_6/prodata//iaa/aa/conv.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	US-08-861-338-15	Sequence 15, App.
2	49	100.0	11	US-08-861-338-15	Sequence 15, App.
3	49	100.0	272	US-08-861-338-15	Sequence 12, App.
4	49	100.0	272	US-08-861-338-15	Sequence 12, App.
5	49	100.0	685	US-08-861-338-15	Sequence 1, Appl
6	49	100.0	685	US-08-861-338-15	Sequence 1, Appl
7	49	100.0	685	US-08-861-338-15	Sequence 2, Appl
8	49	100.0	685	US-08-861-338-15	Sequence 2, Appl
9	46	93.9	9	US-08-861-338-15	Sequence 17, Appl
10	41	83.7	8	US-08-861-338-15	Sequence 10, Appl
11	41	83.7	273	US-08-861-338-15	Sequence 10, Appl
12	41	83.7	273	US-08-861-338-15	Sequence 10, Appl
13	41	83.7	416	US-08-861-338-15	Sequence 2, Appl
14	41	83.7	416	US-08-861-338-15	Sequence 2, Appl
15	41	83.7	464	US-08-861-338-15	Sequence 6, Appl
16	41	83.7	464	US-08-861-338-15	Sequence 6, Appl
17	41	83.7	925	US-08-861-338-15	Sequence 4, Appl
18	41	83.7	925	US-08-861-338-15	Sequence 4, Appl
19	40	81.6	9	US-08-861-338-15	Sequence 18, Appl
20	40	81.6	20	US-08-861-338-15	Sequence 6, Appl
21	40	81.6	272	US-08-861-338-15	Sequence 14, Appl
22	40	81.6	673	US-08-861-338-15	Sequence 14, Appl
23	40	81.6	202	US-08-861-338-15	Sequence 1, Appl
24	40	81.6	603	US-08-861-338-15	Sequence 26, Appl
25	39	79.6	264	US-08-861-338-15	Sequence 17, Appl
26	39	79.6	271	US-08-861-338-15	Sequence 11, Appl
27	39	79.6	271	US-08-861-338-15	Sequence 11, Appl

28	39	79.6	303	4	US-09-739-455-12	Sequence 12, Appl
29	39	79.6	303	4	US-09-739-455-12	Sequence 22, Appl
30	38	77.6	259	4	US-09-252-991A-28679	Sequence 28679, A
31	38	77.6	275	1	US-08-252-9950-13	Sequence 13, Appl
32	38	77.6	275	2	US-08-834-108-13	Sequence 13, Appl
33	38	77.6	344	2	US-08-755-728-3	Sequence 3, Appl
34	38	77.6	344	2	US-08-755-728-3	Sequence 3, Appl
35	38	77.6	344	3	US-09-283-011-3	Sequence 3, Appl
36	38	77.6	347	2	US-09-216-000-4	Sequence 1, Appl
37	38	77.6	403	2	US-08-755-728-4	Sequence 4, Appl
38	38	77.6	403	2	US-08-974-655-4	Sequence 4, Appl
39	38	77.6	403	3	US-09-283-011-4	Sequence 4, Appl
40	38	77.6	737	4	US-09-772-647-4	Sequence 3, Appl
41	37	75.5	20	3	US-08-861-338-3	Sequence 3, Appl
42	37	75.5	182	4	US-09-134-001C-3742	Sequence 3742, Ap
43	37	75.5	220	1	US-08-233-146-2	Sequence 2, Appl
44	37	75.5	220	1	US-08-463-470-2	Sequence 2, Appl
45	37	75.5	264	2	US-07-857-224B-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-861-338-15
Sequence 15, Application US/08861338
Patent No. 6174993
GENERAL INFORMATION:
APPLICANT: Ben-Sasson, Samuel A.
TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861.338
FILING DATE: 21-MAY-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CMCC-590
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "N-Acetyl Methionine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: /note= "Gamma Benzyl Ester of
Glutamic Acid-NH2"
US-08 861-338-15

Query Match 100.0% Score 49; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2,5e-05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGRRPFF 9
 ||||| ||
 DE 1 MLGRRPFF 9

RESULT 2
 US-08-861-338-19
 Sequence 19, Application US/0886138
 Patent No. 619499
 GENERAL INFORMATION:
 APPLICANT: Ben-Sasson, Shmuel A.
 TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.10
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/861-338
 FILING DATE: 21-MAY-1997
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Brock, David E.
 REGISTRATION NUMBER: 22,592
 REFERENCE/DOCKET NUMBER: CMC-590
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781) 861-6240
 TELEFAX: (781) 861-9540
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 FEATURES:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /note= "N-Acetyl Methionine"

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note= "N-Acetyl Methionine"

NAME/KEY: Modified-site

LOCATION: 9

OTHER INFORMATION: /note= "Glutamic Acid Henry Ester"

NAME/KEY: Modified-site

LOCATION: 11

OTHER INFORMATION: /note= "Serine NH2"

US-08-861-338-19

Query Match 100.0% Score 49; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.0e-04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGRRPFF 9
 ||||| ||
 DE 1 MLGRRPFF 9

RESULT 3
 US-08-252-995D-12
 Sequence 12, Application US/08252995D
 Patent No. 5650501
 GENERAL INFORMATION:
 APPLICANT: Dennis, James W
 APPLICANT: Heffernan, Mike
 APPLICANT: Fode, Carol
 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERESKIN & PARR
 STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CY 1 MLGRRPFF 9
 ||||| ||
 DE 1 MLGRRPFF 9

Query Match 100.0% Score 49; DB 1; Length 272;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGRRPFF 9
 ||||| ||
 DE 1 MLGRRPFF 9

RESULT 4
 US-08-834-108-12
 Sequence 12, Application US/08834108
 Patent No. 5976893
 GENERAL INFORMATION:
 APPLICANT: Dennis, James W
 APPLICANT: Heffernan, Mike
 APPLICANT: Fode, Carol
 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERESKIN & PARR
 STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CY 1 MLGRRPFF 9
 ||||| ||
 DE 1 MLGRRPFF 9

Sequence 12, Application US/08252995D
 Patent No. 5650501
 GENERAL INFORMATION:
 APPLICANT: Dennis, James W
 APPLICANT: Heffernan, Mike
 APPLICANT: Fode, Carol
 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERESKIN & PARR
 STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/252,995D
 FILING DATE: 02-JUN-1994
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Kurdydko, Linda M.
 REGISTRATION NUMBER: 34,971
 REFERENCE/DOCKET NUMBER: 3153-96
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 272 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: Mus musculus
 US-08-252-995D-12

Query Match 100.0% Score 49; DB 1; Length 272;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGRRPFF 9
 ||||| ||
 DE 1 MLGRRPFF 9

RESULT 4
 US-08-834-108-12
 Sequence 12, Application US/08834108
 Patent No. 5976893
 GENERAL INFORMATION:
 APPLICANT: Dennis, James W
 APPLICANT: Heffernan, Mike
 APPLICANT: Fode, Carol
 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERESKIN & PARR
 STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CY 1 MLGRRPFF 9
 ||||| ||
 DE 1 MLGRRPFF 9

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/834,108
3 FILING DATE:
4 CLASSIFICATION: 536
5 ATTORNEY/AGENT INFORMATION:
6 NAME: Kurdydyk, Linda M
7 REGISTRATION NUMBER: 34,971
8 REFERENCE/DOCKET NUMBER: 3153-210
9 TELECOMMUNICATION INFORMATION:
10 TELEPHONE: (416) 364-7311
11 TELEFAX: (416) 361-1398
12 INFORMATION FOR SEQ ID NO: 12:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 272 amino acids
15 TYPE: amino acid
16 STRANDEDNESS: single
17 TOPOLOGY: linear
18 MOLECULE TYPE: peptide
19 ORIGINAL SOURCE:
20 ORGANISM: Mus musculus
21 US 08 834-103.12

Query Match 100.0%; Score 49; DB 2; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DT .99 MLGRRPPE 207

RESULT 5

1 US-08-78-989-1
2 Sequence 1, Application US/088-8989
3 Patent No. 5885903
4 GENERAL INFORMATION:
5 APPLICANT: Bardman, Olga
6 APPLICANT: Hillman, Jennifer L.
7 APPLICANT: Corley, Neil C.
8 APPLICANT: Guglier, Karl G.
9 APPLICANT: Lai, Preeti
10 APPLICANT: Goli, Surya K.
11 APPLICANT: Shah, Purvi
12 TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
13 TITLE OF INVENTION: KINASES
14 NUMBER OF SEQUENCES: 2
15 CORRESPONDENCE ADDRESS:
16 ADDRESSEE: Inocyte Pharmaceuticals, Inc.
17 STREET: 1194 Porter Drive
18 CITY: Palo Alto
19 STATE: CA
20 COUNTRY: USA
21 ZIP: 94304
22 COMPUTER READABLE FORM:
23 MEDIUM TYPE: Diskette
24 COMPUTER: IBM Compatible
25 OPERATING SYSTEM: DOS
26 SOFTWARE: FastSeq for Windows Version 2.0
27 CURRENT APPLICATION DATA:
28 APPLICATION NUMBER: US/08/878,989
29 FILING DATE:
30 CLASSIFICATION: 435
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Billings, Lucy J
33 REGISTRATION NUMBER: 36,749
34 REFERENCE/DOCKET NUMBER: PF-0321 US
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 415-855-0555
37 TELEFAX: 415-845-4166
38 TELEX:

1 INFORMATION FOR SEQ ID NO: 1:
2 SEQUENCE CHARACTERISTICS:
3 LENGTH: 685 amino acids
4 TYPE: amino acid
5 STRANDEDNESS: single
6 TOPOLOGY: linear
7 IMMEDIATE SOURCE:
8 LIBRARY: HUVENRO
9 CLONE: 39043
10 US-08-878-989-1

Query Match 100.0%; Score 49; DB 2; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DB 273 MLGRRPPE 281

RESULT 6

1 US-09-136-282-2
2 Sequence 2, Application US/09136282
3 Patent No. 6063609
4 GENERAL INFORMATION:
5 APPLICANT: ANDERSON, KAREN
6 APPLICANT: JACKSON, JEFFREY
7 APPLICANT: HANSBURY, MICHAEL
8 APPLICANT: NERURKAR, SANDHYA
9 APPLICANT: ROSHAK, AMY
10 APPLICANT: BOJZYK, MARK
11 TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
12 NUMBER OF SEQUENCES: 3
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE: Ratner & Prestia
15 STREET: P.O. Box 980
16 CITY: Valley Forge
17 STATE: PA
18 COUNTRY: USA
19 ZIP: 19482
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: Diskette
22 COMPUTER: IBM Compatible
23 OPERATING SYSTEM: DOS
24 SOFTWARE: FastSeq for Windows Version 2.0
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/09/136,282
27 FILING DATE: 20-AUG-1998
28 CLASSIFICATION:
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: 60/056,112
31 FILING DATE: 20-AUG-1997
32 ATTORNEY/AGENT INFORMATION:
33 NAME: Prestia, Paul F
34 REGISTRATION NUMBER: 23,031
35 REFERENCE/DOCKET NUMBER: GH-70231
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: 610-407-0700
38 TELEFAX: 610-407-0700
39 TELEX: 846169
40 INFORMATION FOR SEQ ID NO: 2:
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 685 amino acids
43 TYPE: amino acid
44 STRANDEDNESS: single
45 TOPOLOGY: linear
46 MOLECULE TYPE: protein
47 US-09-136-282-2

Query Match 100.0%; Score 49; DB 3; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPE 9
Db 273 MLLGRPPE 281

RESULT 7

US-09-272-796-1
; Sequence 1, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, O-ga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lai, Freeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/09/272-796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 38/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-032: US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVENOB01
; CLONE: 39043
US-09-272-736-1

Query Match 100.0%; Score 49; DB 3; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPE 9
Db 273 MLLGRPPE 281

RESULT 8

US-09-503-744-2
; Sequence 2, Application US/09503744
; Patent No. 6245544
; GENERAL INFORMATION:
; APPLICANT: Karen M. Anderson

; APPLICANT: Mark M. Bouzyk
; APPLICANT: Michael J. Hansbury
; APPLICANT: Jeffrey R. Jackson
; APPLICANT: Sandhya S. Nerurkar
; APPLICANT: Amy K. Postak
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; FILE REFERENCE: CH-70231-D1
; CURRENT APPLICATION NUMBER: US/09/505,744
; CURRENT FILING DATE: 2000-02-16
; EARLIER APPLICATION NUMBER: 09/136,282
; EARLIER FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 60/056,112
; EARLIER FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 685
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-503-744-2

Query Match 100.0%; Score 49; DB 3; Length 685;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPE 9
Db 273 MLLGRPPE 281

RESULT 9

US-08-861-338-17
; Sequence 17, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"

```

1 FEATURE:
2 NAME/KEY: Modified-site
3 LOCATION: 9
4 OTHER INFORMATION: /note= "Gamma Benzyl Ester of
5 OTHER INFORMATION: Glutamine Acid-NH2"
6 US-08-861-338-17
7
8 Query Match 93.9%; Score 46; DB 1; Length 9;
9 Best Local Similarity 88.9%; Pred. No. 2.5e+05;
10 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
11
12 QY 1 MLGRPPPE 9
13 : : : : :
14 : : : : :
15 Db 1 MLGRPPPE 9
16
17 RESULT 10
18 US-08-861-338-16
19 Sequence 16, Application US/08861338
20 Patent No. 6174993
21 GENERAL INFORMATION:
22 APPLICANT: Ben-Sasson, Shmuel A.
23 TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
24 TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
25 NUMBER OF SEQUENCES: 22
26 CORRESPONDENCE ADDRESS:
27 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
28 STREET: Two Militia Drive
29 CITY: Lexington
30 STATE: Massachusetts
31 COUNTRY: USA
32 ZIP: 02173
33 COMPUTER READABLE FORM:
34 MEDIUM TYPE: Floppy disk
35 COMPUTER: IBM PC compatible
36 OPERATING SYSTEM: PC-DOS/MS-DOS
37 SOFTWARE: PatentIn Release #1.0, Version #1.30
38 CURRENT APPLICATION DATA:
39 APPLICATION NUMBER: US/08/861-338
40 FILING DATE: 21-MAY-1997
41 CLASSIFICATION: 514
42 ATTORNEY/AGENT INFORMATION:
43 NAME: Brock, David E.
44 REGISTRATION NUMBER: 22,592
45 REFERENCE/DOCKET NUMBER: CX2C-550
46 TELECOMMUNICATION INFORMATION:
47 TELEPHONE: (781) 861-6240
48 TELEFAX: (781) 861-9540
49 INFORMATION FOR SEQ ID NO: 16:
50 SEQUENCE CHARACTERISTICS:
51 LENGTH: 8 amino acids
52 TYPE: amino acid
53 STRANDEDNESS: not relevant
54 TOPOLOGY: not relevant
55 MOLECULE TYPE: peptide
56 FEATURE:
57 NAME/KEY: Modified-site
58 LOCATION: 1
59 OTHER INFORMATION: /note= "N-Acetyl Methionine"
60
61 FEATURE:
62 NAME/KEY: Modified-site
63 LOCATION: 8
64 OTHER INFORMATION: /note= "Phenylalanine-NH2"
65
66 US-08-861-338-16
67
68 Query Match 83.7%; Score 41; DB 3; Length 8;
69 Best Local Similarity 87.5%; Pred. No. 2.5e+05;
70 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
71
72 QY 1 MLGRPPPF 8
73 : : : : :
74 : : : : :
75 Db 1 MLGRPPPF 8
76
77 RESULT 11
78 US-08-252-995D-10
79 Sequence 10, Application US/08252995D
80 Patent No. 5650561
81 GENERAL INFORMATION:
82 APPLICANT: Dennis, James W
83 APPLICANT: Heffernan, Mike
84 APPLICANT: Fode, Carol
85 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
86 NUMBER OF SEQUENCES: 14
87 CORRESPONDENCE ADDRESS:
88 ADDRESSEE: BERESKIN & PARR
89 STREET: 40 King Street West
90 CITY: Toronto
91 STATE: Ontario
92 COUNTRY: Canada
93 ZIP: M5H 3Y2
94 COMPUTER READABLE FORM:
95 MEDIUM TYPE: Floppy disk
96 COMPUTER: IBM PC compatible
97 OPERATING SYSTEM: PC-DOS/MS-DOS
98 SOFTWARE: PatentIn Release #1.0, Version #1.30
99 CURRENT APPLICATION DATA:
100 APPLICATION NUMBER: US/08/252,995D
101 FILING DATE: 02-JUN-1994
102 CLASSIFICATION: 536
103 ATTORNEY/AGENT INFORMATION:
104 NAME: Kirdydyk, Linda M
105 REGISTRATION NUMBER: 34,971
106 REFERENCE/DOCKET NUMBER: 3153-96
107 TELECOMMUNICATION INFORMATION:
108 TELEPHONE: (416) 364-7311
109 TELEFAX: (416) 361-1338
110 INFORMATION FOR SEQ ID NO: 10:
111 SEQUENCE CHARACTERISTICS:
112 LENGTH: 273 amino acids
113 TYPE: amino acid
114 STRANDEDNESS: single
115 TOPOLOGY: linear
116 MOLECULE TYPE: peptide
117 ORIGINAL SOURCE:
118 ORGANISM: Homo sapiens
119 US-08-252-995D-10
120
121 Query Match 83.7%; Score 41; DB 1; Length 273;
122 Best Local Similarity 86.7%; Pred. No. 3.3;
123 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
124
125 QY 1 MLGRPPPE 9
126 : : : : :
127 : : : : :
128 Db 200 LLIGRPPFD 208
129
130 RESULT 12
131 US-08-834-108-10
132 Sequence 10, Application US/08834108
133 Patent No. 5976893
134 GENERAL INFORMATION:
135 APPLICANT: Dennis, James W
136 APPLICANT: Heffernan, Mike
137 APPLICANT: Fode, Carol
138 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
139 NUMBER OF SEQUENCES: 14
140 CORRESPONDENCE ADDRESS:
141 ADDRESSEE: BERESKIN & PARR
142 STREET: 40 King Street West
143 CITY: Toronto
144 STATE: Ontario
145 COUNTRY: Canada
146 ZIP: M5H 3Y2
147 COMPUTER READABLE FORM:
148 MEDIUM TYPE: Floppy disk
149
150 QY 1 MLGRPPPF 8
151 : : : : :
152 : : : : :
153 Db 1 MLGRPPPF 8
154
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/834-108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-834-108-10

Query Match 83.7%; Score 41; DB 2; Length 273;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DB 200 LLIGRRPFD 208

RESULT 13
US-08-252-995D-2
Sequence 2, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252-995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-252-995D-2

Query Match 83.7%; Score 41; DB 1; Length 416;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DB 204 LLIGRRPFD 212

RESULT 14
US-08-834-108-2
Sequence 2, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834-108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-834-108-2

Query Match 83.7%; Score 41; DB 2; Length 416;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
DB 204 LLIGRRPFD 212

RESULT 15
US-08-252-995D-6
Sequence 6, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR

STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.10
 CURRENT APPLICATION DATA:
 FILING DATE: 02-JUN-1994
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Kurdydyk, Linda M
 REGISTRATION NUMBER: 34,971
 REFERENCE/DOCKET NUMBER: 3153-96
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 464 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-252-995D-4

Query Match 83.7%; Score 41; DB 1; Length 464;
 Best Local Similarity 66.7%; Pred. No. 5.7;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLGRRPPE 9
 : : : : :
 Db 204 LLIGRRPFD 212

RESULT 16
 US-08-834-108-4
 : Sequence 6, Application US/08834108
 : Patent No. 5976893
 : GENERAL INFORMATION:
 : APPLICANT: Dennis, James W
 : APPLICANT: Hefferman, Mike
 : APPLICANT: Fode, Carol
 : TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 : NUMBER OF SEQUENCES: 14
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BERSKIN & PARR
 : STREET: 40 King Street West
 : CITY: Toronto
 : STATE: Ontario
 : COUNTRY: Canada
 : ZIP: M5H 3Y2
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent in Release #1.0, Version #1.10
 : CURRENT APPLICATION DATA:
 : FILING DATE: 02-JUN-1994
 : CLASSIFICATION: 536
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Kurdydyk, Linda M
 : REGISTRATION NUMBER: 34,971
 : REFERENCE/DOCKET NUMBER: 3153-210
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (416) 364-7311
 : TELEFAX: (416) 361-1398
 : INFORMATION FOR SEQ ID NO: 6:
 : SEQUENCE CHARACTERISTICS:

LENGTH: 464 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-834-108-6

Query Match 83.7%; Score 41; DB 2; Length 464;
 Best Local Similarity 66.7%; Pred. No. 5.7;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLGRRPPE 9
 : : : : :
 Db 204 LLIGRRPFD 212

RESULT 17
 US-08-252-995D-4
 : Sequence 4, Application US/08252995D
 : Patent No. 5650501
 : GENERAL INFORMATION:
 : APPLICANT: Dennis, James W
 : APPLICANT: Hefferman, Mike
 : APPLICANT: Fode, Carol
 : TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 : NUMBER OF SEQUENCES: 14
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BERSKIN & PARR
 : STREET: 40 King Street West
 : CITY: Toronto
 : STATE: Ontario
 : COUNTRY: Canada
 : ZIP: M5H 3Y2
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent in Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/252,995D
 : FILING DATE: 02-JUN-1994
 : CLASSIFICATION: 536
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Kurdydyk, Linda M
 : REGISTRATION NUMBER: 34,971
 : REFERENCE/DOCKET NUMBER: 3153-96
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (416) 364-7311
 : TELEFAX: (416) 361-1398
 : INFORMATION FOR SEQ ID NO: 4:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 925 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-252-995D-4

Query Match 83.7%; Score 41; DB 1; Length 925;
 Best Local Similarity 66.7%; Pred. No. 12;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLGRRPPE 9
 : : : : :
 Db 204 LLIGRRPFD 212

RESULT 18
 US-08-834-108-4
 : Sequence 4, Application US/08834108
 : Patent No. 5976893
 : GENERAL INFORMATION:
 : APPLICANT: Dennis, James W
 : APPLICANT: Hefferman, Mike
 : APPLICANT: Fode, Carol

; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BERESKIN & PARR
 ; STREET: 40 King Street West
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5H 3Y2
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/834,106
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kurydyk, Linda M
 ; REGISTRATION NUMBER: 34,971
 ; REFERENCE/DOCKET NUMBER: 3153 210
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 364-7311
 ; TELEFAX: (416) 361-3398
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 925 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US 08-834-106-4

Query Match 83.7%; Score 41; DB 2; Length 925;
 Best Local Similarity 66.7%; Pred. No. 12;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLGRPPFE 9
 DB : MLGRPPFE 212

RESULT 19
 US-08-861-338-18
 ; Sequence 18, Application US/08861338
 ; Patent No. 6174993
 ; GENERAL INFORMATION:
 ; APPLICANT: Ber-Sasson, Samuel A.
 ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/861,338
 ; FILING DATE: 21-MAY-1997
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brook, David E.
 ; REGISTRATION NUMBER: 22,592
 ; REFERENCE/DOCKET NUMBER: CMCC-590
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (781) 861-6240

; TELEFAX: (781) 861-9540
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 1
 ; OTHER INFORMATION: /note= "N-Acetyl Leucine"
 ; NAME/KEY: Modified-site
 ; LOCATION: 7
 ; OTHER INFORMATION: /note= "Glutamic Acid Benzyl Ester"
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 9
 ; OTHER INFORMATION: /note= "Serine-NH2"
 ; US-08-861-338-18

Query Match 81.6%; Score 40; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGRPPFE 9
 DB 1 LGRPPFE 7

RESULT 20
 US-08-861-338-6
 ; Sequence 6, Application US/08861338
 ; Patent No. 6174993
 ; GENERAL INFORMATION:
 ; APPLICANT: Ber-Sasson, Samuel A.
 ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/861,338
 ; FILING DATE: 21-MAY-1997
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brook, David E.
 ; REGISTRATION NUMBER: 22,592
 ; REFERENCE/DOCKET NUMBER: CMCC-590
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (781) 861-6240
 ; TELEFAX: (781) 861-9540
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide
 ; US-08-861-338-6

Query Match 81.6%; Score 40; DB 3; Length 20;

Best Local Similarity 66.7%; Pred. No. 0.35;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGRRPPE 9
:|:|:|
FH 3 LLVGKPPPE 11

RESULT 21

US-08-252-995D-14
Sequence 14, Application US/0825299-9
Patent No. 5650531
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
City: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 361-1398
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mus musculus

Query Match 81.6%; Score 40; DB 1; Length 272;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGRRPPE 9
:|:|:|
DB 3 LLVGKPPPE 207

RESULT 22

US-08-834-108-14
Sequence 14, Application US/08834106
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR

STREET: 40 King Street West
City: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 361-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mus musculus

Query Match 81.6%; Score 40; DB 2; Length 272;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLGRRPPE 9
:|:|:|
DB 199 LLVGKPPPE 207

RESULT 23

US-09-198-122-2
Sequence 2, Application US/09198122
Patent No. 6180380
GENERAL INFORMATION:
APPLICANT: Sreberhardt, Klaus; Rubsamen-Waigmann, Helga;
APPLICANT: Holtrich, Uwe
TITLE OF INVENTION: CLONING OF A MEMBER OF THE SERINE-
TITLE OF INVENTION: THREONINE-KINASE FAMILY
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRUNG HORN KRAMER & WOODS
STREET: 660 White Plains Road
City: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
MEDIUM TYPE: storage
COMPUTER: NEC Powermate SX-20
OPERATING SYSTEM: DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/198,122
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/601,014
FILING DATE: 23-FEB-1996
APPLICATION NUMBER: PCT/EP94/02863
FILING DATE: 30-AUG-1994

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4329177
; FILING DATE: 30-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 9518-KUB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-09-198-122-2

Query Match 81.6%; Score 40; DB 3; Length 603;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPFE 9
11111111
Db 244 LVLGRRPFE 252

RESULT 24
US-09-311-311C-26
; Sequence 26, Application US/09311311C
; Patent No. 6158738
; GENERAL INFORMATION:
; APPLICANT: Erikson, et al.
; TITLE OF INVENTION: POLO BOX THERAPEUTIC COMPOSITIONS,
; METHODS, AND USES THEREOF
; FILE REFERENCE: 1874/117
; CURRENT APPLICATION NUMBER: US/09/311,311C
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,286
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(602)
; OTHER INFORMATION: P1k protein
US-09-311-311C-26

Query Match 81.6%; Score 40; DB 4; Length 603;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPFE 9
11111111
Db 244 LVLGRRPFE 252

RESULT 25
US-07-957-224B-17
; Sequence 17, Application US/07957245
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Rad,aubstrasse 151

```

```

; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
; FEATURE: Protein Kinase; Table 8 Column 18
; PUBLICATION INFORMATION:
; AUTHORS:
; AUTHORS: Hanks, S. K.
; AUTHORS: Quinn, A. M.
; AUTHORS: Hunter, T.
; TITLE: The protein kinase family
; JOURNAL: Science
; VOLUME: 241
; PAGES: 42-52
; DATE: 1988
US-07-857-224B-17

Query Match 79.6%; Score 39; DB 2; Length 264;
Best Local Similarity 66.7%; Pred. No. 7;5;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPFE 9
11111111
Db 195 MLVGRRPFD 203

RESULT 26
US-08-232-995D-11
; Sequence 11, Application US/08252995D
; Patent No. 5658501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D

```

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; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
;   NAME: Kurdydyk, Linda M
;   REGISTRATION NUMBER: 34,971
;   REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (416) 364-7311
;   TELEFAX: (416) 362-1398
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 271 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
;   ORGANISM: Drosophila melanogaster
; US-08-252-995E-11

Query Match          79.6%; Score 39; DB 1; Length 271;
Best Local Similarity 66.7%; Pred. No. 7.7;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGRPPPE 9
DB      198 LLVGQPPPE 206

RESULT 28
US-09-739-455-12
; Sequence 12, Application US/09739455
; Patent No. 6413756
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; FILE REFERENCE: CLO00653
; CURRENT APPLICATION NUMBER: US/09/739,455
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 303
;   TYPE: PRT
; ORGANISM: Leishmania mexicana
; US-09-739-455-12

Query Match          79.6%; Score 39; DB 4; Length 303;
Best Local Similarity 88.9%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MLLGRPPPE 9
DB      207 MLLGRPPPE 215

RESULT 29
US-09-739-455-22
; Sequence 22, Application US/09739455
; Patent No. 6413756
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; FILE REFERENCE: CLO00653
; CURRENT APPLICATION NUMBER: US/09/739,455
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
;   LENGTH: 303
;   TYPE: PRT
; ORGANISM: Leishmania mexicana
; US-09-739-455-22

Query Match          79.6%; Score 39; DB 4; Length 303;
Best Local Similarity 88.9%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MLLGRPPPE 9
DB      207 MLLGRPPPE 215

RESULT 30
US-09-252-991A-28679
; Sequence 28679, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

```


1 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
2
3 FILE REFERENCE: 137196.136
4
5 CURRENT APPLICATION NUMBER: US/09/252,991A
6
7 PRIOR FILING DATE: 1999-02-18
8
9 PRIOR APPLICATION NUMBER: US 62/074,288
10
11 PRIOR FILING DATE: 1998-02-18
12
13 PRIOR APPLICATION NUMBER: US 62/094,199
14
15 PRIOR FILING DATE: 1998-07-27
16
17 NUMBER OF SEQ ID NOS: 33142
18
19 SEQ ID NO 28673
20
21 LENGTH: 259
22
23 TYPE: PRT
24
25 ORGANISM: Pseudomonas aeruginosa
26
27 US-09-252-991A 28673

Query Match 77.6% Score 38; DB 4; Length 259;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRP 7
111111
DB 152 MLGRRP 158

RESULT 31
US-09-252-991D-13
1 Sequence 13, Application US/0825299D
2 Patent No. 5450501
3 GENERAL INFORMATION:
4 APPLICANT: Dennis, James W
5 APPLICANT: Heffernan, Mike
6 APPLICANT: Fode, Carol
7 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
8
9 NUMBER OF SEQUENCES: 14
10
11 CORRESPONDENCE ADDRESSES:
12 ADDRESSEE: BERESKIN & PARR
13 STREET: 40 King Street West
14 CITY: Toronto
15 STATE: Ontario
16 COUNTRY: Canada
17 ZIP: M5H 3Y2
18
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: Patent'n Release #1.0, Version #1.30
24
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/08/252,991A
27 FILING DATE: 02-JUN-1994
28
29 CLASSIFICATION: 536
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Kurdydyk, Linda M
32 REGISTRATION NUMBER: 34,971
33 REFERENCE/DOCKET NUMBER: 3153-9A
34
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: (416) 364-7311
37 TELEFAX: (416) 361-1398
38
39 INFORMATION FOR SEQ ID NO: 13:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 275 amino acids
42 TYPE: amino acid
43 STRANDEDNESS: single
44 TOPOLOGY: linear
45 MOLECULE TYPE: peptide
46 ORIGINAL SOURCE:
47 ORGANISM: Saccharomyces cerevisiae
48
49 US-09-252-991D-13

Query Match 77.6% Score 38; DB 4; Length 259;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPFE 9
111111
DB 200 LLGKRRPQ 208

RESULT 32
US-08-834-108-13
1 Sequence 13, Application US/08544108
2 Patent No. 5976893
3 GENERAL INFORMATION:
4 APPLICANT: Dennis, James W
5 APPLICANT: Heffernan, Mike
6 APPLICANT: Fode, Carol
7 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
8
9 NUMBER OF SEQUENCES: 14
10
11 CORRESPONDENCE ADDRESSES:
12 ADDRESSEE: BERESKIN & PARR
13 STREET: 40 King Street West
14 CITY: Toronto
15 STATE: Ontario
16 COUNTRY: Canada
17 ZIP: M5H 3Y2
18
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: Patent'n Release #1.0, Version #1.30
24
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/08/834,108
27 FILING DATE:
28
29 CLASSIFICATION: 536
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Kurdydyk, Linda M
32 REGISTRATION NUMBER: 34,971
33 REFERENCE/DOCKET NUMBER: 3153-21C
34
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: (416) 364-7311
37 TELEFAX: (416) 361-1398
38
39 INFORMATION FOR SEQ ID NO: 13:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 275 amino acids
42 TYPE: amino acid
43 STRANDEDNESS: single
44 TOPOLOGY: linear
45 MOLECULE TYPE: peptide
46 ORIGINAL SOURCE:
47 ORGANISM: Saccharomyces cerevisiae
48
49 US-08-834-108-13

Query Match 77.6% Score 38; DB 2; Length 275;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPFE 9
111111
DB 200 LLGKRRPQ 208

RESULT 33
US-08-755-728-3
1 Sequence 3, Application US/08755728
2 Patent No. 5962312
3 GENERAL INFORMATION:
4 APPLICANT: Plowman, Gregory
5 APPLICANT: Mossie, Kevin
6 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
7
8 NUMBER OF SEQUENCES: 29
9
10 CORRESPONDENCE ADDRESSES:
11 ADDRESSEE: Lyon & Lyon
12 STREET: 630 West Fifth Street
13 CITY: Los Angeles
14
15 US-08-755-728-3

STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FASTSEQ for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/755,728
 FILING DATE: December 18, 1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/008,809
 FILING DATE: December 18, 1995
 APPLICATION NUMBER: 60/023,943
 FILING DATE: August 14, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 223/113
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 344 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08 755-728-3

Query Match 77.6%; Score 38; DP 2; Length 344;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
 Db 266 LLVGNPPE 274

RESULT 14
 US-08 974-655-3
 Sequence 3, Application US/0897465
 Patent No. 6207401
 GENERAL INFORMATION:
 APPLICANT: Plowman, Gregory
 APPLICANT: Mossie, Kevin
 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
 TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FASTSEQ for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,655
 FILING DATE:

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/755,728
 FILING DATE: December 25, 1996
 APPLICATION NUMBER: 60/008,809
 FILING DATE: December 18, 1995
 APPLICATION NUMBER: 60/023,943
 FILING DATE: August 14, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 223/113
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 344 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08 974-655-3
 Query Match 77.6%; Score 38; DB 2; Length 344;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
 Db 266 LLVGNPPE 274

RESULT 35
 US-09-283-011-3
 Sequence 3, Application US/09283011
 Patent No. 6207401
 GENERAL INFORMATION:
 APPLICANT: Plowman, Gregory
 APPLICANT: Mossie, Kevin
 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
 TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FASTSEQ for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/283,011
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/012,135
 FILING DATE: January 22, 1998
 APPLICATION NUMBER: 08/755,728
 FILING DATE: December 25, 1996
 APPLICATION NUMBER: 60/023,943
 FILING DATE: August 14, 1996
 APPLICATION NUMBER: 60/008,809
 FILING DATE: December 18, 1995

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 231/282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-283-011-3

Query Match 77.6%; Score 38; DB 3; Length 344;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy : MLGRPPE 9
||: |||
Db 266 LLVGNPPE 274

RESULT 36
US-09-016-000-1
Sequence 1, Application US/C901600
Patent No. 5962332
GENERAL INFORMATION:
APPLICANT: Hallman, Jennifer L.
APPLICANT: La, Preeti
APPLICANT: Bauman, Olga
APPLICANT: Akersblom, Ingrid E.
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Kati G.
TITLE OF INVENTION: PROTEIN KINASE MOLECULES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,000
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Baillings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0465 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: HMCINOT01
CLONE: 2940
US-09-016-000-1
Query Match 77.6%; Score 38; DB 2; Length 347;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MLGRPPE 9
||: |||
Db 269 LLVGNPPE 277

RESULT 37
US-08-755-728-4
Sequence 4, Application US/08755728
Patent No. 5962312
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Mossie, Kevin
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,728
FILING DATE: No. 5962312ember 25, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Watling, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-755-728-4

Query Match 77.6%; Score 38; DB 2; Length 403;
Best Local Similarity 75.3%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy 2 LLGRPPE 9

Db 323 LVGRPPPE 330

RESULT 38
US-09-974-655-4
; Sequence 4, Application US/08974655
; Patent No. 5972676
; GENERAL INFORMATION:
; APPLICANT: P. Bowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR 1
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,655
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 5972676, December 25, 1994
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-351C
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO

Query Match 77.6%; Score 38; DB 2; Length 403;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 2 LLGRPPPE 9
Db 323 LVGRPPPE 330

RESULT 39
US-09-283-011-4
; Sequence 4, Application US/09283011
; Patent No. 620740
; GENERAL INFORMATION:
; APPLICANT: P. Bowman, Gregory

; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/283,011
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/012,135
; FILING DATE: January 22, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 620740, December 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-351C
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEtical: NO
; ANTI-SENSE: NO
US-09-283-011-4

Query Match 77.6%; Score 38; DB 3; Length 403;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 2 LLGRPPPE 9
Db 323 LVGRPPPE 330

RESULT 40
US-09-772-647-4
; Sequence 4, Application US/09772647
; Patent No. 6521815
; GENERAL INFORMATION:
; APPLICANT: Verma, Ajit K
; APPLICANT: Reddig, Peter J
; APPLICANT: Jansen, Aaron P
; TITLE OF INVENTION: Animal Model System for Squamous Cell Carcinoma
; FILE REFERENCE: 960296.97613
; CURRENT APPLICATION NUMBER: US/09/772,647
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1

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: SEQ ID NO 4
: LENGTH: 737
: TYPE: prt
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: T7 tag and
: OTHER INFORMATION: mouse protein kinase C epsilon coding sequence
US 09 772 647-4

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Query Match      77.6%; Score 38, DB 4; Length 737
Best Local Similarity 66.7%; Pred. No. 131
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db      600 VMAGQPPPE 608

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Search completed: November 14, 2003, 13:59:49
Job time : 11.8286 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

Query protein - protein search, using sw model:

Run on: November 14, 2003, 13:28:05 : Search time 22.3714 Seconds
(without alignments)
73.443 Million cell updates/sec

Title: US-09-736-076-15

Perfect score: 49

Sequence: 1 MLLGRPPPE 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 3.5

Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 3%

Maximum Match 100%

Listing first 45 summaries

Database: 1: /cgn2_6/prodata/1/pubaa/US07_PUBOXB.pep.*

- 2: /cgn2_6/prodata/1/pubaa/PC1_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubaa/US06_PUBOXB.pep.*
- 5: /cgn2_6/prodata/1/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/1/pubaa/PC1US_PUBOXB.pep.*
- 7: /cgn2_6/prodata/1/pubaa/US09_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/1/pubaa/US09_PUBOXB.pep.*
- 9: /cgn2_6/prodata/1/pubaa/US09A_PUBOXB.pep.*
- 10: /cgn2_6/prodata/1/pubaa/US09B_PUBOXB.pep.*
- 11: /cgn2_6/prodata/1/pubaa/US09C_PUBOXB.pep.*
- 12: /cgn2_6/prodata/1/pubaa/US09_NEW_PUB.pep.*
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- 17: /cgn2_6/prodata/1/pubaa/US06_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/1/pubaa/US06_PUBOXB.pep.*

Pred. No. is the number of residues predicted to have a score greater than or equal to the score of the hit being printed, and is derived by analysis of the full database.

SUMMARY

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	9	US-09-736-076-15	Sequence 15, Appl
2	49	100.0	10	US-09-736-076-15	Sequence 15, Appl
3	49	100.0	11	US-09-736-076-15	Sequence 19, Appl
4	49	100.0	400	US-10-026-021-7	Sequence 5, Appl
5	49	100.0	469	US-10-059-585-33	Sequence 14, Appl
6	49	100.0	685	US-09-771-161A-123	Sequence 249, Appl
7	49	100.0	685	US-09-771-161A-150	Sequence 250, Appl
8	49	100.0	685	US-09-771-161A-151	Sequence 251, Appl
9	49	100.0	685	US-10-024-828-12	Sequence 10, Appl
10	49	100.0	685	US-09-898-837A-32	Sequence 1, Appl
11	49	100.0	685	US-10-024-828-12	Sequence 10, Appl
12	49	93.9	9	US-09-736-076-15	Sequence 17, Appl
13	49	93.9	8	US-09-736-076-15	Sequence 16, Appl
14	49	93.9	379	US-10-026-021-7	Sequence 3, Appl
15	49	93.9	970	US-10-026-021-7	Sequence 2, Appl

16	40	81.6	9	US-09-736-076-15	Sequence 18, Appl
17	40	81.6	20	US-09-736-076-15	Sequence 6, Appl
18	329	81.6	329	US-09-925-300-1268	Sequence 1268, Appl
19	40	81.6	367	US-10-026-021-7	Sequence 6, Appl
20	40	81.6	516	US-09-771-161A-123	Sequence 123, Appl
21	40	81.6	528	US-10-032-585-7571	Sequence 7571, Appl
22	40	81.6	603	US-09-771-161A-214	Sequence 214, Appl
23	40	81.6	603	US-10-171-311-186	Sequence 186, Appl
24	39	79.6	303	US-10-153-919-12	Sequence 12, Appl
25	39	79.6	303	US-10-153-919-22	Sequence 22, Appl
26	38	77.6	8	US-09-736-076-15	Sequence 32, Appl
27	38	77.6	256	US-09-898-837A-32	Sequence 32, Appl
28	38	77.6	344	US-09-012-135A-3	Sequence 3, Appl
29	38	77.6	344	US-10-059-585-33	Sequence 34, Appl
30	38	77.6	344	US-10-171-311-214	Sequence 214, Appl
31	38	77.6	347	US-09-974-298-136	Sequence 136, Appl
32	38	77.6	348	US-10-291-253A-16	Sequence 16, Appl
33	38	77.6	403	US-09-012-135A-4	Sequence 4, Appl
34	38	77.6	403	US-10-026-021-7	Sequence 7, Appl
35	38	77.6	403	US-10-059-585-33	Sequence 33, Appl
36	38	77.6	403	US-10-209-324-2	Sequence 2, Appl
37	38	77.6	737	US-09-771-161A-195	Sequence 195, Appl
38	38	77.6	737	US-10-228-931-4	Sequence 4, Appl
39	37	75.5	20	US-09-736-076-15	Sequence 3, Appl
40	37	75.5	445	US-09-836-392-15	Sequence 15, Appl
41	37	75.5	499	US-10-024-828-12	Sequence 12, Appl
42	37	75.5	505	US-10-156-761-14310	Sequence 14310, A
43	37	75.5	588	US-10-024-828-16	Sequence 16, Appl
44	37	75.5	672	US-08-681-219-29	Sequence 29, Appl
45	37	75.5	672	US-10-092-138-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-09-736-076-15
: Sequence 15, Application US/09736076
: Patent No. US20020049301A1
: GENERAL INFORMATION:
: APPLICANT: Ben-Sasson Simuel A.
: TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
: FILE REFERENCE: 1242.1015-009
: CURRENT APPLICATION NUMBER: US/09/736,076
: PRIOR FILING DATE: 2000-12-13
: PRIOR APPLICATION NUMBER: US 08/861,338
: PRIOR FILING DATE: 1997-05-21
: NUMBER OF SEQ ID NOS: 68
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 15
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: ACETYLATION
: LOCATION: (1)...(10)
: OTHER INFORMATION: position 9 is benzylester
: NAME/KEY: AMIDATION
: LOCATION: (1)...(9)
: OTHER INFORMATION: J42
US-09-736-076-15

Query Match : 100.0% ; Score 49; DB 9; Length 9;
Best Local Similarity : 100.0% ; Pred. No. 5,9e+05;
Matches : 9; Conservative : 0; Mismatches : 0; Indels : 0; Caps : 0;

QY : MLLGRPPPE 9

DB : MLLGRPPPE 9

RESULT 2

US-09-736-076-57
 ? Sequence 57, Application US/09736076
 ? Patent No. US20020049301A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Ben-Sasson Shmuel A.
 ? TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ? MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 ? FILE REFERENCE: 1242-1015-009
 ? CURRENT FILING DATE: 2000-12-13
 ? PRIOR APPLICATION NUMBER: US/09/736,076
 ? PRIOR FILING DATE: 1997-05-21
 ? NUMBER OF SEQ ID NOS: 68
 ? SOFTWARE: FastSeq for Windows Version 4.0
 ? SEQ ID NO 5:
 ? TYPE: PRT
 ? LENGTH: 10
 ? ORGANISM: Artificial Sequence
 ? FEATURE:
 ? NAME/KEY: MYRISTATE
 ? LOCATION: 1...10
 ? OTHER INFORMATION: position 10 is benzylester
 ? NAME/KEY: AMIDATION
 ? LOCATION: 60...120
 ? OTHER INFORMATION: SNK
 US-09-736-076-57

Query Match 100.0% Score 49; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.029;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
 DB 2 MLGRRPPE 10

US-09-736-076-19
 ? Sequence 19, Application US/09736076
 ? Patent No. US20020049301A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Ben-Sasson Shmuel A.
 ? TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ? MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 ? FILE REFERENCE: 1242-1015-009
 ? CURRENT FILING DATE: 2000-12-13
 ? PRIOR APPLICATION NUMBER: US/09/736,076
 ? PRIOR FILING DATE: 1997-05-21
 ? NUMBER OF SEQ ID NOS: 68
 ? SOFTWARE: FastSeq for Windows Version 4.0
 ? SEQ ID NO 19:
 ? TYPE: PRT
 ? LENGTH: 11
 ? ORGANISM: Artificial Sequence
 ? FEATURE:
 ? NAME/KEY: ACETYLATION
 ? LOCATION: 1...10
 ? OTHER INFORMATION: position 9 is benzylester
 ? NAME/KEY: AMIDATION
 ? LOCATION: 61...111
 ? OTHER INFORMATION: J46
 US-09-736-076-19

Query Match 100.0% Score 49; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.041;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
 DB 1 MLGRRPPE 9

RESULT 4
 US-10-026-021-5
 ? Sequence 5, Application US/10026021
 ? Publication No. US20030027756A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Hitoshi, Yasumichi
 ? APPLICANT: Demo, Susan
 ? APPLICANT: Jenkins, Yonchu
 ? APPLICANT: Riga Pharmaceuticals, Inc.
 ? TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
 ? TREATMENT OF CANCER
 ? FILE REFERENCE: 021044-001210US
 ? CURRENT APPLICATION NUMBER: US/10/026,021
 ? CURRENT FILING DATE: 2002-08-25
 ? PRIOR APPLICATION NUMBER: US 60/309,632
 ? PRIOR FILING DATE: 2001-08-01
 ? NUMBER OF SEQ ID NOS: 8
 ? SOFTWARE: PatentIn Ver. 2.1
 ? SEQ ID NO 5:
 ? TYPE: PRT
 ? LENGTH: 400
 ? ORGANISM: Homo sapiens
 ? FEATURE:
 ? NAME/KEY: DOMAIN
 ? LOCATION: 11...1400
 ? OTHER INFORMATION: human SNK mitotic kinase kinase domain
 US-10-026-021-5

Query Match 100.0% Score 49; DB 15; Length 400;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
 DB 273 MLGRRPPE 281

RESULT 5
 US-10-059-585-14
 ? Sequence 14, Application US/10059585
 ? Publication No. US2003038276A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Ota, Toshio
 ? APPLICANT: Isogai, Takao
 ? APPLICANT: Nishikawa, Tetsuo
 ? APPLICANT: Hayashi, Koji
 ? APPLICANT: Otsuka, Katsuo
 ? APPLICANT: Yamamoto, Jun-ichi
 ? APPLICANT: Ishii, Shizuko
 ? APPLICANT: Sugiyama, Tomoyasu
 ? APPLICANT: Wakamatsu, Ai
 ? APPLICANT: Nagai, Keiichi
 ? APPLICANT: Otsuki, Tetsuji
 ? APPLICANT: Furahashi, Shin-ichi
 ? APPLICANT: Senoo, Chiaki
 ? APPLICANT: Nezu, Jun-ichi
 ? TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
 ? KINASE/PROTEIN PHOSPHATASE
 ? FILE REFERENCE: 06501-098001
 ? CURRENT APPLICATION NUMBER: US/10/059,585
 ? CURRENT FILING DATE: 2002-01-29
 ? PRIOR APPLICATION NUMBER: PCT/JP00/05060
 ? PRIOR FILING DATE: 2000-07-28
 ? PRIOR APPLICATION NUMBER: US 60/183,322
 ? PRIOR FILING DATE: 2000-02-17
 ? PRIOR APPLICATION NUMBER: US 60/159,590
 ? PRIOR FILING DATE: 1999-10-18
 ? PRIOR APPLICATION NUMBER: JP 2000-118776
 ? PRIOR FILING DATE: 2000-01-11
 ? PRIOR APPLICATION NUMBER: JP 2000-183767
 ? PRIOR FILING DATE: 2000-05-02
 ? PRIOR APPLICATION NUMBER: JP 11-248036
 ? PRIOR FILING DATE: 1999-07-29

; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 469
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-059-585 14

Query Match 100.0%; Score 49; DB 15; Length 469;
 Best Local Similarity 100.0%; Pred. No. 1.2; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
 DB 57 MLGRRPPE 65

RESULT 6
 US-09-771-161A-249
 ; Sequence 249, Application US/09771-161A
 ; Patent No. US2002010811A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, et al.
 ; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 ; FILE REFERENCE: 802620-2005.1
 ; CURRENT APPLICATION NUMBER: US/09771-161A
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 09/724,676
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 135619
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 273
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 249
 ; LENGTH: 685
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-771-161A-249

Query Match 100.0%; Score 49; DB 10; Length 685;
 Best Local Similarity 100.0%; Pred. No. 1.7; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
 DB 273 MLGRRPPE 281

RESULT 7
 US-09-771-161A-250
 ; Sequence 250, Application US/09771-161A
 ; Patent No. US2002010811A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, et al.
 ; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 ; FILE REFERENCE: 802620-2005.1
 ; CURRENT APPLICATION NUMBER: US/09771-161A
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 09/724,676
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 136776
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 135619
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 273
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 250
 ; LENGTH: 685
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-771-161A-250

Query Match 100.0%; Score 49; DB 10; Length 685;
 Best Local Similarity 100.0%; Pred. No. 1.7; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
 DB 273 MLGRRPPE 281

RESULT 8
 US-09-771-161A-251
 ; Sequence 251, Application US/09771-161A
 ; Patent No. US2002010811A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, et al.
 ; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 ; FILE REFERENCE: 802620-2005.1
 ; CURRENT APPLICATION NUMBER: US/09771-161A
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 09/724,676
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 136776
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 135619
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 273
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 251
 ; LENGTH: 685
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-771-161A-251

Query Match 100.0%; Score 49; DB 10; Length 685;
 Best Local Similarity 100.0%; Pred. No. 1.7; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
 DB 273 MLGRRPPE 281

RESULT 9
 US-10-024-298A-101
 ; Sequence 101, Application US/10024298A
 ; Publication No. US20030149540A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ASAH; KASEI; KABUSHIKI KAISHA
 ; APPLICANT: AKIO MATSUDA
 ; APPLICANT: GOICHI HONDA
 ; APPLICANT: SHUJI MURAMATSU
 ; APPLICANT: YUKIKO NAGANO
 ; TITLE OF INVENTION: NF-K B Activating Gene
 ; FILE REFERENCE: 1254-0191P
 ; CURRENT APPLICATION NUMBER: US/10/024,298A
 ; CURRENT FILING DATE: 2003-04-08
 ; PRIOR APPLICATION NUMBER: 60/314,385
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: 60/278,641
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: 60/258,355
 ; PRIOR FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: JP254018/2001
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: JPO088912/2001
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: JP402288/2000
 ; PRIOR FILING DATE: 2000-12-28
 ; NUMBER OF SEQ ID NOS: 192
 ; SOFTWARE: Patent in ver. 2.0
 ; SEQ ID NO 101
 ; LENGTH: 685


```

? TYPE: PR7
? ORGANISM: Homo sapiens
US-10-024-299A-101

Query Match      100.0% Score 49; DB 12; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      : MLLGRPPFE 9
DB      : MLLGRPPFE 281

RESULT 10
US-09-769-970-1
? Sequence 1, Application US/09769970
? Publication No. US20030170219A1
? GENERAL INFORMATION:
? APPLICANT: Bandmar, Olga
? Hillman, Jennifer L.
? Corley, Neil C.
? Guegler, Karl G.
? Cal, Preeti
? Goli, Surya K.
? Shah, Purvi
? TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
? KINASES
? NUMBER OF SEQUENCES: 21
? CORRESPONDENCE ADDRESS:
? STREET: 3174 Porter Drive
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/769,970
? FILING DATE: 24-Jan-2001
? CLASSIFICATION: <Unknown>
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: 09/272,796
? FILING DATE: <Unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Billings, Lucy J.
? REGISTRATION NUMBER: 16,747
? REFERENCE/DOCKET NUMBER: 16,747
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-855-3595
? TELEFAX: 415-845-4166
? TELEX: <Unknown>
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 685 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: HUVEN0801
? CLONE: 39043
? SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-769-970-1

Query Match      100.0% Score 49; DB 12; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      : MLLGRPPFE 9
DB      : MLLGRPPFE 281

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Db      273 MLLGRPPFE 281

RESULT 11
US-10-042-211A-101
? Sequence 101, Application US/10042211A
? Publication No. US20030170719A1
? GENERAL INFORMATION:
? APPLICANT: MATSUDA, Akio et al.
? TITLE OF INVENTION: NFkB Activating Gene
? FILE REFERENCE: 1254-0192P
? CURRENT APPLICATION NUMBER: US/10/042,211A
? CURRENT FILING DATE: 2002-01-12
? PRIOR APPLICATION NUMBER: JP 2000-402288
? PRIOR FILING DATE: 2000-12-28
? PRIOR APPLICATION NUMBER: JP 2001-088912
? PRIOR FILING DATE: 2001-03-26
? PRIOR APPLICATION NUMBER: JP 2001-254018
? PRIOR FILING DATE: 2001-08-24
? PRIOR APPLICATION NUMBER: US 60/258,315
? PRIOR FILING DATE: 2000-12-28
? PRIOR APPLICATION NUMBER: US 60/278,640
? PRIOR FILING DATE: 2001-03-26
? PRIOR APPLICATION NUMBER: US 60/314,385
? PRIOR FILING DATE: 2001-08-24
? NUMBER OF SEQ ID NOS: 182
? SOFTWARE: Patentin Ver. 2.0
? SEQ ID NO 101
? LENGTH: 685
? TYPE: PR7
? ORGANISM: Homo sapiens
US-10-042-211A-101

Query Match      100.0% Score 49; DB 12; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      : MLLGRPPFE 9
DB      : MLLGRPPFE 281

RESULT 12
US-09-736-076-17
? Sequence 17, Application US/09736076
? Patent No. US2002004931A1
? GENERAL INFORMATION:
? APPLICANT: Ben-Sasson Shmuel A.
? TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
? MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
? FILE REFERENCE: 1242-1015-039
? CURRENT APPLICATION NUMBER: US/09/736,076
? CURRENT FILING DATE: 2000-12-13
? PRIOR APPLICATION NUMBER: US 08/861,338
? PRIOR FILING DATE: 1997-05-21
? NUMBER OF SEQ ID NOS: 68
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 17
? LENGTH: 9
? TYPE: PR7
? ORGANISM: Artificial Sequence
? FEATURE:
? NAME/KEY: ACETYLATION
? LOCATION: (1)...(9)
? OTHER INFORMATION: position 9 is benzylester
? NAME/KEY: AMIDATION
? LOCATION: (9)...(9)
? OTHER INFORMATION: 243.1
US-09-736-076-17

Query Match      93.9% Score 46; DB 9; Length 9;
Best Local Similarity 89.9%; Pred. No. 5.9e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MLLGRPPE 9
 Db 204 LLIGRPPE 9

RESULT 13
 US-09-736-076-16
 ; Sequence 16, Application US/09736076
 ; Publication No. US2003027756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ben-Sasson Shmuel A.
 ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ; FILE REFERENCE: 1242.1315-009
 ; CURRENT APPLICATION NUMBER: US/09/736.076
 ; PRIOR FILING DATE: 2000-12-13
 ; PRIOR APPLICATION NUMBER: US 08/861,338
 ; PRIOR FILING DATE: 1997-05-21
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: ACETYLATION
 ; LOCATION: (1)...(8)
 ; NAME/KEY: AMIDATION
 ; LOCATION: (1)...(8)
 ; OTHER INFORMATION: J43
 US-09-736-076-16

Query Match 83.7%; Score 41; DB 9; Length 8;
 Best Local Similarity 87.5%; Pred. No. 5.9e+05;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPE 8
 Db 1 MLLGRPPE 8

RESULT 14
 US-10-026-021-3
 ; Sequence 3, Application US/10026021
 ; Publication No. US2003027756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hitoshi, Yasumichi
 ; APPLICANT: Jenkins, Yochu
 ; APPLICANT: Rigel Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
 ; FILE REFERENCE: 021044-00121005
 ; CURRENT APPLICATION NUMBER: US/10/026.021
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/309,632
 ; PRIOR FILING DATE: 2001-08-01
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patent'n Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 379
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: DOVAIN
 ; LOCATION: (1)...(379)
 ; OTHER INFORMATION: SAK serine/threonine kinase domain
 US-10-026-021-3

Query Match 83.7%; Score 41; DB 15; Length 379;
 Best Local Similarity 66.7%; Pred. No. 24;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPE 9
 Db 204 LLIGRPPE 212

RESULT 15
 US-10-026-021-2
 ; Sequence 2, Application US/10026021
 ; Publication No. US2003027756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hitoshi, Yasumichi
 ; APPLICANT: Jenkins, Yochu
 ; APPLICANT: Rigel Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
 ; FILE REFERENCE: 021044-00121005
 ; CURRENT APPLICATION NUMBER: US/10/026.021
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/309,632
 ; PRIOR FILING DATE: 2001-08-01
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patent'n Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 970
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: human SAK serine/threonine kinase
 US-10-026-021-2

Query Match 83.7%; Score 41; DB 15; Length 970;
 Best Local Similarity 66.7%; Pred. No. 59;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPE 9
 Db 204 LLIGRPPE 212

RESULT 16
 US-09-736-076-18
 ; Sequence 18, Application US/09736076
 ; Patent No. US2003049301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ben-Sasson Shmuel A.
 ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ; FILE REFERENCE: 1242.1315-009
 ; CURRENT APPLICATION NUMBER: US/09/736.076
 ; CURRENT FILING DATE: 2000-12-13
 ; PRIOR APPLICATION NUMBER: US 08/861,338
 ; PRIOR FILING DATE: 1997-05-21
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 18
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: ACETYLATION
 ; LOCATION: (1)...(9)
 ; OTHER INFORMATION: position 7 is benzylester
 ; NAME/KEY: AMIDATION
 ; LOCATION: (1)...(9)
 ; OTHER INFORMATION: J45
 US-09-736-076-18

Query Match 81.6%; Score 40; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5.9e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 3 LGRPPPE 9
|||||
DB 1 LGRPPPE 7

RESULT 17
US-09-736-076 6
; Sequence 6, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Bee-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 12421815-039
; CURRENT APPLICATION NUMBER: US/09736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,118
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: POLO
US-09-736-076-6

Query Match 81.6%; Score 40; DB 9; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
|||||
DB 3 LLVGKPPPE 11

RESULT 18
US-09-736-076-1268
; Sequence 1268, Application US/09925400
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antisenses
; FILE REFERENCE: P4301
; CURRENT APPLICATION NUMBER: US/09/925,400
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/00496
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1690
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1268
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; LOCATION: (59)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (107)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (308)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (314)

Query Match 81.6%; Score 40; DB 9; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGRPPPE 9
|||||
DB 1 LGRPPPE 7

RESULT 19
US-10-026-021-6
; Sequence 6, Application US/10026021
; Publication No. US20030027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Demo, Susan
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation Of Cellular Proliferation for
; FILE REFERENCE: 021344-032100S
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(367);
; OTHER INFORMATION: human PLK1 mitotic kinase kinase domain
US-10-026-021-6

Query Match 81.6%; Score 40; DB 15; Length 367;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
|||||
DB 244 LLVGKPPPE 268

RESULT 20
US-09-771-161A-123
; Sequence 123, Application US/09771161A
; Patent No. US2002011811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
```

```
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 123
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-123

Query Match
Best Local Similarity 81.6%; Score 40; DB 10; Length 603;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGRRPPE 9
Db 157 LLVGKPPPE 165

RESULT 21
US-10-032-585-7571
; Sequence 7571, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 0182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7571
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7571

Query Match
Best Local Similarity 81.6%; Score 40; DB 12; Length 528;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGRRPPE 9
Db 454 LLVGKPPPE 462

RESULT 22
US-09-771-161A-214
; Sequence 214, Application US/09771161A
; Patent No. US2002010811A
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 214
```

```
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-214

Query Match
Best Local Similarity 81.6%; Score 40; DB 10; Length 603;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGRRPPE 9
Db 244 LLVGKPPPE 252

RESULT 23
US-10-171-311-186
; Sequence 186, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-186

Query Match
Best Local Similarity 81.6%; Score 40; DB 15; Length 603;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGRRPPE 9
Db 244 LLVGKPPPE 252

RESULT 24
US-10-153-919-12
; Sequence 12, Application US/10153919
; Publication No. US20030166219A1
; GENERAL INFORMATION:
; APPLICANT: VAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO00653DIV
; CURRENT APPLICATION NUMBER: US/10/153,919
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/209,585
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 09/739,455
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 23
```

```

: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 12
: LENGTH: 203
: TYPE: PRT
: ORGANISM: Leishmania mexicana
US 10-151-919-12

Query Match      79.6%  Score 39, DB 12, Length 193
Best Local Similarity 89.9%  Pred. No. 43
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY      1 MLIGRPPFE 9
Db      207 MLIGRPPFE 215

RESULT 26
US-10-151-919-22
: Sequence 22, Application US/10153919
: Publication No. US20030166219A1
: GENERAL INFORMATION:
: APPLICANT: YAN, Chanhua et al.
: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: C000653D1V
: CURRENT APPLICATION NUMBER: US/10-151-919
: PRIOR FILING DATE: 2002-05-24
: PRIOR APPLICATION NUMBER: 60/209,585
: PRIOR FILING DATE: 2000-06-06
: PRIOR APPLICATION NUMBER: 09/739,455
: PRIOR FILING DATE: 2003-12-19
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 22
: LENGTH: 303
: TYPE: PRT
: ORGANISM: Leishmania mexicana
US-10-151-919 22

Query Match      79.6%  Score 39, DB 12, Length 193
Best Local Similarity 88.9%  Pred. No. 43
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY      1 MLIGRPPFE 9
Db      207 MLIGRPPFE 215

RESULT 27
US-09-898-837A-32
: Sequence 32, Application US/09898837A
: Publication No. US200307697A1
: GENERAL INFORMATION:
: APPLICANT: Quinn, Kerry E.
: APPLICANT: Spytek, Kimberly A.
: APPLICANT: Majumder, Kumud
: APPLICANT: Vernet, Corine
: APPLICANT: Herrmann, John L.
: APPLICANT: Burgess, Catherine
: APPLICANT: Fernandes, Elma
: APPLICANT: Taupier Jr., Raymond
: APPLICANT: Rastelli, Luca
: APPLICANT: Curagen Corporation
: APPLICANT: Gerlach, Valerie L.
: APPLICANT: MacDougall, John R.
: TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
: FILE REFERENCE: 15966-598 CIP
: CURRENT APPLICATION NUMBER: US/09/898,837A
: CURRENT FILING DATE: 2001-07-03
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986
: PRIOR FILING DATE: 1999-11-17
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,819
: PRIOR FILING DATE: 2000-04-05
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,637
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/197,080
: PRIOR FILING DATE: 2000-04-13
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/232,677
: PRIOR FILING DATE: 2000-09-15
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347
: PRIOR FILING DATE: 2000-02-09
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195
: PRIOR FILING DATE: 2000-04-03
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,906
: PRIOR FILING DATE: 2000-07-03
: PRIOR APPLICATION NUMBER: U.S.S.N. 09/715,427
: NUMBER OF SEQ ID NOS: 53
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 32
: LENGTH: 256
: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
US-09-898-837A-32

Query Match      77.6%  Score 38, DB 11, Length 256;
Best Local Similarity 55.6%  Pred. No. 54;
Matches      5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

CY      1 MLIGRPPFE 9
Db      193 LLIGKPPFF 201

RESULT 28
US-09-012-135A-3
: Sequence 3, Application US/09012135A
: Patent No. US20030081575A1

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: OTHER INFORMATION: SNK
US-09-736-076-58

Query Match      77.6%  Score 38, DB 9, Length 8;
Best Local Similarity 100.0%  Pred. No. 5.9e+05;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY      1 MLIGRPP 7
Db      2 MLIGRPP 8

RESULT 27
US-09-898-837A-32
: Sequence 32, Application US/09898837A
: Publication No. US200307697A1
: GENERAL INFORMATION:
: APPLICANT: Quinn, Kerry E.
: APPLICANT: Spytek, Kimberly A.
: APPLICANT: Majumder, Kumud
: APPLICANT: Vernet, Corine
: APPLICANT: Herrmann, John L.
: APPLICANT: Burgess, Catherine
: APPLICANT: Fernandes, Elma
: APPLICANT: Taupier Jr., Raymond
: APPLICANT: Rastelli, Luca
: APPLICANT: Curagen Corporation
: APPLICANT: Gerlach, Valerie L.
: APPLICANT: MacDougall, John R.
: TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
: FILE REFERENCE: 15966-598 CIP
: CURRENT APPLICATION NUMBER: US/09/898,837A
: CURRENT FILING DATE: 2001-07-03
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986
: PRIOR FILING DATE: 1999-11-17
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,819
: PRIOR FILING DATE: 2000-04-05
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,637
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/197,080
: PRIOR FILING DATE: 2000-04-13
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/232,677
: PRIOR FILING DATE: 2000-09-15
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347
: PRIOR FILING DATE: 2000-02-09
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195
: PRIOR FILING DATE: 2000-04-03
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,906
: PRIOR FILING DATE: 2000-07-03
: PRIOR APPLICATION NUMBER: U.S.S.N. 09/715,427
: NUMBER OF SEQ ID NOS: 53
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 32
: LENGTH: 256
: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
US-09-898-837A-32

Query Match      77.6%  Score 38, DB 11, Length 256;
Best Local Similarity 55.6%  Pred. No. 54;
Matches      5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

CY      1 MLIGRPPFE 9
Db      193 LLIGKPPFF 201

RESULT 28
US-09-012-135A-3
: Sequence 3, Application US/09012135A
: Patent No. US20030081575A1

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; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,135A
; FILING DATE: January 22, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,268
; FILING DATE: January 9, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: NO. US20020081578A/ember 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard S.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NOS: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYDROPHETICAL: NO
; ANTI-SENSE: NO
; US 09-012 135A-3

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```

Query Match 77.6%, Score 38; DB 9; Length 344;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MLGCRPPE 9
Db 266 LLVGNPPE 274

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RESULT 39

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US-10 059 585-34
; Sequence 34, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Cta, Toshio
; APPLICANT: Isoda, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko

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; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059,585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JPCO/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-059-585-34

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Query Match 77.6%, Score 38; DB 15; Length 344;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 MLGCRPPE 9
Db 266 LLVGNPPE 274

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```

RESULT 30

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```

US-10-171-311-214
; Sequence 214, Application US/10171311
; Publication No. US20030082770A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xume
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerssh, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-171-311-214

```

Query Match 77.6%; Score 38; DB 15; Length 344;
 Best Local Similarity 66.7%; Pred. No. 72;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
 : : : : :
 Db 266 LLVGNPPPE 274

RESULT 31
 US-09-974-298-136
 ; Sequence 136, Application US/09974298
 ; Patent No. US20020156263A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Hui-Mei
 ; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
 ; FILE REFERENCE: PA-0337 P
 ; CURRENT APPLICATION NUMBER: US/09/974,298
 ; CURRENT FILING DATE: 2001-10-04
 ; PRIOR APPLICATION NUMBER: 60/238,133;
 ; PRIOR FILING DATE: 2000-05-10
 ; NUMBER OF SEQ ID NOS: 154
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 136
 ; LENGTH: 347
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Inocyte ID NO. US20020156263A1; C2294CCD;
 US 09 974-298-136

Query Match 77.6%; Score 38; DB 10; Length 347;
 Best Local Similarity 66.7%; Pred. No. 72;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGREPE 9
 : : : : :
 Db 269 LLVGNPPPE 277

RESULT 32
 US 10 291-253A-16
 ; Sequence 16, Application US/0291253A
 ; Publication No. US20030150017A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Botella, Jose
 ; APPLICANT: Graham, Michael
 ; TITLE OF INVENTION: A Method for Facilitating Patented Substance
 ; FILE REFERENCE: Genatode
 ; CURRENT APPLICATION NUMBER: US/10/291,253A
 ; CURRENT FILING DATE: 2003-03-31
 ; PRIOR APPLICATION NUMBER: PR8706
 ; PRIOR FILING DATE: 2001-11-07
 ; PRIOR APPLICATION NUMBER: PR8802
 ; PRIOR FILING DATE: 2001-11-12
 ; PRIOR APPLICATION NUMBER: US60/341404
 ; PRIOR FILING DATE: 2001-12-14
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 16
 ; LENGTH: 348
 ; TYPE: PRT
 ; ORGANISM: Meloidogyne incognita
 US-10-291-253A-16

Query Match 77.6%; Score 38; DB 12; Length 348;
 Best Local Similarity 66.7%; Pred. No. 73;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGREPPE 9

Db 210 MMAGOPPE 218
 : : : : :
 RESULT 33
 US-09-012-135A-4
 ; Sequence 4, Application US/09012135A
 ; Patent No. US20020081578A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Plowman, Gregory
 ; APPLICANT: Mossie, Kevin
 ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
 ; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
 ; NUMBER OF SEQUENCES: 39
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: FastSeq for Windows 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/012,135A
 ; FILING DATE: January 22, 1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/005,268
 ; FILING DATE: January 9, 1998
 ; APPLICATION NUMBER: 08/755,728
 ; FILING DATE: No. US20020081578A1ember 25, 1996
 ; APPLICATION NUMBER: 06/023,943
 ; FILING DATE: August 14, 1996
 ; APPLICATION NUMBER: 60/008,909
 ; FILING DATE: December 18, 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 231/282
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 403 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-09-012-135A-4
 Query Match 77.6%; Score 38; DB 9; Length 403;
 Best Local Similarity 75.0%; Pred. No. 84;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LLGRPPPE 9
 : : : : :
 Db 323 LVGRPPPE 330
 RESULT 34
 US-10-026-021-7
 ; Sequence 7, Application US/10c26021
 ; Publication No. US20030027756A1

GENERAL INFORMATION:
 APPLICANT: Hicoshi, Yasumichi
 APPLICANT: Demo, Susan
 APPLICANT: Jenkins, Yonchu
 APPLICANT: Rigel Pharmaceuticals, Inc.
 TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
 TREATMENT OF CANCER
 FILE REFERENCE: 021044-001210US
 CURRENT APPLICATION NUMBER: US/10/026,021
 CURRENT FILING DATE: 2002-06-25
 PRIOR APPLICATION NUMBER: US 62/309,432
 PRIOR FILING DATE: 2001-08-01
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 7
 LENGTH: 403
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: human ARK mitotic kinase
 US-10-026-021-7

Query Match 77.6% Score 38; DB 15; Length 403;
 Best Local Similarity 75.0%; Pred. No. 84;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPFE 9
 DB 323 LVGRPPFE 330

RESULT 35

US-10-059-585-33
 Sequence 33, Application US/10059585
 Publication No. US20030082776A1
 GENERAL INFORMATION:
 APPLICANT: Ota, Toshio
 APPLICANT: Isogai, Takao
 APPLICANT: Nishikawa, Tetsuo
 APPLICANT: Hayashi, Koji
 APPLICANT: Otsuka, Kaoru
 APPLICANT: Yamamoto, Jun-ichi
 APPLICANT: Ishii, Shizuko
 APPLICANT: Sugiyama, Tomoyasu
 APPLICANT: Wakamatsu, Ai
 APPLICANT: Nagai, Keiichi
 APPLICANT: Otsuki, Tetsuji
 APPLICANT: Funabashi, Shin-ichi
 APPLICANT: Sano, Chiaki
 APPLICANT: Nezu, Jun-ichi

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
 TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
 FILE REFERENCE: 06501-098001
 CURRENT APPLICATION NUMBER: US/10/059,585
 CURRENT FILING DATE: 2002-01-29
 PRIOR APPLICATION NUMBER: PCT/JP00/05860
 PRIOR FILING DATE: 2000-07-28
 PRIOR APPLICATION NUMBER: US 60/183,322
 PRIOR FILING DATE: 2000-02-17
 PRIOR APPLICATION NUMBER: US 60/159,570
 PRIOR FILING DATE: 1999-10-18
 PRIOR APPLICATION NUMBER: JP 2000-118776
 PRIOR FILING DATE: 2000-01-11
 PRIOR APPLICATION NUMBER: JP 2000-183767
 PRIOR FILING DATE: 2000-05-02
 PRIOR APPLICATION NUMBER: JP 11-248036
 PRIOR FILING DATE: 1999-07-29
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 33
 LENGTH: 403
 TYPE: PRT
 ORGANISM: Homo sapiens

US-10-059-585-33

Query Match 77.6% Score 38; DB 15; Length 403;
 Best Local Similarity 75.0%; Pred. No. 84;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPFE 9
 DB 323 LVGRPPFE 330

RESULT 36

US-10-209-324-2
 Sequence 2, Application US/10209324
 Publication No. US20030108910A1
 GENERAL INFORMATION:
 APPLICANT: UNIVERSITY OF CALIFORNIA SAN FRANCISCO
 APPLICANT: TOLAND, Amanda E.
 APPLICANT: BALMAIN, Allan
 TITLE OF INVENTION: STK15 (STK6) GENE POLYMORPHISM AND METHODS OF DETERMINING CANCER
 FILE REFERENCE: UCSF1120-2
 CURRENT APPLICATION NUMBER: US/10/209,324
 CURRENT FILING DATE: 2002-07-29
 PRIOR APPLICATION NUMBER: US 60/334,146
 PRIOR FILING DATE: 2001-11-28
 PRIOR APPLICATION NUMBER: US 60/308,911
 PRIOR FILING DATE: 2001-07-27
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 2
 LENGTH: 403
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: MISC FEATURE
 LOCATION: (31)-(33)
 OTHER INFORMATION: Xaa is Ile or Phe
 US-10-209-324-2

Query Match 77.6% Score 38; DB 15; Length 403;
 Best Local Similarity 75.0%; Pred. No. 84;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPFE 9
 DB 323 LVGRPPFE 330

RESULT 37

US-09-771-161A 195
 Sequence 195, Application US/0977161A
 Patent No. US2002011081A1
 GENERAL INFORMATION:
 APPLICANT: LEVINE, et al.
 TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 FILE REFERENCE: 802620-2005.1
 CURRENT APPLICATION NUMBER: US/09/771,161A
 CURRENT FILING DATE: 2001-01-26
 PRIOR APPLICATION NUMBER: 09/724,676
 PRIOR FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: 138776
 PRIOR FILING DATE: 2000-06-15
 PRIOR APPLICATION NUMBER: 135619
 PRIOR FILING DATE: 2000-04-12
 NUMBER OF SEQ ID NOS: 273
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 195
 LENGTH: 737
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-771-161A-195

Query Match 77.6% Score 38; DB 10; Length 737;

Best Local Similarity 66.7%; Pred. No. 1.5e-02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY : MLIGRPPE 9
| : |||||
DB 600 MNAGQPPPE 608

RESULT 38
US-10-228-931-4
Sequence 4: Application US/10228911
Publication No. US2003051259A1
GENERAL INFORMATION:
APPLICANT: Verma, Amit K
APPLICANT: Reddig, Peter J
APPLICANT: Jansen, Aaron F
TITLE OF INVENTION: Animal Model System for Squamous Cell Carcinoma
FILE REFERENCE: 960396.97613
CURRENT APPLICATION NUMBER: US/10/248,911
PRIOR FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: US/09/772,647
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 717
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: T1 rag and
OTHER INFORMATION: mouse protein kinase C epsilon coding sequence
US 10-228-931-4

Query Match 77.6%; Score 38; DB 15; Length 717;
Best Local Similarity 66.7%; Pred. No. 1.5e-02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY : MLIGRPPE 9
| : |||||
DB 600 MNAGQPPPE 608

RESULT 39
US-09-736-076-3
Sequence 3: Application US/09736076
Patent No. US2002004901A1
GENERAL INFORMATION:
APPLICANT: Ben Sarsion, Samuel A.
TITLE OF INVENTION: SHORT PEPTIDES WITH SELECTIVE Y
TITLE OF INVENTION: MODULATE THE ACTIVITY OF SEVERAL KINASES
FILE REFERENCE: 1421015-009
CURRENT APPLICATION NUMBER: US/09/736,076
PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: US 08/811,496
PRIOR FILING DATE: 1997-05-21
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 20
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: PKC
US-09-736-076-3

Query Match 75.5%; Score 37; DB 9; Length 20;
Best Local Similarity 66.7%; Pred. No. 6.8e-01;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY : MLIGRPPE 9
| : |||||
DB 3 MNAGQPPPE 11

RESULT 40
US-09-836-392-15
Sequence 15: Application US/09836392
Patent No. US20020173459A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptide
FILE REFERENCE: PTO20P
CURRENT APPLICATION NUMBER: US/09/836,392
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: PCT/US00/28066
PRIOR FILING DATE: 2000-10-11
PRIOR APPLICATION NUMBER: 60/159,542
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/165,914
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/189,027
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 15
LENGTH: 445
TYPE: PRT
ORGANISM: Homo sapiens
US-09-836-392-15

Query Match 75.5%; Score 37; DB 10; Length 445;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY : MLIGRPPE 8
| : |||||
DB 263 MLVGQPPPE 270

Search completed: November 14, 2003, 13:43:26
Job time : 22:37:4 secs

GenCore version 5.1.6
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QM protein protein search, using sw model

Run on: November 14, 2003, 13:20:05, Search time 10.8 Seconds

(without alignment)
#0:141 Million cell updates/sec

Title: US-09-736-076-15

Perfect score: 49

Sequence: 1 MLLGRPPPE 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96169682 residues

Total number of hits satisfying chosen parameters: 183368

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: PIR761*
2: PIR2*
3: PIR3*
4: PIR4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	682	A44493	serum-inducible kinase - mouse
2	41	83.7	465	B55748	protein kinase (EC
3	41	83.7	521	D88640	protein F55A8.2 [
4	41	83.7	925	A55748	protein kinase (EC
5	40	81.6	603	S14151	protein/threonine-s
6	40	81.6	603	A47545	protein kinase (EC
7	40	81.6	603	A54339	protein kinase - m
8	39	79.6	576	A22127	protein kinase pol
9	39	79.6	639	A12545	protein kinase C (
10	38	77.6	305	T43221	serine/threonine-s
11	38	77.6	329	B87750	protein B0207.4 [
12	38	77.6	389	S52342	protein kinase (EC
13	38	77.6	403	JC5974	arora-related kin
14	38	77.6	407	S52243	phosphatase protein -
15	38	77.6	547	T44841	K05H7.1 protein -
16	38	77.6	547	T22856	hypothetical prote
17	38	77.6	634	B12332	protein kinase C (
18	38	77.6	648	T43337	protein-like kinase-1
19	38	77.6	683	T38254	serine/threonine-s
20	38	77.6	705	A48144	protein kinase CDC
21	38	77.6	707	A53530	protein kinase C (
22	38	77.6	736	K1R80E	protein kinase C (
23	38	77.6	737	S28942	protein kinase C (
24	38	77.6	737	K1R70E	protein kinase C (
25	38	77.6	737	K1R50E	protein kinase C (
26	37	75.5	220	B42725	multile hydratase
27	37	75.5	380	S70964	phos protein - Myx
28	37	75.5	672	K1H02A	protein kinase C (
29	37	75.5	672	K1R70E	protein kinase C (

30	37	75.5	672	1	KIMSCA	protein kinase C (
31	37	75.5	672	1	K1RBC	protein kinase C (
32	37	75.5	672	1	K1BCC	protein kinase C (
33	37	75.5	676	2	A37237	protein kinase C (
34	37	75.5	682	1	K1B00C	protein kinase C (
35	37	75.5	697	1	K1R70C	protein kinase C (
36	37	75.5	697	1	K1R80C	protein kinase C (
37	37	75.5	697	2	JN0548	protein kinase C (
38	37	75.5	697	2	D24664	protein kinase C (
39	37	75.5	766	2	S69657	hypothetical prote
40	37	75.5	861	2	T15903	protein kinase C h
41	37	75.5	1099	2	A56155	tumor suppressor p
42	36	73.5	217	2	S28754	NADH2 dehydrogenas
43	36	73.5	345	2	JC4665	protein kinase (EC
44	36	73.5	363	2	H97464	nitrogen regulatio
45	36	73.5	371	2	T16391	hypothetical prote

ALIGNMENTS

RESULT 1

A44493
serum-inducible kinase - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 10-Sep-1997
C:Accession: A44493
R:Simmons, D.L.; Neel, B.G.; Stevens, R.; Evett, G.; Erikson, R.L.
Mol. Cell. Biol. 12, 4164-4169, 1992
A:Title: Identification of an early-growth-response gene encoding a novel putative p
A:Reference number: A44493; MUID:92375085; PMID:150821
A:Accession: A44493
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-682 <SM>
A:Experimental source: F-2 cells
A>Note: sequence extracted from NCBI backbone (NCBI:111721, NCBIP:111722)
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho
C:Keywords: ATP
F:77-331/Domain: protein kinase homology <Kin>

Query Match 100.0% Score 49; DB 2; Length 682;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
DB 276 MLLGRPPPE 278
|||||

RESULT 2

B55748
protein kinase (EC 2.7.1.37) Sak-b - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 19-Dec-1997
C:Accession: B55748
R:Fode, C.; Motro, B.; Yousefi, S.; Heffernan, M.; Dennis, J.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 6388-6392, 1994
A:Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosop
A:Reference number: A55748; MUID:94294387; PMID:8022793
A:Accession: B55748
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-465 <FOD>
A:Cross-references: GB:L29480
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho
C:Keywords: ATP; phosphotransferase
F:10-265/Domain: protein kinase homology <Kin>
F:18-26/Region: protein kinase ATP-binding motif

Query Match 83.7% Score 41; DB 2; Length 465;
Best Local Similarity 66.7%; Pred. No. 5.4;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MLLGRPFPE 9
   |||||
DB 204 LLVGRPFPE 212

RESULT 3
Protein F55A8.2 (imported) - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
C:Accession: D88640
R:Annotation: D88640
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
Science 282, 2012-2018, 1998
A:Reference number: A75000; MUID:9905961; PID:39851916
A:Note: see websites genome.wustl.edu/asc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: D88640
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-521 <STO>
A:Cross-references: GB:chr_IV; PIDN:AACT13.86.1; PID:g3133.145; GSPDB:GN000022; CESP:F55A8
C:Genetics:
A:Gene: F55A8.2
A:Map position: 4
C:Superfamily: cGMP-dependent protein kinase; cAMP receptor protein cyclic nucleotide-bi
Query Match 83.7%; Score 41; DB 2; Length 521;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPFPE 9
   |||||
DB 401 LLVGRPFPE 409

RESULT 4
A55748
C:Species: Mus musculus (house mouse)
C:Date: 22-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 24-Sep-1999
C:Accession: A55748
R:Feeder, C.; Votro, H.; Yousefi, S.; Heffernan, M.; Dennis, J.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 6389-6392, 1994
A:Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosophila
F:113-26/Region: protein kinase ATP-binding motif
Reference number: A55748; MUID:94564343; PMID:8022793
A:Accession: A55748
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-925 <ECN>
A:Cross-references: GR:529479; NID:g4040.1; PID:AA330.4.1; PID:g487870
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP; phosphotransferase
F:113-26/Domain: protein kinase homology <KIN>
Query Match 83.7%; Score 41; DB 2; Length 925;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPFPE 9
   |||||
DB 204 LLVGRPFPE 212

RESULT 5
S34130
A:Title: serine/threonine-specific protein kinase Plk (EC 2.7.1.1) - human
K:Alternate names: polo-like protein kinase; protein kinase p-lk-1
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C:Accession: S34130; I38123; S61543

```

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R:Goistein, R.M.; Schultz, S.J.; Bartek, J.; Ziemiecki, A.; Ried, T.; Nigg, E.A.
submitted to the EMBL Data Library, June 1993
A:Description: Cloning and characterization of a novel human protein kinase plk-1 a
through mitosis.
A:Reference number: S34130
A:Accession: S34130
A:Molecule type: mRNA
A:Residues: 1-603 <GCC>
A:Cross-references: EMBL:X73459; NID:g112997; PIDN:CAAS1837.1; PID:g312998
A:Experimental source: nasopharyngeal carcinoma
R:Heitrich, U.; Wolf, G.; Grauning, A.; Karn, T.; Bohme, B.; Rubsamen-Waigmann, H.
Proc. Natl. Acad. Sci. U.S.A. 91, 1736-1740, 1994
A:Title: Induction and down-regulation of PLK, a human serine/threonine kinase expre
A:Reference number: A5134; MUID:9473904; PMID:8127874
A:Accession: I38123
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-140; 'P', 142-226 'E', 228-603 <RES>
A:Cross-references: EMBL:X75932; NID:g460768; PIDN:CAAS3536.1; PID:g460769
R:Braeuninger, A.; Strebhardt, K.; Rubsamen-Waigmann, H.
Oncogene 11, 1793-1800, 1995
A:Title: Identification and functional characterization of the human and murine polo
A:Reference number: S61543; MUID:96068906; PMID:7478607
A:Accession: S61543
A:Molecule type: DNA
A:Residues: 1-122, 'T', 124-136 <BRA>
A:Cross-references: EMBL:X90725; NID:g1061143; PIDN:CAA62260.1; PID:g1061144
A:Experimental source: Placenta
A:Note: the authors translated the codon AOC for residue 107 as Met
C:Genetics:
A:Gene: GDB:PJK
A:Cross-references: GDB:331C03
A:Map position: 17pter-17p12
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hc
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:51-305/Domain: protein kinase homology <KIN>

Query Match 81.6%; Score 40; DB 2; Length 603;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPFPE 9
   |||||
DB 244 LLVGRPFPE 252

RESULT 6
A47545
Protein kinase (EC 2.7.1.17) Plk - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C:Accession: A47545
R:Clay, F.C.; McGwen, S.J.; Beatoncello, I.; Wilks, A.F.; Dunn, A.R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4892-4896, 1993
A:Title: Identification and cloning of a protein kinase-encoding mouse gene, Plk, r
A:Reference number: A47545; MUID:93281660; PMID:8099445
A:Accession: A47545
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-603 <CLA>
A:Cross-references: GB:L06144; NID:g309461; PIDN:AAA39948.1; PID:g309462
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hc
C:Keywords: ATP; phosphotransferase
F:51-305/Domain: protein kinase homology <KIN>

Query Match 81.6%; Score 40; DB 2; Length 603;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPFPE 9
   |||||
DB 244 LLVGRPFPE 252

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A:Cross-references: GB:X05076; NID:g8352; PIDN:CAA28736.1; PID:g8353; GB:Y00042
C:Genetics:
A:Gene: FlyBase:Pk53E
A:Cross-references: FlyBase:FBgn0003091
C:Superfamily: protein kinase C alpha; protein kinase C 2 region homology; protein k
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:46-95/Domain: protein kinase C zinc-binding repeat homology <K21>
F:111-160/Domain: protein kinase C zinc-binding repeat homology <K21>
F:161-273/Domain: protein kinase C 2 region homology <K22>
F:339-599/Domain: protein kinase C 2 region homology <K22>
F:347-355/Region: protein kinase ATP-binding motif

Query Match 79.6%; Score 39; DB 2; Length 639;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGKPPPE 9
Db 533 MLVGQPPPE 541

RESULT 10
T43221
serine/threonine-specific protein kinase (EC 2.7.1.1) 2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C:Accession: T43221
R:Schumacher, J.M.; Golden, A.; Donovan, P.J.
J. Cell Biol. 143, 1635-1646, 1998
A:Title: AIR-2: An aurora/pl1-related protein kinase associated with chromosomes and
A:Reference number: 222347; MUID:99069487; PMID:9852156
A:Accession: T43221
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-305 <SCH>
A:Cross-references: EMBL:AF071207; PIDN:AAC70945.1
C:Genetics:
A:Gene: AIR-2
A:Map position: 1
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: phosphotransferase

Query Match 77.6%; Score 38; DB 2; Length 305;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLGRPPPE 9
Db 220 LVGKPPPE 227

RESULT 11
B87790
protein BC207.4 (imported) - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: B87790
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: B87790
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-329 <STO>
A:Cross-references: GB:chr_1; PIDN:AAB52459.1; PID:g1943805; GSPDB:GN00019; CESP:E020
C:Genetics:
A:Gene: BC207.4
A:Map position: 1
C:Superfamily: kinase-related transforming protein; protein kinase homology

```

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Query Match      77.6%; Score 38; DB 2; Length 329;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPPE 9
    |||||
DB 244 LVGKPPPE 25;

RESULT 10
protein kinase (EC 2.7.1.1) p46Xleq22 African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 19-Jun-1999
A:Accession: S52242
R:Roghi, C.; Le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A:Description: Eg2, selected by differential screening encodes a new Xenopus protein kin
A:Reference number: S52242
A:Accession: S52242
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-389 <ROG>
A:Cross-references: EMBL:Z17206; NID:g609280; PIDN:CAA76914.1; PID:g609280
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase
F:129-311/Domain: protein kinase homology <KIN>
F:127-135/Region: protein kinase ATP-binding motif

Query Match      77.6%; Score 38; DB 2; Length 359;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPPE 9
    |||||
DB 311 LVGKPPPE 318

RESULT 13
aureora related kinase 1 (EC 2.7.1.1) human
C:Species: Homo sapiens (man)
C>Date: 05-Feb-1999 #sequence_revision 03-Feb-1999 #text_change 21-Jan-2000
A:Accession: J05974
R:Shimada, M.; Nakano, H.; Kuroyanagi, H.; Shirasawa, T.; Mihara, M.; Gilbert, D.J.; Jenk
Biochem. Biophys. Res. Commun. 244, 285-292, 1998
A:Title: cDNA cloning, expression, subcellular localization, and chromosomal assignment
A:Reference number: J05974; MJD:98183430; PID:g54916
A:Accession: J05974
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-403 <SH1>
A:Cross-references: GB:AF008551
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
F:131-383/Domain: protein kinase homology <KIN>

Query Match      77.6%; Score 38; DB 2; Length 403;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPPE 9
    |||||
DB 323 LVGKPPPE 330

RESULT 14
p46Eg265 protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 07-May-1995 #sequence_revision 01-Aug-1995 #text_change 24-Sep-1999
A:Accession: S52243; S34642; I51695
R:Roghi, C.; Le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A:Description: Eg2, selected by differential screening encodes a new Xenopus protein kin
A:Reference number: S52243
A:Accession: S52243
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-407 <ROG>
A:Cross-references: EMBL:Z17207; NID:g609281; PIDN:CAA76915.1; PID:g609282
R:Bouvet, P.; Omilli, F.; Arlot-Bonnemair, Y.; Legagneux, V.; Roghi, C.; Bassez, T.;
submitted to the EMBL Data Library, June 1993
A:Description: Targetted deadenylation of specific mRNAs in Xenopus embryos by a mecl
A:Reference number: S34642
A:Accession: S34642
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 328-407 <BOJ>
A:Cross-references: EMBL:Z24453; NID:g394756; PIDN:CAA80826.1; PID:g394757
R:Bouvet, P.; Omilli, F.; Arlot-Bonnemair, Y.; Legagneux, V.; Roghi, C.; Bassez, T.;
Mol. Cell. Biol. 14, 1893-1900, 1994
A:Title: The deadenylation conferred by the 3' untranslated region of a developmental
A:Reference number: I51695; MJD:94158861; PID:D8114721
A:Accession: I51695
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 328-407 <BO2>
A:Cross-references: EMBL:Z24453; NID:g394756; PIDN:CAA80826.1; PID:g394757
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: ATP; phosphotransferase; protein kinase
F:138-390/Domain: protein kinase homology <KIN>
F:146-154/Region: protein kinase ATP-binding motif

Query Match      77.6%; Score 38; DB 2; Length 407;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGRPPPE 9
    |||||
DB 330 LVGKPPPE 337

RESULT 15
K06H7.1 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
A:Accession: S44841
R:Favell, A.D.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid K06H7.
A:Reference number: S44842
A:Accession: S44841
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-547 <FAV>
A:Cross-references: EMBL:L15314; NID:g289690; PIDN:AAA28084.1; PID:g289691
C:Genetics:
A:Introns: 25/3; 36/3; 80/3; 149/3; 186/2; 229/3; 311/3
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho
C:Keywords: ATP; serine/threonine-specific protein kinase
F:265-518/Domain: protein kinase homology <KIN>

Query Match      77.6%; Score 38; DB 2; Length 547;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPPE 9
    |||||
DB 457 LLFGQPPPE 465

RESULT 16
T22856
hypothetical protein F57P5.5 - Caenorhabditis elegans

```

C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Jun-2002
 C:Accession: T22856
 R:Harits, B.
 submitted to the EMBL Data Library, July 1996
 A:Reference number: 219627
 A:Accession: T22856
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-547 <MIL>
 A:Cross references: EMBL:Z75933; FIDN:GAB00101.1; GSPDB:GN00023; CESP:F57F5.5
 A:Experimental source: clone F57F5
 C:Genetics:
 A:Gene: CESP:F57F5.5
 A:Map position: 5
 A:Introns: 43/1; 129/2; 166/3; 187/1; 289/3; 341/2; 450/4; 499/1
 Full-60/Domain: protein kinase C zinc binding repeat homology <K2N1>
 F:89-135/Domain: protein kinase C zinc-binding repeat homology <K2N2>

Query Match 77.6%; Score 38; DB 2; Length 547;
 Best Local Similarity 66.7%; Pred. No. 24;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPFE 9
 :|||:
 Db 410 VVAGQPPFE 418

RESULT 17
 E32392
 protein kinase C (EC 2.7.1.1) epsilon related - fruit fly *Drosophila melanogaster*;
 N:Alternate names: protein kinase C 98F
 C:Species: *Drosophila melanogaster*
 C:Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 11-Jun-1999
 C:Accession: B32392
 R:Schaeffer, E.; Smith, D.; Mardon, G.; Quinn, W.; Zuker, C.
 Cell 57, 403-412, 1993
 A:Title: Isolation and characterization of two new *Drosophila* protein kinase C genes, in
 A:Reference number: B32392; MUID:89243302; PMID:7270775
 A:Accession: B32392
 A:Molecule type: mRNA
 A:Residues: 1-634 <SCH>
 A:Cross references: GB:J04648; NID:G158108; FIDN:AA4428.6.1; PID:G158129
 C:Genetics:
 A:Gene: FlyBase:PkcsE
 A:Cross references: FlyBase:FBgn0003093
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine phosphate or peptidyl-threonin
 A>Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
 C:Superfamily: protein kinase C delta; protein kinase C zeta binding repeat homology; pr
 C:Keywords: ATP; duplication; phorbol ester binding; phosphatidyl binding; phosphotransf
 F:84-63/Region: pseudophosphorylation motif
 F:72-117/Domain: protein kinase C zinc-binding repeat homology <K1>
 F:47-194/Domain: protein kinase C zinc-binding repeat homology <K2>
 F:301-560/Domain: protein kinase C zinc-binding repeat homology <KIN>
 F:309-317/Region: protein kinase ATP-binding motif
 F:72-102,105,121/Binding site: zinc His, Cys, Cys, Cys #status predicted
 F:85,110,113/Binding site: zinc Cys, Cys, His, Cys #status predicted
 F:147,177,180,195/Binding site: zinc His, Cys, Cys #status predicted
 F:160,167,185,189/Binding site: zinc Cys, Cys, His, Cys #status predicted
 F:332,351,427,429/Active site: Lys, Glu, Asp, Cys #status predicted

Query Match 77.6%; Score 38; DB 1; Length 634;
 Best Local Similarity 66.7%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPFE 9
 :|||:
 Db 495 VVAGQPPFE 503

RESULT 18
 T43317

polo-like kinase-1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 01-Dec-2000
 C:Accession: T43317; S44761
 R:Chase, D.; Rafaninas, C.; Ashcroft, N.; Kosinski, M.; Longo, D.; Ferris, D.K.; Gol
 submitted to the EMBL Data Library, July 1998
 A:Description: The polo-like kinase PLK-1 is required for nuclear envelope breakdown
 A:Reference number: 222438
 A:Accession: T43317
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-648 <CHA>
 A:Cross references: EMBL:AF080581; PIDN:AAC34661.1
 R:Favella, A. D.
 submitted to the EMBL Data Library, May 1993
 A:Description: Sequence of the *C. elegans* cosmid C14B9.
 A:Reference number: S44617
 A:Accession: S44761
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 'MKTLL' 282-648 <FAV>
 A:Cross references: EMBL:L15188; NID:G289640; PID:G289648
 C:Genetics:
 A:Gene: plk-1
 A:Map position: 3
 A:Introns: 391/3; 540/3; 578/3
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

Query Match 77.6%; Score 38; DB 2; Length 648;
 Best Local Similarity 66.7%; Pred. No. 28;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPFE 9
 :|||:
 Db 228 LFGQPPFE 236

RESULT 19
 T38254
 serine/threonine-specific protein kinase p101 (EC 2.7.1.1) - fission yeast (*Schizosar*
 C:Species: *Schizosaccharomyces pombe*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
 C:Accession: T38254; T45128
 R:Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 submitted to the EMBL Data Library, August 1995
 A:Reference number: Z21781
 A:Accession: T38254
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-683 <BRC>
 A:Cross references: EMBL:Z98559; FIDN:CAB1167.1; GSPDB:GN00066; SPDB:SPAC23C11.16
 A:Experimental source: strain 9728; cosmid c23C11
 R:Okura, H.; Hagan, I.M.; Glover, D.M.
 Genes Dev. 9, 1059-1073, 1995
 A:Title: The conserved *Schizosaccharomyces pombe* kinase p101, required to form a bip
 A:Reference number: Z22921; MUID:95262899; PMID:7744248
 A:Accession: T45128
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-683 <OHK>
 A:Cross references: EMBL:X85758; NID:G887640; PIDN:CAA59766.1; PID:G887641
 A:Experimental source: strain 972 derivative
 C:Genetics:
 A:Gene: p101; SPAC23C11.16
 A:Map position: 1
 C:Function:
 A:Description: required to form a bipolar spindle and early in the regulatory casc
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
 C:Keywords: phosphotransferase; protein kinase

Query Match 77.6%; Score 38; DB 2; Length 683;
 Best Local Similarity 55.6%; Pred. No. 30;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY : MLJGRPPPE 9
DB 243 LLJGKPPFQ 241

RESULT 23
A88144
Protein kinase CUC5 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein kinase PKX2; protein YMD373.133; protein YMR001c
C:Species: Saccharomyces cerevisiae
C:Date: 30-Jun-1995 #sequence revision 30-Jun-1995 #text_change 24-Sep-1999
C:Accession: A48144, S51030, S27445
R:Kitada, K.; Johnson, A.L.; Johnston, L.H.; Sugino, A
Yeast Cell. Bio. 22, 4445-4457, 1993
A:Title: A multicopy suppressor gene of the Saccharomyces cerevisiae G1 cell cycle mutation
A:Reference number: A48144; MUID:9309479; PMID:8321244
A:Accession: A48144
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-705 <Kin>
A:Cross-references: EXBL:M84220; NID:q172186; PIDN:AAA-2576.1; PID:q172187
R:Devlin, K.; Churcher, C.M.
Submitted to the EMBL Data Library, March 1995
A:Reference number: S51028
A:Accession: S51030
A:Molecule type: DNA
A:Residues: 1-705 <Dev>
A:Cross-references: EXBL:248613; NID:q1728645; PIDN:CAA-2576.1; PID:q1728646; MIPS:YMR001c
A:Experimental source: strain AB472
C:Genetics:
A:Gene: SSG1/CDC5; PKX2
A:Cross-references: SSG1:SC004603; MIPS:YMP001C
A:Map position: 13k
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases, protein kinase homodimeric
C:Keywords: ATP; cell cycle control; phosphotransferase; protein kinase
F:80-337/Domain: protein kinase homology <Kin>

Query Match 77.6% Score 38; DB 2; Length 705;
Best Local Similarity 55.6% Pred. No. 31;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY : MLJGRPPPE 9
DB 243 LLJGKPPFQ 282

RESULT 21
A53530
Protein kinase C (EC 2.7.1.1) epsilon-related - Caenorhabditis elegans
N:Alternate names: Protein kinase C PKC1B, PKC1B1
C:Species: Caenorhabditis elegans
C:Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 11-Jun-1999
C:Accession: A53530
R:Land, M.; Islas-Trejo, A.; Freedman, J.H.; Rucinski, G.
J. Biol. Chem. 269, 9234-9244, 1994
A:Title: Structure and expression of a novel, neuronal protein kinase C (PKC1B) from Caenorhabditis elegans
A:Reference number: A53530; MUID:9417945; PMID:8132661
A:Accession: A53530
A:Molecule type: mRNA
A:Residues: 1-707 <KAN>
A:Cross-references: GB:U00181; NID:9494065; PIDN:AAA18-199.1; PID:9392435
C:Genetics:
A:Gene: kin-13
A:Map position: V
A:Note: Located near myo-3, col-1, and CPR-72 genes
C:Function:
A:Description: catalyzes the formation of triphosphatide or peptidyl-threonine
A:Note: activity is calcium-independent, phospholipid-dependent, and activated by diacylglycerol
C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; phospholipid binding; phosphotransferase
C:Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotransferase
F:157-162/Region: pseudophosphorylation motif

F:171-220/Domain: protein kinase C zinc-binding repeat homology <K21>
F:249-298/Domain: protein kinase C zinc-binding repeat homology <K22>
F:376-638/Domain: protein kinase homology <KIN>
F:384-392/Region: protein kinase ATP-binding motif
F:171-201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:184,187,209,212/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:249,279,282,298/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:262,265,287,290/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:407,426,502,504/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 77.6% Score 38; DB 1; Length 707;
Best Local Similarity 66.7% Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY : MLJGRPPPE 9
DB 570 MMAGQPPPE 578

RESULT 22
KIR3CE
protein kinase C (EC 2.7.1.1) epsilon - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 21-Nov-1997
C:Accession: A29880
R:Ohno, S.; Akita, Y.; Konno, Y.; Imajoh, S.; Suzuki, K.
Cell. 55, 731-741, 1988
A:Title: A novel phorbol ester receptor/protein kinase, nPKC, distantly related to protein kinase C
A:Reference number: A29880; MUID:88223367; PMID:3370672
A:Accession: A29880
A:Molecule type: mRNA
A:Residues: 1-736 <GRN>
A:Cross-references: GB:M20314
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A:Note: activity is calcium-independent, phospholipid-dependent, and activated by diacylglycerol
C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology
C:Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid binding; pseudophosphorylation motif
F:156-161/Region: pseudophosphorylation motif
F:170-220/Domain: protein kinase C zinc-binding repeat homology <K21>
F:243-292/Domain: protein kinase C zinc-binding repeat homology <K22>
F:435-667/Domain: protein kinase homology <KIN>
F:413-421/Region: protein kinase ATP-binding motif
F:170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:183,186,209,212/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:436,455,531,533/Active site: Lys, Glu, Asp, Lys #status predicted
F:702,709/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status

Query Match 77.6% Score 38; DB 1; Length 736;
Best Local Similarity 66.7% Pred. No. 32;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY : MLJGRPPPE 9
DB 599 MMAGQPPPE 607

RESULT 23
S28942
protein kinase C (EC 2.7.1.1) epsilon - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 11-Jun-1999
C:Accession: S28942
R:Basta, P.; Strickland, M.B.; Holmes, W.; Loomis, C.R.; Ballas, L.M.; Burns, D.J.
Biochim. Biophys. Acta 1132, 154-163, 1992
A:Title: Sequence and expression of human protein kinase C-epsilon.
A:Reference number: S28942; MUID:93003318; PMID:1382605
A:Accession: S28942
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-737 <BAS>

Db 118 ITRGRPF 125

RESULT 27

S70964

pkx5 protein - Myxococcus xanthus

N:Alternate names: serine protein kinase homolog

C:Species: Myxococcus xanthus

C>Date: 12-Feb-1998 #sequence_revision 20-Feb-1999 #text_change 28-Oct-1999

C:Accession: S70964

R:Zhang, W.; Inouye, K.; Inouye, S.

Mol. Microbiol. 20, 435-447, 1996

A:Title: Reciprocal regulation of the differentiation of Myxococcus xanthus by Pkn5 and A

A:Reference number: S70964

A:Accession: S70964

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-380 <2HA>

A:Cross-references: EMBL:U00656; NID:g111924; PIDN:AA34004.1; P:G1113925

A:Note: The nucleotide sequence was submitted to the EMBL Data Library, November 1995

C:Genetics:

A:Gene: pkx5

Query Match 75.5% Score 37; DB 2; Length 380;

Best Local Similarity 66.7% Pred. No. 25;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRPF 9

DB 314 ITRGRPF 322

RESULT 28

K:HUCA

protein kinase C (EC 2.7.1.1) alpha - human

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999

C:Accession: S09496

R:Pinkenzeller, G.; Yarnes, D.; Hug, H.

Nucleic Acids Res. 18, 2183, 1990

A:Title: Sequence of human protein kinase C alpha.

A:Reference number: S09496; MUID:9024567; PMID:2336401

A:Accession: S09496

A:Molecule type: mRNA

A:Residues: 1-672 <FIN>

A:Cross-references: EMBL:X52479; NID:g35482; PIDN:CAA3618.1; PID:g35483

C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-sp

f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters,

C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may

C:Comment: The zinc stabilized regions bind diacylglycerol and phorbol esters.

C:Genetics:

A:Gene: G35:PRKCA

A:Cross-references: GDB:128015; OMIM:176960

A:Map position: 17q22-17q23.2

C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kin

C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bindi

F:10-23/Region: pseudophosphorylation motif

F:22-27/Region: pseudophosphorylation motif

F:37-86/Domain: protein kinase C zinc-binding repeat homology <K21>

F:102-151/Domain: protein kinase C zinc-binding repeat homology <K22>

F:152-264/Domain: protein kinase C C2 region homology <K2>

F:337-597/Domain: protein kinase homology <KIN>

F:345-353/Region: protein kinase ATP-binding motif

F:368/Active site: Lys #status predicted

F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query Match 75.5% Score 37; DB 1; Length 672;

Best Local Similarity 66.7% Pred. No. 45;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRPF 9

DB 531 MLGRPF 539

RESULT 29

KIRIC

protein kinase C (EC 2.7.1.1) alpha - rat

N:Alternate names: protein kinase C type III

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999

C:Accession: S02248

R:Ono, Y.; Fujii, T.; Igarashi, K.; Kikkawa, U.; Ogita, K.; Nishizuka, Y.

C:Accession: S02248; S02620

A:Title: Nucleotide sequences of cDNAs for alpha and gamma subtypes of rat brain pr

A:Reference number: S02129; MUID:88262515; PMID:3387228

A:Accession: S02248

A:Molecule type: mRNA

A:Residues: 1-672 <ONO>

A:Cross-references: EMBL:X07286; NID:g56913; PIDN:CAA30266.1; PID:g56914

C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine

f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol este

C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane

C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.

C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein k

C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bin

F:19-29/Region: phospholipid binding #status experimental

F:22-27/Region: pseudophosphorylation motif

F:37-86/Domain: protein kinase C zinc-binding repeat homology <K21>

F:102-151/Domain: protein kinase C zinc-binding repeat homology <K22>

F:152-264/Domain: protein kinase C C2 region homology <K2>

F:337-597/Domain: protein kinase homology <KIN>

F:345-353/Region: protein kinase ATP-binding motif

F:368/Active site: Lys #status predicted

F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status F

Query Match 75.5% Score 37; DB 1; Length 672;

Best Local Similarity 66.7% Pred. No. 45;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRPF 9

DB 531 MLGRPF 539

RESULT 30

KIMSCA

protein kinase C (EC 2.7.1.1) alpha - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999

C:Accession: S07104; JS0078

R:Segidish, T.; Mazurek, N.

Nature 342, 807-811, 1989

A:Title: A mutant protein kinase C that can transform fibroblasts.

A:Reference number: S07104; MUID:90098082; PMID:2601739

A:Accession: S07104

A:Molecule type: mRNA

A:Residues: 1-672 <MEG>

A:Cross-references: GDB:X52685; GB:X51603; NID:g49938; PIDN:CAA36908.1; PID:g49939

A:Experimental source: strain Balb/c

R:Rose-John, S.; Dietrich, A.; Marks, F.

Gene 74, 465-471, 1988

A:Title: Molecular cloning of mouse protein kinase C (PKC) cDNA from Swiss 3T3 fibro

A:Reference number: JS0078; MUID:89232737; PMID:2469625

A:Accession: JS0078

A:Molecule type: mRNA

A:Residues: 1-146, 'D', 148-217, 'N', 219-276, 'AH', 279-312, 'V', 314-466, 'N', 468-471, 'N', 4

A:Cross-references: GB:M25811

A:Note: The authors translated the codon AAC for residue 141 as Lys; the sequence sh

C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonin

f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol est

C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane

Query Match 75.5% Score 37; DB 1; Length 672;

Best Local Similarity 66.7% Pred. No. 45;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRPF 9

DB 531 MLGRPF 539

C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 11-Jun-1999

R;Accession: A06621

R;Parker, P.J.; Coussens, L.; Totty, N.; Rhee, L.; Young, S.; Chen, E.; Stabel, S.; W Science 233, 853-859, 1986

A>Title: The complete primary structure of protein kinase C - the major phorbol ester A:Reference number: A06621; MUID:862899425; PMID:3755547

A:Accession: A06621

A:Molecule type: mRNA

A:Residues: 1-672 <PAR>

A:Cross-references: GB:MJ973; NID:g:63529; PIDN:AAA30706.1; PID:g:63530

A:Experimental source: brain

C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine dependent phospholipids. This protein is a receptor for tumor-promoting phorbol ester C:Comment: Binding to acidic phospholipids (phosphatidyserine) in the cell membrane C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.

C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein k C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bin F:19-29/Region: phospholipid binding #status experimental

F:22-27/Region: pseudophosphorylation motif

F:37-86/Domain: protein kinase C zinc-binding repeat homology <KZ1>

F:102-151/Domain: protein kinase C zinc-binding repeat homology <KZ2>

F:152-264/Domain: protein kinase C C2 region homology <KC2>

F:337-597/Domain: protein kinase homology <KIN>

F:345-353/Region: protein kinase ATP-binding motif

F:37,67,70,86/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F:50,53,75,78/Binding site: zinc (Cys, Cys, His, Cys) #status predicted

F:102,132,135,151/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F:115,118,140,143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted

F:368/Active site: lys #status predicted

F:631,638/Binding site: phosphate (thr) (covalent) (by autophosphorylation) #status p

Query Match 75.5%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGGRPFPE 9
||| :|||
Db 531 MLAGQPFPD 539

RESULT 33

A37237

C:protein kinase C (EC 2.7.1.1) i - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 28-Feb-1997

C:Accession: A37237

R;Chen, K.; Peng, Z.; Javala, S.; Kung, H.
Second Messengers Phosphoproteins 12, 251-260, 1989

A>Title: Molecular cloning and sequence analysis of two distinct types of Xenopus lae A:Reference number: A37237; MUID:9C172233; PMID:3722298

A:Accession: A37237

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A:Molecule type: mRNA

A:Residues: 1-676 <HE>

C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein k C:Keywords: ATP; phosphotransferase

F:42-91/Domain: protein kinase C zinc-binding repeat homology <KZ1>

F:107-156/Domain: protein kinase C zinc-binding repeat homology <KZ2>

F:157-267/Domain: protein kinase C C2 region homology <KC2>

F:341-601/Domain: protein kinase homology <KIN>

F:349-357/Region: protein kinase ATP-binding motif

```

Query Match      75.5%  Score 37;  DB 2;  Length 676;
Best Local Similarity 66.7%  Pred. NO. 45;
Matches 6;  Conservative 2;  Mismatches 1;  Indels 0;  Gaps 0;

Qy      1  MLLGRPFPE 9
      ||:||||:
Db      535  MLAGQPFDF 543

RESULT 34
KIBQGC

```

Protein: kinase C (EC 2.7.1.1) gamma - bovine (fragment)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 C/Accession: C24664
 R/Coussens, L.; Parker, P.J.; Rhee, L.; Yang-Feng, T.L.; Chen, E.; Waterfield, M.D.; Fra-
 Science 213, 859-866, 1986
 A/Title: Multiple, distinct forms of bovine and human protein kinase C suggest diversity
 A/Reference number: A94291; MUID:86289426; PMID:3755532
 A/Accession: C24664
 A/Molecule type: mRNA
 A/Residues: 1-682 <ON>
 A/Cross-references: GB:M13976; NID:9163525; PDB:AAA10704; PDB:5G3526
 C/Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-sp
 f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters,
 C/Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may
 C/Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
 C/Superfamily: protein kinase C alpha; protein kinase C2 region homology; protein kina
 C/Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bindin
 F:31-11/Region: pseudophosphorylation motif
 F:6-11/Region: pseudophosphorylation motif
 F:21-70/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:86-135/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:136-249/Domain: protein kinase C2 region homology <KC2>
 F:334-570/Domain: protein kinase homology <KIN>
 F:342-552/Region: protein kinase ATP-binding motif
 F:21-51,54,70/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:34,37,59,62/Binding site: zinc (His, Cys, His, Cys) #status predicted
 F:86,116,119,135/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:99,122,124,127/Binding site: zinc (His, Cys, Cys, His, Cys) #status predicted
 F:365/Active site: Lys #status predicted
 F:633,640/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query Match: 75.5%; Score 37; DB 1; Length 697;
 Best Local Similarity: 66.7%; Pred. No. 47;
 Matches: 6; Conservative: 2; Mismatches: 1; Indels: 0; Gaps: 0;

QY 1 MLLGRPPE 9
 |||||
 DB 548 MLAGQPPFD 541

RESULT 15
 KIR73C
 Protein: kinase C (EC 2.7.1.1) gamma - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 C/Accession: A55105; S02129; I55317
 R/Kinjo, J.; Lee, M.H.; Sultzman, L.A.; Kikkawa, K.; Hewick, R.W.; Bell,
 Cell 44, 491-502, 1986
 A/Title: Cloning and expression of multiple protein kinase C subse
 A/Reference number: A95883; MUID:86272697; PMID:375337
 A/Accession: A55105
 A/Molecule type: mRNA
 A/Residues: 1-697 <KC>
 A/Cross-references: GB:M13707; NID:9226196; PDB:AAA11274; PDB:3Z06187
 A/Note: the authors translated the cDNA JUV for residue 432 as Glu
 R/Ono, Y.; Fujii, T.; Igasaki, K.; Kikkawa, K.; Ogita, K.; Kishizuka, Y.
 Nucleic Acids Res. 16, 5199-5200, 1988
 A/Title: Nucleotide sequences of cDNAs for alpha and gamma subtypes of rat brain prote
 A/Reference number: S02129; MUID:89262515; PMID:3387225
 A/Accession: S02129
 A/Molecule type: mRNA
 A/Residues: 1-697 <ON>
 A/Cross-references: EMBL:X07287; NID:956917; PDB:CAA3026717; PDB:956918
 R/Chen, K.
 J. Biol. Chem. 265, 19961-19965, 1990
 A/Title: Characterization of the 5'-flanking region of the rat protein kinase C gamma ge
 A/Reference number: I55317; MUID:91060619; PMID:2246211
 A/Accession: I55317
 A/Status: translated from GB/EMBL/DDEC
 A/Molecule type: DNA
 A/Residues: 1-56 <RES>
 A/Cross-references: GB:M55417; NID:3206184; PDB:AAA11274; PDB:3554487

C/Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonin
 f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol est
 C/Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membra
 C/Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
 C/Genetics:
 A/Genes: PRKC-gamma
 C/Superfamily: protein kinase C alpha; protein kinase C2 region homology; protein
 C/Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bu
 F:18-28/Region: pseudophosphorylation motif
 F:21-26/Region: pseudophosphorylation motif
 F:36-85/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:101-150/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:151-264/Domain: protein kinase C2 region homology <KC2>
 F:349-614/Domain: protein kinase homology <KIN>
 F:357-365/Region: protein kinase ATP-binding motif
 F:36,66,69,85/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:49,52,74,77/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:101,131,134,150/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:114,117,139,142/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:380/Active site: Lys #status predicted
 F:648,655/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status

Query Match: 75.5%; Score 37; DB 1; Length 697;
 Best Local Similarity: 66.7%; Pred. No. 47;
 Matches: 6; Conservative: 2; Mismatches: 1; Indels: 0; Gaps: 0;

QY 1 MLLGRPPE 9
 |||||
 DB 548 MLAGQPPFD 556

RESULT 36
 KIRBGC
 Protein: kinase C (EC 2.7.1.1) gamma - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 C/Accession: A28708
 R/Ohno, S.; Kawasaki, H.; Konno, Y.; Inagaki, M.; Hidaka, H.; Suzuki, K.
 Biochemistry 27, 2083-2087, 1989
 A/Title: A fourth type of rabbit protein kinase C.
 A/Reference number: A28708; MUID:88241336; PMID:2837282
 A/Accession: A28708
 A/Molecule type: mRNA
 A/Residues: 1-697 <ON>
 A/Cross-references: PDB:AAA31449.1; PDB:9165652
 C/Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonin
 f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol est
 C/Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membra
 C/Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
 C/Superfamily: protein kinase C alpha; protein kinase C2 region homology; protein
 C/Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester b
 F:18-28/Region: pseudophosphorylation motif
 F:21-26/Region: pseudophosphorylation motif
 F:36-85/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:101-150/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:151-264/Domain: protein kinase C2 region homology <KC2>
 F:349-614/Domain: protein kinase homology <KIN>
 F:357-365/Region: protein kinase ATP-binding motif
 F:36,66,69,85/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:49,52,74,77/Binding site: zinc (His, Cys, Cys, His, Cys) #status predicted
 F:101,131,134,150/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:114,117,139,142/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:380/Active site: Lys #status predicted
 F:648,655/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status

Query Match: 75.5%; Score 37; DB 1; Length 697;
 Best Local Similarity: 66.7%; Pred. No. 47;
 Matches: 6; Conservative: 2; Mismatches: 1; Indels: 0; Gaps: 0;

QY 1 MLLGRPPE 9
 |||||
 DB 548 MLAGQPPFD 556

XX SQ Sequence 429 AA;
Query Match 87.8%; Score 43; DB 21; Length 129;
Best Local Similarity 77.8%; Pred. No. 7;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLGKPPPE 9
Dc 260 LLVGKPPPE 268
RESULT 20
ID ABP73734
XX AC ABP73734;
XX DT 30-JAN-2003 (first entry)
XX DE Candida albicans essential protein SEQ ID NO 7571.
XX KW Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal.
XX OS Candida albicans.
XX PN WC20C253728-A2.
XX PD 11-JUL-2002.
XX PE 26-DEC-2001; 2001WO-US49486.
XX PR 29-DEC-2000; 2000US-259128P.
XX PR 20-FEB-2001; 2001US-C792024.
XX PR 22-AUG-2001; 2001US-314050P.
XX PA (ELT-); ELTRA PHARM INC.
XX PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX DR WP1; 2002-566634/60.
XX DR N-PSDB; AB212284.
XX PT Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele
PT of a gene and placing other allele of the gene under conditional
PT expression.
XX PS Claim 44; SEQ ID NO 7571; 167pp • Sequence listing; English.
XX CC The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of an

CC essential Candida albicans protein used in the method of the invention.
CC Note: The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied to Derwent by
CC the European Patent Office.
XX SQ Sequence 528 AA;
Query Match 87.8%; Score 43; DB 23; Length 528;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLGKPPPE 9
Dc 454 LLVGKPPPE 462
RESULT 21
AAU74656
ID AAU74656 standard; Protein; 531 AA.
XX AC AAU74656;
XX DT 09-APR-2002 (first entry)
XX DE Mammalian polo-like kinase (Plk).
XX KW Polo-like kinase; PLK; polo-box; cytostatic; neoplasm;
KW hyperproliferative disorder; cytokinesis; solid tumour;
KW carcinoma; sarcoma; cancer; small cell carcinoma; adenocarcinoma;
KW Mullerian tumour; squamous cell carcinoma; protein.
XX OS Mammalia.
XX PH Key Location/Qualifiers
FT Misc-difference 130 /label= Unknown;
FT Misc-difference 131 /label= Unknown
FT Misc-difference 132 /label= Unknown
FT Misc-difference 133 /label= Unknown
FT Misc-difference 134 /label= Unknown
FT Misc-difference 135 /label= Unknown
FT Misc-difference 136 /label= Unknown
FT Misc-difference 137 /label= Unknown
FT Misc-difference 138 /label= Unknown
FT Misc-difference 139 /label= Unknown
FT Misc-difference 140 /label= Unknown
FT Misc-difference 141 /label= Unknown
FT Misc-difference 147 /label= Unknown
FT Misc-difference 148 /label= Unknown
FT Misc-difference 149 /label= Unknown
FT Misc-difference 150 /label= Unknown
FT Misc-difference 151 /label= Unknown
FT Misc-difference 152 /label= Unknown
FT Misc-difference 153 /label= Unknown
FT Misc-difference 154 /label= Unknown

FT /label= Unknown
 FT Misc difference 355
 FT /label= Unknown
 FT Misc difference 356
 FT /label= Unknown
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 FT Misc difference 362
 FT /label= Unknown
 FT Misc difference 363
 FT /label= Unknown
 FT Misc difference 364
 FT /label= Unknown
 FT Misc difference 365
 FT /label= Unknown
 FT Region 412..439
 FT /label= Polo box
 FT /note= "Core polo box consensus sequence"
 XX
 XX WQ20013040: A2.
 XX
 XX 29 NOV-2001.
 XX
 XX 23-MAY-2001: 2001WO-US16903.
 XX
 XX 23-MAY 2000: 2000JUS-206588P.
 XX
 XX GRASD : HARVARD COLLEGE
 XX CUSH : US DEPT. HEALTH & HUMAN SERVICES.
 XX CUSH : US NAT. INST OF HEALTH.
 XX
 XX See KS, Song S, Erikson R;
 XX WPI: 2002-05210/14.
 XX

Identifying polo-like kinase modulators by contacting eukaryotic cells expressing polo box peptides with test compounds and evaluating changes in dominant negative cytokinesis-defective growth patterns.

Example 2: Fig 5: 57pp; English.

The invention describes a novel method of identifying compounds with polo-like kinase (PLK) modulating activity. This comprises contacting eukaryotic cells expressing polo-box or polo-box related peptides, binding peptides comprising 25 contiguous residues from a polo-like kinase C-terminal region, with a test compound. Ectopic expression of a polo-box in a eukaryotic cell causes a severe cytokinetic defect in the cell. These eukaryotic cells can also be tested with the test compound used in the method of the invention. The polo-box related peptides and polo-like kinase activity modulatory compounds can be used to inhibit or enhance cellular proliferation and subsequently for treating hyperproliferative disorders including neoplasia, solid tumors, carcinomas, sarcomas and cancers e.g. small cell carcinoma, adenocarcinoma, Mullerian tumors and squamous cell carcinomas. This is the amino acid sequence of a mammalian polo like kinase (PLK), uncontrolled expression of the PLK family is implicated in the development of human cancers, discussed in the method of the invention.

XX Sequence 531 AA;

Query Match 87.8%; Score 43; DB 23; Length 511;
 Best Local Similarity 77.8%; Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY : MLGKPPFE 9

DB 204 LMGKPPFE 212

RESULT 22

AAR74620

ID AAR74620 standard; Protein: 603 AA.

XX AAR74620;

XX 25-MAR-2003 (updated)

DT 26-OCT-1995 (first entry)

XX Human lung tumour Polo-like kinase.

XX Polo-like kinase; PLK; serine threonine kinase; human; lung tumour;

KW autoimmune disease; lymphocyte activity.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Binding-site 60..86

FT /label= ATP-binding_motif

FT Region 174..177

FT /note= "motif that is highly conserved in protein

FT kinases"

FT Region 194..196

FT /note= "motif that is highly conserved in protein

FT kinases"

XX DE4329177-A1.

XX 02-MAR-1995.

XX 30-AUG-1993: 93DE-4329:77.

XX 30-AUG-1993: 93DE-4329:77.

XX (CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.

XX Holtrich U, Rubsamen-Waigmann H, Strebhardt K;

PI Rubsamen-Waigmann H;

XX WPI: 1995-059454/14.

XX N-PSDB: AAC88155.

XX A polo-like serine threonine kinase-protein - isolated from

XX proliferating human tissue, useful in the determin of lymphocyte

XX activity, eg in auto-immune diseases

XX Claim 1; Page 8-10; 11pp; German.

XX A human lung tumour-derived cDNA (AAO88155) was found to have high

XX homology with sequences from members of the serine/threonine kinase

XX family. Due to the strong homology with the Drosophila polo gene,

XX the protein encoded by the new cDNA (AAR74620) was designated a polo-

XX like kinase (PLK). PLK mRNA is expressed in proliferating cells such

XX as placenta, colon and tumours of the lung, oesophagus, gut and

XX intestine. Resting lymphocytes do not express the PLK gene but after

XX stimulation with phytohaemagglutinin, PLK is expressed and can be

XX used as an indicator of lymphocyte stimulation.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 603 AA;

Query Match 87.8%; Score 43; DB 16; Length 603;

Best Local Similarity 77.8%; Pred. No. 13;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY : MLGKPPFE 9

DB 244 LMGKPPFE 12

```

RESULT 23
AAU79306
ID AAU79306 standard; Peptide; 603 AA.
XX AC AAU79306;
XX DT 02 JUL-2002 (first entry)
XX DE Mouse polo-like kinase (Plk).
XX KW Polo box; PBI; cytostatic; fungicide; protozoicide; antihelminthic;
XX KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
XX KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX KW cancer of the uterus; ovarian cancer; cervical cancer;
XX KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
XX KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
XX KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX KW arthropod infection; mouse; polo-like kinase; Plk.
XX OS Mus musculus.
XX XX
XX PN US6358738-B1.
XX PD 19-MAR-2002.
XX PF 13-MAY-1999; 99US-0311311.
XX PR 13-MAY-1998; 98US-085296P.
XX PA (HARD ) HARVARD COLLEGE.
XX PI Erikson RL, Lee KS;
XX DR WPI; 2002-314756/35.
XX PT Administering polo kinase inhibitors for the treatment of cancers and
XX PT fungal infections
XX PS Example 1; Column 59-64; 47pp; English.
XX CC The invention describes a method of inhibiting growth of an isolated
XX CC population of cells by inhibiting a cell polo kinase by administering a
XX CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX CC carboxy terminal domain of the polo kinase which excludes the polo
XX CC kinase catalytic domain. The method is used for the treatment of cancer
XX CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, and the
XX CC cervix), the epithelium, the brain, the retina, the prostate, and the
XX CC throat, infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX CC This is the amino acid sequence of the polo like kinase (Plk), a
XX CC protein from which mitotic protein polo kinase inhibitory peptides are
XX CC derived.
XX SQ Sequence 603 AA;
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGKPPFE 9
DE 244 LLVGKPPFE 252
RESULT 24
AAU79306
ID AAU79306 standard; Peptide; 603 AA.
XX AC AAU79306;
XX DT 02 JUL-2002 (first entry)
XX DE Mouse polo-like kinase (Plk).
XX KW Polo box; PBI; cytostatic; fungicide; protozoicide; antihelminthic;
XX KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
XX KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX KW cancer of the uterus; ovarian cancer; cervical cancer;
XX KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
XX KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
XX KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX KW arthropod infection; mouse; polo-like kinase; Plk.
XX OS Mus musculus.
XX XX
XX PN US6358738-B1.
XX PD 19-MAR-2002.
XX PF 13-MAY-1999; 99US-0311311.
XX PR 13-MAY-1998; 98US-085296P.
XX PA (HARD ) HARVARD COLLEGE.
XX PI Erikson RL, Lee KS;
XX DR WPI; 2002-314756/35.
XX PT Administering polo kinase inhibitors for the treatment of cancers and
XX PT fungal infections
XX PS Example 1; Column 59-64; 47pp; English.
XX CC The invention describes a method of inhibiting growth of an isolated
XX CC population of cells by inhibiting a cell polo kinase by administering a
XX CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX CC carboxy terminal domain of the polo kinase which excludes the polo
XX CC kinase catalytic domain. The method is used for the treatment of cancer
XX CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, and the
XX CC cervix), the epithelium, the brain, the retina, the prostate, and the
XX CC throat, infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX CC This is the amino acid sequence of the polo like kinase (Plk), a
XX CC protein from which mitotic protein polo kinase inhibitory peptides are
XX CC derived.
XX SQ Sequence 603 AA;
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGKPPFE 9
DE 244 LLVGKPPFE 252

```

```

DE XX Mouse polo-like kinase (Plk) T2:0D mutant.
KW Polo box; PBI; cytostatic; fungicide; protozoicide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutcin.
XX OS Mus musculus.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 210
XX FT /note= "Wild type Thr substituted by Asp"
XX PN US6358738-B1.
XX PD 19-MAR-2002.
XX PF 13-MAY-1999; 99US-0311311.
XX PR 13-MAY-1998; 98US-085296P.
XX PA (HARD ) HARVARD COLLEGE.
XX PI Erikson RL, Lee KS;
XX DR WPI; 2002-314756/35.
XX PT Administering polo kinase inhibitors for the treatment of cancers and
XX PT fungal infections
XX PS Example 1; Page 1; 47pp; English.
XX CC The invention describes a method of inhibiting growth of an isolated
XX CC population of cells by inhibiting a cell polo kinase by administering a
XX CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX CC carboxy terminal domain of the polo kinase which excludes the polo
XX CC kinase catalytic domain. The method is used for the treatment of cancer
XX CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, and the
XX CC cervix), the epithelium, the brain, the retina, the prostate, and the
XX CC throat, infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX CC mutant, used to determine the residues required for kinase activity.
XX CC Note: This sequence does not appear in the specification but has been
XX CC created from the wild type sequence shown in AAU79306 using information
XX CC given in the invention.
XX SQ Sequence 603 AA;
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGKPPFE 9
DB 244 LLVGKPPFE 252
RESULT 25
AAU79309
ID AAU79309 standard; Peptide; 603 AA.
XX AC AAU79309;
XX DT 02 JUL-2002 (first entry)
XX DE Mouse polo-like kinase (Plk) T2:0E mutant.
XX XX

```

KW Polo box; PBl; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
 XX
 OS Mus musculus.
 CS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 210 /note= "Wild type Thr substituted by Glu"
 FT
 XX
 XX
 PN US6358738-B1.
 XX
 XX 19-MAR-2002.
 XX
 PD
 XX
 PF 13-MAY-1999; 98US-0311311.
 XX
 XX 13-MAY-1998; 98US-085296P.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA
 XX Erikson RL, Lee KS;
 PI
 XX
 XX
 DR WPI; 2002-314756/35.
 XX
 XX
 PT Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections .
 PT
 XX
 PS Example 1; Page : 47pp; English.
 XX
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79310 using information
 CC given in the invention.
 XX
 SQ Sequence 603 AA;
 Query Match 87.8%; Score 43; DB 23; Length 603;
 Best Local Similarity 77.8%; Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGKPPPE 9
 Db :|||:|
 244 LLVGKPPPE 252
 RESULT 26
 AAU79310
 ID AAU79310 standard; Peptide; 603 AA.
 XX
 AC AAU79310;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Mouse polo-like kinase (Plk) T210V mutant.
 XX
 KW Polo box; PBl; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;

KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
 XX
 OS Mus musculus.
 CS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 210 /note= "Wild type Thr substituted by Val"
 FT
 XX
 XX
 PN US6358738-B1.
 XX
 XX 19-MAR-2002.
 XX
 PD
 XX
 PF 13-MAY-1999; 98US-0311311.
 XX
 XX 13-MAY-1998; 98US-085296P.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA
 XX Erikson RL, Lee KS;
 PI
 XX
 XX
 DR WPI; 2002-314756/35.
 XX
 XX
 PT Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections .
 PT
 XX
 PS Example 1; Page : 47pp; English.
 XX
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information
 CC given in the invention.
 XX
 SQ Sequence 603 AA;
 Query Match 87.8%; Score 43; DB 23; Length 603;
 Best Local Similarity 77.8%; Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGKPPPE 9
 Db :|||:|
 244 LLVGKPPPE 252
 RESULT 27
 AAU79311
 ID AAU79311 standard; Peptide; 603 AA.
 XX
 AC AAU79311;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Mouse polo-like kinase (Plk) E206V mutant.
 XX
 KW Polo box; PBl; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;

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KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW thyroid cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 206 /note= "Wild type Glu substituted by Val"
XX
XX US6358738-B1.
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99JUS-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections -
XX
XX Example 1; Page -; 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk);
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
SQ Sequence 603 AA;
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
:|:|:|:|
Db 244 LLVGKPPPE 252

RESULT 28
AAU79312
ID AAU79312 standard; Peptide: 603 AA.
XX
XX AAU79312;
AC
XX AAU79312;
DT 02-JUL-2002 (first entry)
XX
XX Mouse polo-like kinase (Plk) E206N mutant.
XX
XX Polo box; PBI; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.

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KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 206 /note= "Wild type Glu substituted by Asn"
XX
XX US6358738-B1.
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99JUS-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections -
XX
XX Example 1; Page -; 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk);
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
SQ Sequence 603 AA;
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
:|:|:|:|
Db 244 LLVGKPPPE 252

RESULT 29
AAU79313
ID AAU79313 standard; Peptide: 603 AA.
XX
XX AAU79313;
AC
XX AAU79313;
DT 02-JUL-2002 (first entry)
XX
XX Mouse polo-like kinase (Plk) E206V/T210V mutant.
XX
XX Polo box; PBI; cytostatic; fungicide; protozoacide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.

```



```

XX Mus musculus.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 206 /note= "Wild type Glu substituted by Val"
FT
FI Misc-difference 210 /note= "Wild type Thr substituted by Val"
FT
XX
XX US6358738-B1.
XX
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections
XX
XX Example 1; Page -: 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
XX Sequence 603 AA;
SQ
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CY 1 MLGKPPFE 9
DB 244 LLVGKPPFE 252
:::|||||
RESULT 30
AAU79314
ID AAU79314 standard; Peptide; 603 AA.
XX
XX AAU79314;
AC
XX 02-JUL-2002 (first entry)
DT
XX
XX Mouse polo-like kinase (Plk) D:94N mutant.
DE
XX
XX Polo box; Pbl; cyostatic; fungicide; protozoicide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.
KW

```

```

XX Mus musculus.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 194 /note= "Wild type Asp substituted by Asn"
FT
XX
XX US6358738-B1.
XX
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections
XX
XX Example 1; Page -: 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
XX Sequence 603 AA;
SQ
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
CY 1 MLGKPPFE 9
DB 244 LLVGKPPFE 252
:::|||||
RESULT 31
AAU79315
ID AAU79315 standard; Peptide; 603 AA.
XX
XX AAU79315;
AC
XX 02-JUL-2002 (first entry)
DT
XX
XX Mouse polo-like kinase (Plk) D:94R mutant.
DE
XX
XX Polo box; Pbl; cyostatic; fungicide; protozoicide; antihelminthic;
KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
KW cancer of the uterus; ovarian cancer; cervical cancer;
KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.
XX
XX Mus musculus.
OS

```

```

OS Synthetic.
FH Key Location/Qualifiers
FT Misc difference 194 /note= "Wild type Asp substituted by Arg"
XX
XX US6358738-B1.
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99US-031131.1.
XX
XX 13-MAY-1998; 98US-085296P.
XX (HARD ) HARVARD COLLEGE.
XX Erikson RL, Lee KS;
XX WPI; 2002-314756/35.
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections -
XX Example 1; Page -; 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Pik)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
XX Sequence 603 AA;
XX
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 3; Gaps 0;
QY 1 MLGKPPFE 9
DB 244 LLVGKPPFE 252
RESULT 32
AAU79316
ID AAU79316 standard; Peptide; 603 AA.
XX
XX AAU79316;
XX
XX 02 JUL 2002 (first entry)
XX
XX Mouse polo-like kinase (Pik) K28X mutant.
XX
XX Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX cancer of the uterus; ovarian cancer; cervical cancer;
XX epithelial cancer; brain cancer; retina cancer; prostate cancer;
XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;
XX Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX arthropod infection; mouse; polo-like kinase; Pik; mutant; mutain.
XX
XX Mus musculus.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc difference 415
XX

```

```

FH Key Location/Qualifiers
FT Misc difference 28 /note= "Wild type Lys substituted by Met"
XX
XX US6358738-B1.
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99US-031131.1.
XX
XX 13-MAY-1998; 98US-085296P.
XX (HARD ) HARVARD COLLEGE.
XX Erikson RL, Lee KS;
XX WPI; 2002-314756/35.
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections -
XX Example 2; Page -; 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Pik)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
XX Sequence 603 AA;
XX
Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGKPPFE 9
DB 244 LLVGKPPFE 252
RESULT 33
AAU79317
ID AAU79317 standard; Peptide; 603 AA.
XX
XX AAU79317;
XX
XX 02 JUL 2002 (first entry)
XX
XX Mouse polo-like kinase (Pik) V415A mutant.
XX
XX Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX cancer of the uterus; ovarian cancer; cervical cancer;
XX epithelial cancer; brain cancer; retina cancer; prostate cancer;
XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;
XX Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX arthropod infection; mouse; polo-like kinase; Pik; mutant; mutain.
XX
XX Mus musculus.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc difference 415
XX

```

/note= "wild type Val substituted by Ala"

FT XX US6358738-B1.
 PN XX
 PD XX 19-MAR-2002.
 XX
 PF XX 13-MAY-1999; 99US-0311311.
 XX
 PR XX 13-MAY-1999; 98US-085296P.
 XX
 PA XX (HARD) HARVARD COLLEGE.
 XX
 PI Erikson RL, Lee KS;
 XX
 DR WPI; 2002-3:4756/35.
 XX

PT Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections
 XX
 PS Example 7; Page : 47pp; English.
 XX

CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information
 CC given in the invention.
 XX

SQ Sequence 603 AA;

Query Match 87.8%; Score 43; DB 23; Length 603;
 Best Local Similarity 77.8%; Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
 |||
 DB 244 LLVGKPPPE 252

RESULT 34

AAU79316
 ID AAU79316 standard; Peptide: 603 AA.
 XX
 AC AAU79316;
 XX

DT 02-JUL-2002 (first entry)

DE Mouse polo like kinase (Plk); L427A mutant.

XX Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.

OS Mus musculus.
 OS Synthetic.

FT Key Location/Qualifiers
 FT Misc-difference 427

PN /note= "wild type Lys substituted by Ala"

PN US6358738-B1.

PD 19-MAR-2002.

PF 13-MAY-1999; 99US-0311311.

PR 13-MAY-1999; 98US-085296P.

PA (HARD) HARVARD COLLEGE.

PI Erikson RL, Lee KS;

DR WPI; 2002-3:4756/35.

PT Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections

PS Example 7; Page : 47pp; English.

CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information
 CC given in the invention.
 XX

SQ Sequence 603 AA;

Query Match 87.8%; Score 43; DB 23; Length 603;
 Best Local Similarity 77.8%; Pred. No. 13;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
 |||
 DB 244 LLVGKPPPE 252

RESULT 35

AAU79319
 ID AAU79319 standard; Peptide: 603 AA.
 XX
 AC AAU79319;
 XX

DT 02-JUL-2002 (first entry)

DE Mouse polo-like kinase (Plk); M437I mutant.

XX Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.

OS Mus musculus.
 OS Synthetic.

FT Key Location/Qualifiers
 FT Misc-difference 437

PN /note= "wild type Asn substituted by Ile"

PN US6358738-B1.

```

PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
XX WP1; 2002-314756/35.
DR
XX Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections.
XX
XX Example 7; Page -: 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (PLK)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;

Query Match: 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. NO. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLUGKPPFE 9
LF 244 LLVGKPPFE 252

RESULT 36
AAU79320
XX AAU79320 standard; Peptide; 603 AA.
XX
XX AAU79320;
XX
XX 02-JUL-2002 (first entry)
XX
XX Mouse polo-like kinase (PLK) W414P/T2100 mutant.
XX
XX Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
XX arthropodicide; Mitotic protein polo kinase; polo kinase inhibitor;
XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX cancer of the uterus; ovarian cancer; cervical cancer;
XX epithelial cancer; brain cancer; retina cancer; prostate cancer;
XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;
XX Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX arthropod infection; mouse; polo-like kinase; PLK; mutant; mutain.
XX
XX Yus musculus.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX
XX MISC-difference 414
XX /note="Wild type Trp substituted by Phe"
XX
XX MISC-difference 210
XX /note="Wild type Thr substituted by Asp"
XX
XX US6359738-B1.
XX

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PD 19-MAR-2002.
XX
PF 13-MAY-1999; 99US-0311311.
XX
PR 13-MAY-1998; 98US-085296P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Erikson RL, Lee KS;
XX
XX WP1; 2002-314756/35.
DR
XX Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections.
XX
XX Example 10; Page -: 47pp; English.
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (PLK)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
SQ Sequence 603 AA;

Query Match: 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. NO. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLUGKPPFE 9
DB 244 LLVGKPPFE 252

RESULT 37
ABR48196
XX ABR48196 standard; Protein; 603 AA.
XX
XX ABR48196;
XX
XX 12-JUN-2003 (first entry)
XX
XX Human bladder cancer associated protein sequence SEQ ID NO.110.
XX
XX Human; bladder cancer; cytostatic; gene therapy; vaccine.
XX
XX Homo sapiens.
XX
XX WO2003003906-A2.
XX
XX 16-JAN-2003.
XX
XX 03-JUL-2002; 2002WO-US21338.
XX
XX 03-JUL-2001; 2001US-302814P.
XX
XX 03-AUG-2001; 2001US-310099P.
XX
XX 08-NOV-2001; 2001US-343705P.
XX
XX 13-NOV-2001; 2001US-350666P.
XX
XX 12-APR-2002; 2002US-372246P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Mack DH, Aziz N.
XX

```

DR WPI: 2003-201532/19.
 XX N-PSDB; ACCS1009.
 PT Detecting a bladder cancer-associated transcript in a cell from a
 PT patient, comprises contacting a biological sample from the patient with
 PT a bladder cancer-associated polynucleotide or antibody.
 XX
 PS Claim 10; Page 269; 307pp; English.
 XX
 CC The present invention describes a method for detecting a bladder cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with a polynucleotide
 CC that selectively hybridises to a sequence that is 80 % identical to a
 CC table of sequences (see ACCS095; to ACCS1059). ACCS095 to ACCS1059
 CC encode the human bladder cancer-associated proteins given in ABR48146 to
 CC ABR48242). Bladder cancer-associated sequences from the present invention
 CC have cytostatic activities, and can be used in antisense gene therapy and
 CC in vaccine production. The method can be used for detecting a bladder
 CC cancer associated transcript in a cell from a patient. The method is
 CC useful in diagnosing or treating bladder cancer and in screening for
 CC compounds that modulate bladder cancer, such as hormones or antibodies.
 CC The nucleic acid molecules from the present invention may be used in
 CC various screening and diagnostic methods, and for gene therapy, vaccine
 CC and/or antisense/inhibition applications.
 XX
 SQ Sequence 603 AA;
 Query Match 87.8%; Score 43; DB 24; Length 603;
 Best Local Similarity 77.8%; Pred No. 13;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 XLGKPPFE 9
 DB 244 LVGKPPFE 252
 RESULT OK
 AAW18084
 ID AAW18084 standard; Protein; 403 AA.
 XX
 AC AAW18084;
 XX
 DT 07-SEP-1997 (first entry)
 XX
 DE Human Aurora-2.
 XX
 KW Aurora-2; AUR-2; signal transduction; protein kinase; tumour;
 KW cancer; protein kinase; gene therapy; diagnosis; antibody.
 XX
 OS Homo sapiens.
 XX
 FE Key Location/Qualifiers
 FT Domain 1..130
 FT /label= N-terminal_domain
 FT Domain 131..403
 FT /label= Kinase_domain
 FT Misc-difference 50
 FT /note= "deduced residue from some cDNA clones is
 FT Leu"
 FT Misc-difference 57
 FT /note= "deduced residue from some cDNA clones is
 FT Ile"
 FT Modified-site 288
 FT /label= Phosphorylation;
 FT /note= "cAMP-dependent protein kinase
 FT phosphorylation site conserved in AUR-2
 FT and yeast and Drosophila homologues"
 FT Modified-site 334
 FT /label= Phosphorylation
 FT /note= "tyrosine phosphorylation consensus site
 FT conserved in Drosophila aurora but not
 FT in AUR-1 or yeast IPL1"
 FT Modified-site 342

FT /label= Phosphorylation
 FT /note= "cAMP-dependent protein kinase
 FT phosphorylation site conserved in AUR-2
 FT and yeast and Drosophila homologues"
 FT Misc-difference 50
 FT /note= "deduced residue from some cDNA clones is
 FT Leu"
 FT Misc-difference 57
 FT /note= "deduced residue from some cDNA clones is
 FT Ile"
 XX
 PN W09722702-A1.
 XX
 PD 26-JUN-1997.
 XX
 PF 25-NOV-1996; 96WO-US18859.
 XX
 PR 14-AUG-1996; 96US-0023943.
 PR 18-DEC-1995; 95US-0008909.
 XX
 PA (SUGB-) SUGEN INC.
 XX
 PI Mossie KG, Plowman GD;
 XX
 DR WPI: 1997-341693/31.
 DR N-PSDB; AAT67290.
 XX
 PT Aurora-1 and Aurora-2 and related genes - useful in tumour gene
 PT therapy
 XX
 PS Claim 3; Page 83-85; 98pp; English.
 XX
 CC Novel human proteins, termed Aurora-1 (AAW18083) and Aurora-2
 CC (AAW18084) (AUR-1 and AUR-2), are related serine/threonine kinases
 CC with short N-terminal extensions that appear to be involved in
 CC cancer and/or signal transduction disorders. Their amino acid
 CC sequences were deduced from pancreatic tumour cDNA clones (AAT67289-
 CC 90). AUR-1 and AUR-2 appear to regulate nuclear division, with
 CC disruption of their signaling resulting in polyploid cells. AUR-2
 CC RNA is low or absent in most normal tissues, and abundant in a
 CC subset of tumour-derived cell lines, partic. those of colorectal
 CC origin. AUR polypeptides can be expressed in host cells and used
 CC to raise diagnostic antibodies and to screen for compounds that
 CC interact with AUR-1 and/or AUR-2.
 XX
 SQ Sequence 403 AA;
 Query Match 83.7%; Score 41; DB 18; Length 403;
 Best Local Similarity 87.5%; Pred No. 20;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DLGKPPFE 9
 DB 323 LVGKPPFE 330
 RESULT 39
 AAY22476
 ID AAY22476 standard; Protein; 403 AA.
 XX
 AC AAY22476;
 XX
 DT 29-SEP-1999 (first entry);
 XX
 DE Human AUR2 protein sequence.
 XX
 KW AUR1; AUR2; human; AUR modulator; cancer; glioma; medullablastoma;
 KW chondrosarcoma; pancreatic tumour; proliferative disease; diagnosis;
 KW therapy.
 XX
 OS Homo sapiens.
 XX
 PN W09937788-A2.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 13:23:00 ; Search time 11.8286 Seconds
(without alignments)
32.193 Million cell updates/sec

Title: US-09-736-076-17

Perfect score: 49

Sequence: MLLGKPPPE 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 423:0858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Xatch 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:

- 1: /cgn2_6/prodata/1/aa/5A_CCMB.pep:
- 2: /cgn2_6/prodata/1/aa/5B_CCMB.pep:
- 3: /cgn2_6/prodata/1/aa/5A_CCMB.pep:
- 4: /cgn2_6/prodata/1/aa/5B_CCMB.pep:
- 5: /cgn2_6/prodata/1/aa/5A_CCMB.pep:
- 6: /cgn2_6/prodata/1/aa/5B_CCMB.pep:

Note: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	3	US-08-861-338-17
2	46	93.9	9	3	US-08-861-338-15
3	46	93.9	9	3	US-08-861-338-13
4	46	93.9	272	1	US-08-861-338-12
5	46	93.9	272	2	US-08-834-108-12
6	46	93.9	685	2	US-08-878-589-1
7	46	93.9	685	3	US-09-136-282-2
8	46	93.9	685	3	US-09-272-796-1
9	46	93.9	685	3	US-09-505-744-2
10	44	89.8	8	3	US-08-861-338-16
11	43	87.8	20	3	US-08-861-338-6
12	43	87.8	272	1	US-08-252-995D-14
13	43	87.8	272	2	US-08-834-108-14
14	43	87.8	603	3	US-09-198-122-2
15	43	87.8	603	4	US-09-311-311-C-26
16	41	83.7	275	1	US-08-252-995D-13
17	41	83.7	275	2	US-08-834-108-13
18	41	83.7	403	2	US-08-755-728-4
19	41	83.7	403	2	US-08-974-655-4
20	41	83.7	403	3	US-09-283-011-4
21	39	79.6	264	2	US-07-857-224B-17
22	39	79.6	271	1	US-08-252-995D-12
23	39	79.6	271	2	US-08-834-108-11
24	38	77.6	273	1	US-08-252-995D-10
25	38	77.6	273	2	US-08-834-108-10
26	38	77.6	344	2	US-08-755-728-3
27	38	77.6	344	2	US-08-974-655-3

28	38	77.6	344	3	US-09-283-011-3	Sequence 3, Appl
29	38	77.6	347	2	US-09-016-000-1	Sequence 1, Appl
30	38	77.6	416	1	US-08-252-995D-2	Sequence 2, Appl
31	38	77.6	464	1	US-08-834-108-2	Sequence 2, Appl
32	38	77.6	464	1	US-08-252-995D-6	Sequence 6, Appl
33	38	77.6	464	2	US-08-834-108-6	Sequence 6, Appl
34	38	77.6	737	4	US-09-772-647-4	Sequence 4, Appl
35	38	77.6	925	1	US-08-252-995D-4	Sequence 4, Appl
36	38	77.6	925	2	US-08-834-108-4	Sequence 4, Appl
37	38	77.6	1037	4	US-09-428-711A-21	Sequence 21, Appl
38	37	75.5	9	3	US-08-861-338-18	Sequence 18, Appl
39	37	75.5	20	3	US-08-861-338-3	Sequence 3, Appl
40	37	75.5	264	2	US-07-857-224B-10	Sequence 10, Appl
41	37	75.5	269	2	US-07-857-224B-15	Sequence 15, Appl
42	37	75.5	269	2	US-07-857-224B-14	Sequence 14, Appl
43	37	75.5	269	2	US-07-857-224B-16	Sequence 16, Appl
44	37	75.5	499	4	US-09-509-902A-12	Sequence 12, Appl
45	37	75.5	588	4	US-09-509-902A-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-861-338-17
; Sequence 17, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: ~~Sanofi-Schering-Plough~~ A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Gamma Benzyl Ester of
; OTHER INFORMATION: Glutamine Acid-NH2"
US-08-861-338-17

Query Match 100.0%; Score 49; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
 |||||
 CB 1 MLLGKPPPE 9

RESULT 2
 US-08-861-338-15
 ; Sequence 15, Application US/08861338
 ; Patent No. 617499;
 ; GENERAL INFORMATION:
 ; APPLICANT: Ben-Sasson, Shmuel A.
 ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/861-338
 ; FILING DATE: 21-MAY-1997
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brook, David E.
 ; REGISTRATION NUMBER: 22,592
 ; REFERENCE/DOCKET NUMBERS: CMCC-590
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (781) 861-6240
 ; TELEFAX: (781) 861-9540
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amine acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 1
 ; OTHER INFORMATION: /note= "N-Acetyl Methionine"

QY 1 MLLGKPPPE 9
 |||||
 CB 1 MLLGKPPPE 9

RESULT 1
 US-08-861-338-19
 ; Sequence 19, Application US/08861338
 ; Patent No. 617499;
 ; GENERAL INFORMATION:
 ; APPLICANT: Ben-Sasson, Shmuel A.
 ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/861-338
 ; FILING DATE: 21-MAY-1997
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brook, David E.
 ; REGISTRATION NUMBER: 22,592
 ; REFERENCE/DOCKET NUMBERS: CMCC-590
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (781) 861-6240
 ; TELEFAX: (781) 861-9540
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amine acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 1
 ; OTHER INFORMATION: /note= "N-Acetyl Methionine"

Query Match 93.9%; Score 46; DB 3; Length 9;
 Best Local Similarity 88.9%; Pred. No. 2.5e+05;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
 |||||
 CB 1 MLLGKPPPE 9

RESULT 1
 US-08-861-338-19
 ; Sequence 19, Application US/08861338
 ; Patent No. 617499;
 ; GENERAL INFORMATION:
 ; APPLICANT: Ben-Sasson, Shmuel A.
 ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/861-338
 ; FILING DATE: 21-MAY-1997
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brook, David E.
 ; REGISTRATION NUMBER: 22,592
 ; REFERENCE/DOCKET NUMBERS: CMCC-590
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (781) 861-6240
 ; TELEFAX: (781) 861-9540
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amine acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide
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 ; NAME/KEY: Modified-site
 ; LOCATION: 1
 ; OTHER INFORMATION: /note= "N-Acetyl Methionine"

APPLICANT: Ben-Sasson, Shmuel A.
 TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/861-338
 FILING DATE: 21-MAY-1997
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Brook, David E.
 REGISTRATION NUMBER: 22,592
 REFERENCE/DOCKET NUMBERS: CMCC-590
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781) 861-6240
 TELEFAX: (781) 861-9540
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amine acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /note= "N-Acetyl Methionine"

QY 1 MLLGKPPPE 9
 |||||
 CB 1 MLLGKPPPE 9

RESULT 4
 US-08-252-995D-12
 ; Sequence 12, Application US/09252995D
 ; Patent No. 5650501
 ; GENERAL INFORMATION:
 ; APPLICANT: Dennis, James W
 ; APPLICANT: Heffernan, Mike
 ; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BERESKIN & PARR
 ; STREET: 40 King Street West
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada

Query Match 93.9%; Score 46; DB 3; Length 11;
 Best Local Similarity 88.9%; Pred. No. 0.013;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
 |||||
 CB 1 MLLGKPPPE 9

CY 1 MLLGKPPPE 9
|||.||||
DB 273 MLLGPPPE 281

RESULT 7
US-09-136-282 2
; Sequence 2, Application US/09136282
; Patent No. 6063609
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, KAREN
; APPLICANT: JACKSON, JEFFREY
; APPLICANT: HANSBURY, MICHAEL
; APPLICANT: NERURKAR, SANDHYA
; APPLICANT: ROSHAK, AMY
; APPLICANT: BOUZYSK, MARK
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rauter & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136.282
; FILING DATE: 20-AUG-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,112
; FILING DATE: 20-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-722:1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-136-282-2

Query Match 93.9%; Score 46; DB 3; Length 685;
Best Local Similarity 88.9%; Pred. No. 0.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLLGKPPPE 9
|||.||||
DB 273 MLLGPPPE 281

RESULT 8
US-09-272-796.1
; Sequence 1, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.

; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272.796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVENOB01
; CLONE: 39043
US-09-272-796-1

Query Match 93.9%; Score 46; DB 3; Length 685;
Best Local Similarity 88.9%; Pred. No. 0.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLLGKPPPE 9
|||.||||
DB 273 MLLGPPPE 281

RESULT 9
US-09-505-744-2
; Sequence 2, Application US/09505744
; Patent No. 6245544
; GENERAL INFORMATION:
; APPLICANT: Karen M. Anderson
; APPLICANT: Mark M. Bouzyk
; APPLICANT: Michael J. Hansbury
; APPLICANT: Jeffrey R. Jackson
; APPLICANT: Sandhya S. Neturkar
; APPLICANT: Amy K. Roshak
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; FILE REFERENCE: GH-70231-D1
; CURRENT APPLICATION NUMBER: US/09/505.744
; CURRENT FILING DATE: 2000-C2-16
; EARLIER APPLICATION NUMBER: 09/136.282
; EARLIER FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 60/056,112
; EARLIER FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2
LENGTH: 685
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-505-744-2

Query Match 93.9% Score 46; DB 3; Length 685;
Best Local Similarity 88.9%; Pred. No. 2.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGKPPFE 9
|||
Db 273 LLVGKPPFE 281

RESULT 10

US-08-861-338-16

Sequence 16, Application US/08861338

Patent No. 6174993

GENERAL INFORMATION:

APPLICANT: Ben-Sasson, Shmuel A.

TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY

MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/861,338

FILING DATE: 21-MAY-1997

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: CMCC-590

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781) 861-6240

TELEFAX: (781) 861-9540

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note= "N-Acetyl Methionine"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 8

OTHER INFORMATION: /note= "phenylalanine NH2"

US-08-861-338-16

Query Match 89.8% Score 44; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGKPPFE 8

|||||

Db 1 MLGKPPFE 8

RESULT 11

US-08-861-338-6

Sequence 6, Application US/08861338

Patent No. 6174993

GENERAL INFORMATION:

APPLICANT: Ben-Sasson, Shmuel A.

TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY

MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/861,338

FILING DATE: 21-MAY-1997

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: CMCC-590

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781) 861-6240

TELEFAX: (781) 861-9540

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

US-08-861-338-6

Query Match 87.8% Score 43; DB 3; Length 20;

Best Local Similarity 77.8%; Pred. No. 0.087;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGKPPFE 9

|||||

Db 3 LLVGKPPFE 11

RESULT 12

US-08-252-995D-14

Sequence 14, Application US/09252995D

Patent No. 5650501

GENERAL INFORMATION:

APPLICANT: Dennis, James W

APPLICANT: Heffernan, Mike

APPLICANT: Fode, Carol

TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: BERESKIN & PARR

STREET: 40 King Street West

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5H 3Y2

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

```

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/252,995D
3 FILING DATE: 02-JUN-1994
4 CLASSIFICATION: 536
5 ATTORNEY/AGENT INFORMATION:
6 NAME: Kurdydyk, Linda M
7 REGISTRATION NUMBER: 34,971
8 REFERENCE/DOCKET NUMBER: 3153 9#
9 TELECOMMUNICATION INFORMATION:
10 TELEPHONE: (416) 364-7311
11 TELEFAX: (416) 361-1398
12 INFORMATION FOR SEQ ID NO: 14:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 272 amino acids
15 TYPE: amino acid
16 STRANDEDNESS: single
17 TOPOLOGY: linear
18 MOLECULE TYPE: peptide
19 ORIGINAL SOURCE:
20 ORGANISM: Mus musculus
21 US-08 252-995D-14
22
23 Query Match 87.8%; Score 43; DB 1; Length 272;
24 Best Local Similarity 77.8%; Pred. No. 1.3;
25 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
26
27 QY 1 MLVGKPPPE 9
28 :||:||||
29 DB 199 LLVGKPPPE 207
30
31 RESULT 13
32 US-08-834-108-14
33 Sequence 14, Application US/08834108
34 Patent No. 5976893
35 GENERAL INFORMATION:
36 APPLICANT: Dennis, James W
37 APPLICANT: Heffernan, Mike
38 APPLICANT: Fode, Carol
39 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
40 NUMBER OF SEQUENCES: 14
41 CORRESPONDENCE ADDRESS:
42 ADDRESSEE: HRESKIN & PARR
43 STREET: 40 King Street West
44 CITY: Toronto
45 STATE: Ontario
46 COUNTRY: Canada
47 ZIP: M5H 3Y2
48 COMPUTER READABLE FORM:
49 MEDIUM TYPE: Floppy disk
50 COMPUTER: IBM PC compatible
51 OPERATING SYSTEM: PC-DOS/MS DOS
52 SOFTWARE: Patent Release #1.0, Version #1.10
53 CURRENT APPLICATION DATA:
54 APPLICATION NUMBER: US/08/834,108
55 FILING DATE:
56 CLASSIFICATION: 536
57 ATTORNEY/AGENT INFORMATION:
58 NAME: Kurdydyk, Linda M
59 REGISTRATION NUMBER: 34,971
60 REFERENCE/DOCKET NUMBER: 3153-210
61 TELECOMMUNICATION INFORMATION:
62 TELEPHONE: (416) 364-7311
63 TELEFAX: (416) 361-1398
64 INFORMATION FOR SEQ ID NO: 14:
65 SEQUENCE CHARACTERISTICS:
66 LENGTH: 272 amino acids
67 TYPE: amino acid
68 STRANDEDNESS: single
69 TOPOLOGY: linear
70 MOLECULE TYPE: peptide
71 ORIGINAL SOURCE:
72 ORGANISM: Mus musculus

```

```

US-08-834-108-14
Query Match 87.8%; Score 43; DB 2; Length 272;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLVGKPPPE 9
:||:||||
DB 199 LLVGKPPPE 207
RESULT 14
US-09-198-122-2
Sequence 2, Application US/09198122
Patent No. 6180180
GENERAL INFORMATION:
APPLICANT: Streibhardt, Klaus; Rubsammen-Waigmann, Helga;
APPLICANT: Holtzrich, Jwe
TITLE OF INVENTION: CLONING OF A MEMBER OF THE SERINE-
TITLE OF INVENTION: THREONINE-KINASE FAMILY
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRUNG HORN KRAMER & WOODS
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
MEDIUM TYPE: storage
COMPUTER: NEC Powermate SX-20
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/198,122
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/601,014
FILING DATE: 23-FEB-1996
APPLICATION NUMBER: PCT/EP94/02863
FILING DATE: 30-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4329177
FILING DATE: 30-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9516-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1703
TELEFAX: (914) 332-1844
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 603 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-09-198-122-2
Query Match 87.8%; Score 43; DB 3; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLVGKPPPE 9
:||:||||
DB 244 LLVGKPPPE 252
RESULT 15
US-09-311-311C-2#

```

; Sequence 26, Application US/C931111C
; Patent No. 6358738
; GENERAL INFORMATION:
; APPLICANT: Erikson, et al.
; TITLE OF INVENTION: POLO BOX THERAPEUTIC COMPOSITIONS,
; FILE REFERENCE: 1874/117
; CURRENT APPLICATION NUMBER: US/09/311.311C
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/395,296
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(603)
; OTHER INFORMATION: plx protein
US-09-311-311C-26

Query Match 87.8%; Score 43; DB 4; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY : MLLGKPPFE 9
Db 244 LLIGKPPFQ 252

RESULT 16
US-08-252-995D-13
; Sequence 13, Application US/C8252995D
; Patent No. 5652501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252.995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae

; ORGANISM: Saccharomyces cerevisiae
US-08-252-995D-13
Query Match 83.7%; Score 41; DB 1; Length 275;
Best Local Similarity 66.7%; Pred. No. 3.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPFE 9
Db 200 LLIGKPPFQ 208

RESULT 17
US-08-834-108-13
; Sequence 13, Application US/C8834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834.108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 275 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
US-08-834-108-13

Query Match 83.7%; Score 41; DB 2; Length 275;
Best Local Similarity 66.7%; Pred. No. 3.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLLGKPPFE 9
Db 200 LLIGKPPFQ 208

RESULT 18
US-08-755-728-4
; Sequence 4, Application US/08755728
; Patent No. 5962312
; GENERAL INFORMATION:
; APPLICANT: P. O'Mann, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1

```

1  TITLE OF INVENTION:  AND/OR AUR-2 RELATED DISORDERS
2  NUMBER OF SEQUENCES:  29
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE:  Lyon & Lyon
5  STREET:  633 West Fifth Street
6  CITY:  Suite 4700
7  STATE:  Los Angeles
8  COUNTRY:  California
9  ZIP:  90071-2066
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
12 MEDIUM TYPE:  storage
13 COMPUTER:  IBM Compatible
14 OPERATING SYSTEM:  IBM P.C. DOS 5.0
15 SOFTWARE:  FastSEQ for Windows 2.0
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER:  US/08/755,728
18 FILING DATE:  August 14, 1996
19 PRIORITY APPLICATION DATA:
20 APPLICATION NUMBER:  5962312ember 25, 1996
21 CLASSIFICATION:  530
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER:  60/008,809
24 FILING DATE:  December 18, 1995
25 APPLICATION NUMBER:  60/023,943
26 FILING DATE:  August 14, 1996
27 ATTORNEY/AGENT INFORMATION:
28 NAME:  Wartburg, Richard J.
29 REGISTRATION NUMBER:  32,327
30 REFERENCE/DOCKET NUMBER:  223/113
31 TELEPHONE:  (213) 489-1600
32 TELEFAX:  (213) 955-0440
33 TELEX:  67-3510
34 INFORMATION FOR SEQ ID NO:  4:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH:  403 amino acids
37 TYPE:  amino acid
38 STRANDEDNESS:  single
39 TOPOLOGY:  linear
40 MOLECULE TYPE:  protein
41 HYPOTHETICAL:  NO
42 ANTI-SENSE:  NO
43 US-08-736-076-17-4

```

```

Query Match      83.7%; Score 41; DB 2; Length 403;
Best Local Similarity 87.5%; Pred. No. 4.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2  LKGPPE 9
DB      323  LKGPPE 330

```

```

RESULT 14
US-08-974 655-4
1  Sequence 4, Application US/08974655
2  Patent No. 5972676
3  GENERAL INFORMATION:
4  APPLICANT:  Picman, Gregory
5  APPLICANT:  Mossie, Kevin
6  TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF AUR-1
7  NUMBER OF SEQUENCES:  29
8  CORRESPONDENCE ADDRESS:
9  ADDRESSEE:  Lyon & Lyon
10 STREET:  633 West Fifth Street
11 CITY:  Suite 4700
12 STATE:  Los Angeles
13 COUNTRY:  California
14 ZIP:  90071-2066
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE:  3.5" Diskette, 1.44 Mb

```

```

1  MEDIUM TYPE:  storage
2  COMPUTER:  IBM Compatible
3  OPERATING SYSTEM:  IBM P.C. DOS 5.0
4  SOFTWARE:  FastSEQ for Windows 2.0
5  CURRENT APPLICATION DATA:
6  APPLICATION NUMBER:  US/08/974,655
7  FILING DATE:
8  CLASSIFICATION:  435
9  PRIOR APPLICATION DATA:
10 APPLICATION NUMBER:  08/755,728
11 FILING DATE:  No. 5972676ember 25, 1996
12 APPLICATION NUMBER:  60/008,809
13 FILING DATE:  December 18, 1995
14 APPLICATION NUMBER:  60/023,943
15 FILING DATE:  August 14, 1996
16 ATTORNEY/AGENT INFORMATION:
17 NAME:  Wartburg, Richard J.
18 REGISTRATION NUMBER:  32,327
19 REFERENCE/DOCKET NUMBER:  223/113
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE:  (213) 489-1600
22 TELEFAX:  (213) 955-0440
23 TELEX:  67-3510
24 INFORMATION FOR SEQ ID NO:  4:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH:  403 amino acids
27 TYPE:  amino acid
28 STRANDEDNESS:  single
29 TOPOLOGY:  linear
30 MOLECULE TYPE:  protein
31 HYPOTHETICAL:  NO
32 ANTI-SENSE:  NO
33 US-08-974-655-4

```

```

Query Match      83.7%; Score 41; DB 2; Length 403;
Best Local Similarity 87.5%; Pred. No. 4.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2  LKGPPE 9
DB      323  LKGPPE 330

```

```

RESULT 20
US-09-283-011-4
1  Sequence 4, Application US/09283011
2  Patent No. 6207401
3  GENERAL INFORMATION:
4  APPLICANT:  Picman, Gregory
5  APPLICANT:  Mossie, Kevin
6  TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF AUR-1
7  NUMBER OF SEQUENCES:  39
8  CORRESPONDENCE ADDRESS:
9  ADDRESSEE:  Lyon & Lyon
10 STREET:  633 West Fifth Street
11 CITY:  Suite 4700
12 STATE:  Los Angeles
13 COUNTRY:  California
14 ZIP:  90071-2066
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
17 MEDIUM TYPE:  storage
18 COMPUTER:  IBM Compatible
19 OPERATING SYSTEM:  IBM P.C. DOS 5.0
20 SOFTWARE:  FastSEQ for Windows 2.0
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER:  US/09/283,011
23 FILING DATE:
24 CLASSIFICATION:
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER:  09/012,135

```

```

; FILING DATE: January 22, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: NO. 6207401ember 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYDROPHILIC: NO
; ANTI-SENSE: NO
; US-09-253-011-4

Query Match 83.6% Score 417 DB 3: Length 403;
Best Local Similarity 87.5% Pred. No. 4.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMGKPPFE 9
DB 123 LVGQPPFE 330

RESULT 2:
US-07-857-224B-17
; Sequence 17, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) 8005 12
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 4: 1 632 3930
; TELEFAX: (International) 4: 2 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster

```

```

; FEATURE: Protein kinase; Table 8 Column 18
; PUBLICATION INFORMATION:
; AUTHORS: Hanks, S. K.
; AUTHORS: Quinn, A. M.
; AUTHORS: Hunter, T.
; TITLE: The protein kinase family
; JOURNAL: Science
; VOLUME: 241
; PAGES: 42-52
; DATE: 1988
; US-07-857-224B-17

Query Match 79.6% Score 39; DB 2; Length 264;
Best Local Similarity 66.7% Pred. No. 7;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
DB 195 MLVGQPPFD 203

RESULT 22
US-08-252-995D-11
; Sequence 11, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdzyk, Linda X
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
; US-08-252-995D-11

Query Match 79.6% Score 39; DB 1; Length 271;
Best Local Similarity 66.7% Pred. No. 7.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
DB 198 LLVGQPPFE 206

```

```

RESULT 23
US-08-834-108-11
; Sequence 11, Application US/08934108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdvdyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
US-08-834-108-11

Query Match 79.6%; Score 39; DB 2; Length 271;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
Db 198 LLVGPPPE 206

RESULT 24
US-08-252-995D-10
; Sequence 10, Application US/08252995D
; Patent No. 5650561
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdvdyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-252-995D-10

Query Match 77.6%; Score 38; DB 1; Length 273;
Best Local Similarity 55.6%; Pred. No. 11;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
Db 200 LLGKPPPE 208

RESULT 25
US-08-834-108-10
; Sequence 10, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdvdyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

```



```
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
US-08-834-108-10

Query Match 77.6%; Score 38; DB 2; Length 344;
Best Local Similarity 55.6%; Pred. No. 14;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
DB 200 LLVGPNPPE 208

RESULT 28
US-08-755-728-3
; Sequence 3, Application US/08755728
; Patent No. 5962312
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,728
; FILING DATE: No. 5962312e-ber 25, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-755-728-3

Query Match 77.6%; Score 38; DB 2; Length 344;
Best Local Similarity 55.6%; Pred. No. 14;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
DB 200 LLVGPNPPE 208
```

```
DB 266 LLVGPNPPE 274

RESULT 27
US-08-974-655-3
; Sequence 3, Application US/08974655
; Patent No. 5972676
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,655
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 5972676ember 25, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 62/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-974-655-3

Query Match 77.6%; Score 38; DB 2; Length 344;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
DB 266 LLVGPNPPE 274

RESULT 28
US-09-283-011-3
; Sequence 3, Application US/C9283011
; Patent No. 6207421
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
```

1 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR 1
2 TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
3 NUMBER OF SEQUENCES: 39
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: Lyon & Lyon
6 STREET: 633 West Fifth Street
7 STREET: Suite 4700
8 CITY: Los Angeles
9 STATE: California
10 COUNTRY: U.S.A.
11 ZIP: 90071-2066
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
15 MEDIUM TYPE: storage
16 COMPUTER: IBM Compatible
17 OPERATING SYSTEM: IBM P.C. DOS 5.0
18 SOFTWARE: FastSeq for Windows 2.0
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/09/283,011
21 FILING DATE:
22 CLASSIFICATION:
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 09/012,135
25 FILING DATE: January 22, 1998
26 APPLICATION NUMBER: 08/755,728
27 FILING DATE: NO. 627401ember 25, 1996
28 APPLICATION NUMBER: 60/023,943
29 FILING DATE: August 14, 1996
30 APPLICATION NUMBER: 60/008,809
31 FILING DATE: December 18, 1995
32 ATTORNEY/AGENT INFORMATION:
33 NAME: Walburg, Richard J.
34 REGISTRATION NUMBER: 32,329
35 REFERENCE/DOCKET NUMBER: 321/282
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: (213) 489-1600
38 TELEFAX: (213) 955-0440
39 TELEX: 67-3512
40
41 INFORMATION FOR SEQ ID NO: 3:
42 SEQUENCE CHARACTERISTICS:
43 LENGTH: 344 amino acids
44 TYPE: amino acid
45 STRANDEDNESS: single
46 TOPOLOGY: linear
47 MOLECULE TYPE: protein
48 HYDROTHERMAL: NO
49 ANTI-SENSE: NO
50 US-09-283 011.3
51
52 Query Match 77.6% Score 38; DB 1; Length 344;
53 Best Local Similarity 66.7%; Pred. No. 14;
54 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
55
56 QY 1 MLLGKPPPE 9
57 1 1 1 1 1
58 DB 266 LLVGNPPPE 274
59 1 1 1 1 1
60
61 RESULT 39
62 US-09-016-000-1
63 Sequence 1, Application US/09016000
64 Patent No. 5962232
65 GENERAL INFORMATION:
66 APPLICANT: Hillman, Jennifer L.
67 APPLICANT: Lai, Preeti
68 APPLICANT: Bandman, Olga
69 APPLICANT: Aketblom, Ingrid E.
70 APPLICANT: Shah, Purvi
71 APPLICANT: Corley, Neil C.
72 APPLICANT: Guebler, Karl G.
73 TITLE OF INVENTION: PROTEIN KINASE MOLECULES
74 NUMBER OF SEQUENCES: 12
75 CORRESPONDENCE ADDRESS:

1 ADDRESSEE: Incyte Pharmaceuticals, Inc.
2 STREET: 3174 Porter Drive
3 CITY: Palo Alto
4 STATE: CA
5 COUNTRY: USA
6 ZIP: 94304
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Diskette
9 COMPUTER: IBM Compatible
10 OPERATING SYSTEM: DOS
11 SOFTWARE: FastSeq for Windows Version 2.0
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/09/016,000
14 FILING DATE: HEREWITH
15 CLASSIFICATION:
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER:
18 FILING DATE:
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Billings, Lucy J.
21 REGISTRATION NUMBER: 36,749
22 REFERENCE/DOCKET NUMBER: PF-0465 US
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: 650-855-0555
25 TELEFAX: 650-845-4166
26 TELEX:
27 INFORMATION FOR SEQ ID NO: 1:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 347 amino acids
30 TYPE: amino acid
31 STRANDEDNESS: single
32 TOPOLOGY: linear
33 IMMEDIATE SOURCE:
34 LIBRARY: HMCINOT01
35 CLONE: 2943
36 US-09-016-000-1
37
38 Query Match 77.6% Score 38; DB 2; Length 347;
39 Best Local Similarity 66.7%; Pred. No. 14;
40 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
41
42 QY 1 MLLGKPPPE 9
43 1 1 1 1 1
44 DB 269 LLVGNPPPE 277
45 1 1 1 1 1
46
47 RESULT 30
48 US-08-252-9950-2
49 Sequence 2, Application US/08252995D
50 Patent No. 5659501
51 GENERAL INFORMATION:
52 APPLICANT: Dennis, James W
53 APPLICANT: Hefferman, Mike
54 APPLICANT: Fode, Carol
55 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
56 NUMBER OF SEQUENCES: 14
57 CORRESPONDENCE ADDRESS:
58 ADDRESSEE: BERESKIN & PARR
59 STREET: 40 King Street West
60 CITY: Toronto
61 STATE: Ontario
62 COUNTRY: Canada
63 ZIP: M5H 3Y2
64
65 COMPUTER READABLE FORM:
66 MEDIUM TYPE: Floppy disk
67 COMPUTER: IBM PC compatible
68 OPERATING SYSTEM: PC-DOS/MS-DOS
69 SOFTWARE: Patent In Release #1.0, Version #1.30
70 CURRENT APPLICATION DATA:
71 APPLICATION NUMBER: US/08/252,995D
72 FILING DATE: 02-JUN-1994
73 CLASSIFICATION: 536
74 ATTORNEY/AGENT INFORMATION:

```

; NAME: Kurdvdyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-06-252-995D-2

```

```

Query Match 77.6%; Score 38; DB 1; Length 416;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MLLGKPPPE 9
Db 204 LLIGRPPFD 212

```

```

RESULT 31
US-08-834-108-2
; Sequence 2, Application US/58834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdvdyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-213
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 416 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-834-108-2

```

```

Query Match 77.6%; Score 38; DB 2; Length 416;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MLLGKPPPE 9
Db 204 LLIGRPPFD 212

```

```

RESULT 32
US-08-252-995D-6
; Sequence 6, Application US/08252395D
; Patent No. 5850501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdvdyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-252-995D-6

```

```

Query Match 77.6%; Score 38; DB 1; Length 464;
Best Local Similarity 55.6%; Pred. No. 19;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MLLGKPPPE 9
Db 204 LLIGRPPFD 212

```

```

RESULT 33
US-08-834-108-6
; Sequence 6, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 364-1398
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-834-108-6

Query Match 77.6%; Score 38; DB 2; Length 464;
Best Local Similarity 55.6%; Pred. No. 19;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
DB 204 LLIGRPPD 212

RESULT 34
US-09-772-647-4
Sequence 4, Application US/C9772647
Patent No. 65218:5
GENERAL INFORMATION:
APPLICANT: Verma, Ajit K
APPLICANT: Reddig, Peter J
APPLICANT: Jansen, Aaron P
TITLE OF INVENTION: Animal Model System for Squamous Cell Carcinoma
FILE REFERENCE: 960296, 97613
CURRENT APPLICATION NUMBER: US/99/772,647
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 737
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 17 tag and
OTHER INFORMATION: mouse protein kinase C epsilon coding sequence
US-09-772-647-4

Query Match 77.6%; Score 38; DB 4; Length 737;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
DB 600 MMAGQPPPE 608

RESULT 35
US-08-252-995D-4
Sequence 4, Application US/08/252995D
Patent No. 56505:1
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto

STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-252-995D-4

Query Match 77.6%; Score 38; DB 1; Length 925;
Best Local Similarity 55.6%; Pred. No. 39;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
DB 204 LLIGRPPD 212

RESULT 36
US-08-834-108-4
Sequence 4, Application US/08834:08
Patent No. 597699:3
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 amino acids
TYPE: amino acid

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;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-834-108-4
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;   Query Match      77.6%; Score 18; DB 2; Length 925;
;   Best Local Similarity 55.6%; Pred. No. 19;
;   Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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;   QY 1 MLLGKPPFE 9
;       : : : : :
;   Db 264 LVLGKPPFE 212
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;   RESULT 37
;   US-09-428-711A-21
;   ; Sequence 21; Application US/09428711A
;   ; Patent No. 6358720
;   ; GENERAL INFORMATION:
;   ; APPLICANT: Muramatsu, Masaaki
;   ; APPLICANT: Shirasawa, Takuji
;   ; APPLICANT: Tokumitsu, Hiroshi
;   ; APPLICANT: No. 6358720uchi, Teruhisa
;   ; TITLE OF INVENTION: SERINE/THREONINE PROTEIN KINASE
;   ; FILE REFERENCE: C6501-C45001
;   ; CURRENT APPLICATION NUMBER: US/09/428-711A
;   ; CURRENT FILING DATE: 1999-10-28
;   ; PRIOR APPLICATION NUMBER: PCT/JP98/C1246
;   ; PRIOR FILING DATE: 1998-03-23
;   ; PRIOR APPLICATION NUMBER: JP 9/124798
;   ; PRIOR FILING DATE: 1997-04-28
;   ; NUMBER OF SEQ ID NOS: 21
;   ; SOFTWARE: FastSeq for Windows Version 4.0
;   ; SEQ ID NO 21
;   ; LENGTH: 1037
;   ; TYPE: PRI
;   ; ORGANISM: Mus musculus
;   ; US-09-428-711A-21
;
;   Query Match      77.6%; Score 18; DB 4; Length 1037;
;   Best Local Similarity 75.0%; Pred. No. 44;
;   Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
;
;   QY 2 LVLGKPPFE 9
;       : : : : :
;   Db 208 LVLGKPPFE 215
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;
;   RESULT 38
;   US-08-861-338-19
;   ; Sequence 18; Application US/08861338
;   ; Patent No. 674993
;   ; GENERAL INFORMATION:
;   ; APPLICANT: Ben-Sasson, Shmuel A.
;   ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
;   ; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
;   ; NUMBER OF SEQUENCES: 22
;   ; CORRESPONDENCE ADDRESS:
;   ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;   ; STREET: Two Militia Drive
;   ; CITY: Lexington
;   ; STATE: Massachusetts
;   ; COUNTRY: USA
;   ; ZIP: 02173
;   ; COMPUTER READABLE FORM:
;   ; MEDIUM TYPE: Floppy disk
;   ; COMPUTER: IBM PC compatible
;   ; OPERATING SYSTEM: PC-DOS/MS-DOS
;   ; SOFTWARE: PatentIn Release #1.0, Version #1.30
;   ; CURRENT APPLICATION DATA:
;   ; APPLICATION NUMBER: US/08/861.338
;   ; FILING DATE: 21-MAY-1997
;   ; CLASSIFICATION: 514
;   ; ATTORNEY/AGENT INFORMATION:
;   ; NAME: Brook, David E.
;   ; REGISTRATION NUMBER: 22,592
;   ; REFERENCE/DOCKET NUMBER: CMCC-590
;   ; TELECOMMUNICATION INFORMATION:
;   ; TELEPHONE: (781) 861-6240
;   ; TELEFAX: (781) 861-9540
;   ; INFORMATION FOR SEQ ID NO: 3:
;   ; SEQUENCE CHARACTERISTICS:
;   ; LENGTH: 20 amino acids
;   ; TYPE: amino acid
;   ; STRANDEDNESS: not relevant
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;   US-08-861-338-3
;   ; Sequence 3; Application US/08861338
;   ; Patent No. 6174993
;   ; GENERAL INFORMATION:
;   ; APPLICANT: Ben-Sasson, Shmuel A.
;   ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
;   ; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
;   ; NUMBER OF SEQUENCES: 22
;   ; CORRESPONDENCE ADDRESS:
;   ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;   ; STREET: Two Militia Drive
;   ; CITY: Lexington
;   ; STATE: Massachusetts
;   ; COUNTRY: USA
;   ; ZIP: 02173
;   ; COMPUTER READABLE FORM:
;   ; MEDIUM TYPE: Floppy disk
;   ; COMPUTER: IBM PC compatible
;   ; OPERATING SYSTEM: PC-DOS/MS-DOS
;   ; SOFTWARE: PatentIn Release #1.0, Version #1.30
;   ; CURRENT APPLICATION DATA:
;   ; APPLICATION NUMBER: US/08/861.338
;   ; FILING DATE: 21-MAY-1997
;   ; CLASSIFICATION: 514
;   ; ATTORNEY/AGENT INFORMATION:
;   ; NAME: Brook, David E.
;   ; REGISTRATION NUMBER: 22,592
;   ; REFERENCE/DOCKET NUMBER: CMCC-590
;   ; TELECOMMUNICATION INFORMATION:
;   ; TELEPHONE: (781) 861-6240
;   ; TELEFAX: (781) 861-9540
;   ; INFORMATION FOR SEQ ID NO: 3:
;   ; SEQUENCE CHARACTERISTICS:
;   ; LENGTH: 20 amino acids
;   ; TYPE: amino acid
;   ; STRANDEDNESS: not relevant
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;   Query Match      75.5%; Score 37; DB 3; Length 9;
;   Best Local Similarity 85.7%; Pred. No. 2.5e+05;
;   Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
;   QY 3 LGRPPFE 9
;       : : : : :
;   Db 1 LGRPPFE 7
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;
;   RESULT 39
;   US-08-861-338-3
;   ; Sequence 3; Application US/08861338
;   ; Patent No. 6174993
;   ; GENERAL INFORMATION:
;   ; APPLICANT: Ben-Sasson, Shmuel A.
;   ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
;   ; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
;   ; NUMBER OF SEQUENCES: 22
;   ; CORRESPONDENCE ADDRESS:
;   ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;   ; STREET: Two Militia Drive
;   ; CITY: Lexington
;   ; STATE: Massachusetts
;   ; COUNTRY: USA
;   ; ZIP: 02173
;   ; COMPUTER READABLE FORM:
;   ; MEDIUM TYPE: Floppy disk
;   ; COMPUTER: IBM PC compatible
;   ; OPERATING SYSTEM: PC-DOS/MS-DOS
;   ; SOFTWARE: PatentIn Release #1.0, Version #1.30
;   ; CURRENT APPLICATION DATA:
;   ; APPLICATION NUMBER: US/08/861.338
;   ; FILING DATE: 21-MAY-1997
;   ; CLASSIFICATION: 514
;   ; ATTORNEY/AGENT INFORMATION:
;   ; NAME: Brook, David E.
;   ; REGISTRATION NUMBER: 22,592
;   ; REFERENCE/DOCKET NUMBER: CMCC-590
;   ; TELECOMMUNICATION INFORMATION:
;   ; TELEPHONE: (781) 861-6240
;   ; TELEFAX: (781) 861-9540
;   ; INFORMATION FOR SEQ ID NO: 3:
;   ; SEQUENCE CHARACTERISTICS:
;   ; LENGTH: 20 amino acids
;   ; TYPE: amino acid
;   ; STRANDEDNESS: not relevant
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Job time : 11.8286 secs

TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-861-338-3

Query Match: 75.5%; Score 37; DB 3; Length: 20;
Best Local Similarity 66.7%; Pred. No. 1.2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
DB 3 MLGQPPFD 11

RESULT 40
US-07-857-224B-10
Sequence 10; Application US/07857224B
Patent No. 5959784
GENERAL INFORMATION:
APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 15;
CITY: Zurich
STATE: none
COUNTRY: Switzerland
ZIP: note: this is an international post code: CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIORITY APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2810
TELEFAX: (International) 41 1 262 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 264
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: bovine
FEATURE: Protein Kinase; Table 8 Column 1;
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
VOLUME: 241
PAGES: 42-52
DATE: 1988
US-07-857-224B-10

Query Match: 75.5%; Score 37; DB 2; Length: 264;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
DB 195 MLGQPPFD 203

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OW protein - Protein search, using sw mode:

Run on: November 14, 2003, 13:38:35 ; Search time 22.3/14 Seconds
(without alignments)
73.443 Million cell updates/sec

Title: US-09-736-076-17

Perfect score: 49

Sequence: 1 MLLGKPPPE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 666:88 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666:88

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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- 2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/1/pubaa/US08_PUBCCMB.pep.*
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- 15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCCMB.pep.*
- 16: /cgn2_6/ptodata/1/pubaa/US10C_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/1/pubaa/US10C_PUBCCMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	9	9	US-09-736-076-17
2	46	93.9	9	9	Sequence 15, Appl
3	46	93.9	10	9	US-09-736-076-57
4	46	93.9	11	9	Sequence 19, Appl
5	46	93.9	400	15	US-10-026-021-5
6	46	93.9	469	15	US-10-059-585-14
7	46	93.9	685	10	US-09-771-161A-249
8	46	93.9	685	10	US-09-771-161A-250
9	46	93.9	685	10	US-09-771-161A-251
10	46	93.9	685	12	US-10-024-238A-101
11	46	93.9	685	12	US-09-763-97C-1
12	46	93.9	685	12	US-10-042-211A-101
13	44	89.8	8	9	US-09-736-076-16
14	43	87.8	20	9	US-09-736-076-6
15	43	87.8	329	10	US-09-923-330-1266

16	43	87.8	367	15	US-10-026-021-6	Sequence 6, Appl
17	43	87.8	516	10	US-09-771-161A-123	Sequence 123, App
18	43	87.8	528	12	US-10-032-585-7571	Sequence 7571, Ap
19	43	87.8	603	10	US-09-771-161A-214	Sequence 214, App
20	43	87.8	603	15	US-10-171-311-186	Sequence 186, App
21	41	83.7	256	11	US-09-898-837A-32	Sequence 32, Appl
22	41	83.7	403	9	US-09-012-135A-4	Sequence 4, Appl
23	41	83.7	403	15	US-10-026-021-7	Sequence 7, Appl
24	41	83.7	403	15	US-10-059-585-33	Sequence 33, Appl
25	41	83.7	403	15	US-10-209-324-2	Sequence 2, Appl
26	39	79.6	40	10	US-09-842-582-9	Sequence 9, Appl
27	39	79.6	122	10	US-09-515-806-24	Sequence 24, Appl
28	39	79.6	183	15	US-10-172-088-12	Sequence 12, Appl
29	38	77.6	8	9	US-09-736-076-55	Sequence 55, Appl
30	38	77.6	344	9	US-09-012-135A-3	Sequence 3, Appl
31	38	77.6	344	15	US-10-059-585-34	Sequence 34, Appl
32	38	77.6	344	15	US-10-171-311-214	Sequence 214, App
33	38	77.6	347	10	US-09-974-298-136	Sequence 136, App
34	38	77.6	348	12	US-10-291-253A-16	Sequence 16, App
35	38	77.6	379	15	US-10-026-021-3	Sequence 3, Appl
36	38	77.6	419	10	US-09-893-737-106	Sequence 106, App
37	38	77.6	627	9	US-09-949-970-2	Sequence 2, Appl
38	38	77.6	627	9	US-09-738-626-3546	Sequence 3546, Ap
39	38	77.6	737	10	US-09-771-161A-195	Sequence 195, App
40	38	77.6	737	15	US-10-228-931-4	Sequence 4, Appl
41	38	77.6	970	15	US-10-026-021-2	Sequence 2, Appl
42	38	77.6	970	9	US-09-736-076-18	Sequence 18, Appl
43	37	75.5	20	9	US-09-736-076-3	Sequence 3, Appl
44	37	75.5	445	10	US-09-836-392-15	Sequence 15, Appl

ALIGNMENTS

RESULT :

US-09-736-076-17
; Sequence 17, Application US/C9736076
; Patent No. US2002049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Gasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: J43.1
US-09-736-076-17

Query Match 100.0%; Score 49; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.9e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGKPPPE 9

Db 1 MLLGKPPPE 9

RESULT 2

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US-09-736-076-15
; Sequence 15, Application US/09736076
; Patent No. US2002049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242.1015-009
; CURRENT FILING DATE: 2003-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (9)...(9)
; OTHER INFORMATION: J42
US-09-736-076-15

Query Match 93.9%; Score 46; DB 9; Length 9;
Best Local Similarity 88.9%; Pred. No. 5.9e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : MLLGKPPPE 9
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CD : MLLGKPPPE 9

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US-09-736-076-57
; Sequence 57, Application US/09736076
; Patent No. US2002049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242.1015-009
; CURRENT FILING DATE: 2003-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MYRISTATE
; LOCATION: (1)...(10)
; OTHER INFORMATION: position 10 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (10)...(10)
; OTHER INFORMATION: SNK
US-09-736-076-57

Query Match 93.9%; Score 46; DB 9; Length 10;
Best Local Similarity 88.9%; Pred. No. 6.077;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : MLLGKPPPE 9
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CD : MLLGKPPPE 10

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RESULT 4
US-09-736-076-19
; Sequence 19, Application US/09736076
; Patent No. US2002049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242.1015-009
; CURRENT FILING DATE: 2003-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(10)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (9)...(11)
; OTHER INFORMATION: J46
US-09-736-076-19

Query Match 93.9%; Score 46; DB 9; Length 11;
Best Local Similarity 88.9%; Pred. No. 0.085;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : 1 MLLGKPPPE 9
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DB : 1 MLLGKPPPE 9

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RESULT 5
US-10-026-021-5
; Sequence 5, Application US/10026021
; Publication No. US2003027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi Yasutich;
; APPLICANT: Demo, Susan;
; APPLICANT: Jenkins, Yonchu;
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; FILE REFERENCE: C21044-001210US
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US/10/026,021
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(400)
; OTHER INFORMATION: human SNK mitotic kinase kinase domain
US-10-026-021-5

Query Match 93.9%; Score 46; DB 15; Length 400;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : 1 MLLGKPPPE 9
   |||:||||
DB : 273 MLLGKPPPE 281

```


RESULT 6

US-10-059-585-14
 ; Sequence 14, Application US/10059585
 ; Publication No. US2003008276A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ota, Toshio
 ; APPLICANT: Isogai, Takao
 ; APPLICANT: Nishikawa, Tetsuo
 ; APPLICANT: Hayashi, Koji
 ; APPLICANT: Otsuka, Kaoru
 ; APPLICANT: Yamamoto, Jun-ichi
 ; APPLICANT: Ishii, Shizuko
 ; APPLICANT: Sugiyama, Tomoyasu
 ; APPLICANT: Wakamatsu, Ai
 ; APPLICANT: Nagai, Keiichi
 ; APPLICANT: Otsuki, Tetsuji
 ; APPLICANT: Funahashi, Shin-ichi
 ; APPLICANT: Senoo, Chiaki
 ; APPLICANT: Nezu, Jun-ichi
 ; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
 ; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
 ; FILE REFERENCE: 06501-098001
 ; CURRENT APPLICATION NUMBER: US/10/059,585
 ; CURRENT FILING DATE: 2002-01-29
 ; PRIOR APPLICATION NUMBER: PCT/JP00/35060
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: US 60/183,322
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: US 60/159,590
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: JP 2000-118776
 ; PRIOR FILING DATE: 2000-05-11
 ; PRIOR APPLICATION NUMBER: JP 2000-183767
 ; PRIOR FILING DATE: 2000-05-02
 ; PRIOR APPLICATION NUMBER: JP 11-248336
 ; PRIOR FILING DATE: 1999-07-29
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 14
 ; LENGTH: 469
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-059-585 14

Query Match 93.9%; Score 46; DB 15; Length 469;
 Best Local Similarity 88.9%; Pred. No. 3.6;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY

1 MLGKPPFE 9

|||||

Db

57 MLGRRPFE 65

RESULT 7

US-09-771-161A-249
 ; Sequence 249, Application US/09771161A
 ; Patent No. US20020110811A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, et al.
 ; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 ; FILE REFERENCE: 802620-2005.1
 ; CURRENT APPLICATION NUMBER: US/09/771,161A
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 09/724,676
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 136776
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 135619
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 273
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 249

; LENGTH: 685
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-771-161A-249

Query Match 93.9%; Score 46; DB 10; Length 685;
 Best Local Similarity 88.9%; Pred. No. 5.2;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy

1 MLGKPPFE 9

|||||

Db

273 MLGRRPFE 281

RESULT 8

US-09-771-161A-250
 ; Sequence 250, Application US/09771161A
 ; Patent No. US20020110811A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, et al.
 ; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 ; FILE REFERENCE: 802620-2005.1
 ; CURRENT APPLICATION NUMBER: US/09/771,161A
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 09/724,676
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 136776
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 135619
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 273
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 250
 ; LENGTH: 685
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-771-161A-250

Query Match 93.9%; Score 46; DB 10; Length 685;
 Best Local Similarity 88.9%; Pred. No. 5.2;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy

1 MLGKPPFE 9

|||||

Db

273 MLGRRPFE 281

RESULT 9

US-09-771-161A-251
 ; Sequence 251, Application US/09771161A
 ; Patent No. US20020110811A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, et al.
 ; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 ; FILE REFERENCE: 802620-2005.1
 ; CURRENT APPLICATION NUMBER: US/09/771,161A
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 09/724,676
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 136776
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 135619
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 273
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 251
 ; LENGTH: 685
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-771-161A-251

Query Match 93.9%; Score 46; DB 10; Length 685;
 Best Local Similarity 88.9%; Pred. No. 5.2;

```
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CY 1 MLGKPPPE 9
    |||||
DB 273 MLGKPPPE 281

RESULT 10
US-10-024-298A-101
; Sequence 101, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAH KASEI KASUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAWATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 6C/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254218/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101:
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-101

Query Match 93.9%; Score 46; DB 12; Length 685;
Best Local Similarity 88.9%; Pred. No. 5.2;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGKPPPE 9
    |||||
DB 273 MLGKPPPE 281

RESULT 11
US-09-769-970-1
; Sequence 1, Application US/09769970
; Publication No. US20030170219A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hailman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegier, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
```

```
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769,970
FILING DATE: 24-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/272,796
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-032; US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-3555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 685 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: HUVEBO01
CLONE: 39043
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-769-970-1

Query Match 93.9%; Score 46; DB 12; Length 685;
Best Local Similarity 88.9%; Pred. No. 5.2;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGKPPPE 9
    |||||
DB 273 MLGKPPPE 281

RESULT 12
US-10-042-211A-101
; Sequence 101, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NFkB Activating Gene
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101:
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-101

Query Match 93.9%; Score 46; DB 12; Length 685;
Best Local Similarity 88.9%; Pred. No. 5.2;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      1 MLGKPPPE 9
      1 :|||
Db      273 MLGKPPPE 281

RESULT 13
US-09-736-076-16
; Sequence 16, Application US/09736076
; Patent No. US20020349301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-039
; CURRENT APPLICATION NUMBER: US/09/736.076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861.338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PR
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(8)
; NAME/KEY: AMIDATION
; LOCATION: (10)...(8)
; OTHER INFORMATION: J43
US-09-736-076-16

Query Match      89.8%; Score 43; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.9e+05;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 MLGKPPPE 8
      1 :|||
Db      1 MLGKPPPE 8

RESULT 14
US-09-736-076-6
; Sequence 6, Application US/09736076
; Patent No. US20020349301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-039
; CURRENT APPLICATION NUMBER: US/09/736.076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861.338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PR
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: POLO
US-09-736-076-6

Query Match      87.8%; Score 43; DB 9; Length 20;
Best Local Similarity 77.8%; Pred. No. 3.52;
Matches      7; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

```

```

RESULT 15
US-09-925-300-1268
; Sequence 1268, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925.300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124.270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1268
; LENGTH: 329
; TYPE: PR
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (59)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (307)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (308)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (314)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (317)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (323)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (327)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (328)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (329)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1268

Query Match      87.8%; Score 43; DB 10; Length 329;
Best Local Similarity 77.8%; Pred. No. 8.5;
Matches      7; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

QY      1 MLGKPPPE 9
      1 :|||
Db      260 LLVGKPPPE 268

RESULT 16
US-10-026-021-6
; Sequence 6, Application US/10026021
; Publication No. US2003027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi Yasumichi
; APPLICANT: Demo, Susan
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.

```

1 TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
2 TITLE OF INVENTION: Treatment of Cancer
3 FILE REFERENCE: 021044-001210US
4 CURRENT APPLICATION NUMBER: US/10/026,021
5 CURRENT FILING DATE: 2002-06-25
6 PRIOR APPLICATION NUMBER: US 60/309,632
7 PRIOR FILING DATE: 2001-08-01
8 NUMBER OF SEQ ID NOS: 8
9 SOFTWARE: PatentIn Ver. 2.1
10 SEQ ID NO 6
11 LENGTH: 167
12 TYPE: PRT
13 ORGANISM: Homo sapiens
14 FEATURE:
15 NAME/KEY: DOMAIN
16 LOCATION: 11...1367;
17 OTHER INFORMATION: human PKC: mitotic kinase kinase domain
18 US-10-026-021-6

Query Match 87.8%; Score 43; DB 15; Length 167;
Best Local Similarity 77.8%; Pred. No. 9.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
DB 244 LLVGKPPPE 252

RESULT 19
US-09-771-161A-123
1 Sequence 123, Application US/09771161A
2 Patent No. US20020110811A1
3 GENERAL INFORMATION:
4 APPLICANT: LEVINE, et al.
5 TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
6 FILE REFERENCE: 802620-2005.1
7 CURRENT APPLICATION NUMBER: US/09771161A
8 CURRENT FILING DATE: 2001-01-26
9 PRIOR APPLICATION NUMBER: 09/724,676
10 PRIOR FILING DATE: 2000-11-28
11 PRIOR APPLICATION NUMBER: 136776
12 PRIOR FILING DATE: 2000-06-15
13 PRIOR APPLICATION NUMBER: 135619
14 PRIOR FILING DATE: 2000-04-12
15 NUMBER OF SEQ ID NOS: 273
16 SOFTWARE: PatentIn version 3.0
17 SEQ ID NO 123
18 LENGTH: 516
19 TYPE: PRT
20 ORGANISM: Homo sapiens
21 US-09-771-161A-123

Query Match 87.8%; Score 43; DB 10; Length 516;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
DB 157 LLVGKPPPE 165

RESULT 18
US-10-032-585-742;
1 Sequence 7571, Application US/10032585;
2 Publication No. US20030180953A1
3 GENERAL INFORMATION:
4 APPLICANT: Terry, Roemer D.
5 APPLICANT: Bo, Jiang
6 APPLICANT: Charles, Boone
7 APPLICANT: Howard, Bussey
8 TITLE OF INVENTION: Gene Disruption Technologies for Drug Target Discovery
9 FILE REFERENCE: 10182-005-999
10 CURRENT APPLICATION NUMBER: US/10-032-585

1 CURRENT FILING DATE: 2001-12-20
2 NUMBER OF SEQ ID NOS: 8000
3 SOFTWARE: PatentIn version 3.1
4 SEQ ID NO 7571
5 LENGTH: 528
6 TYPE: PRT
7 ORGANISM: Candida albicans
8 US-10-032-585-7571

Query Match 87.8%; Score 43; DB 12; Length 528;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
DB 454 LLVGKPPPE 462

RESULT 19
US-09-771-161A-214
1 Sequence 214, Application US/09771161A
2 Patent No. US20020110811A1
3 GENERAL INFORMATION:
4 APPLICANT: LEVINE, et al.
5 TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
6 FILE REFERENCE: 802620-2005.1
7 CURRENT APPLICATION NUMBER: US/09771161A
8 CURRENT FILING DATE: 2001-01-26
9 PRIOR APPLICATION NUMBER: 09/724,676
10 PRIOR FILING DATE: 2000-11-28
11 PRIOR APPLICATION NUMBER: 136776
12 PRIOR FILING DATE: 2000-06-15
13 PRIOR APPLICATION NUMBER: 135619
14 PRIOR FILING DATE: 2000-04-12
15 NUMBER OF SEQ ID NOS: 273
16 SOFTWARE: PatentIn version 3.0
17 SEQ ID NO 214
18 LENGTH: 603
19 TYPE: PRT
20 ORGANISM: Homo sapiens
21 US-09-771-161A-214

Query Match 87.8%; Score 43; DB 10; Length 603;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
DB 244 LLVGKPPPE 242

RESULT 20
US-10-171-311-186
1 Sequence 186, Application US/0171311;
2 Publication No. US200308727CA1
3 GENERAL INFORMATION:
4 APPLICANT: Schlegel, Robert
5 APPLICANT: Chen, Yan
6 APPLICANT: Zhao, Xumei
7 APPLICANT: Monahan, John
8 APPLICANT: Kamatkar, Shubhangi
9 APPLICANT: Glatt, Karen
10 APPLICANT: Gannavarapu, Manjula
11 APPLICANT: Hoersch, Sebastian
12 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
13 TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
14 TITLE OF INVENTION: OF CERVICAL CANCER
15 FILE REFERENCE: MRI-035
16 CURRENT APPLICATION NUMBER: US/10/171,311
17 CURRENT FILING DATE: 2002-06-12
18 PRIOR APPLICATION NUMBER: US 60/298,159
19 PRIOR FILING DATE: 2001-06-13
20 PRIOR APPLICATION NUMBER: US 60/298,155

? PRIOR FILING DATE: 2001-06-13
 ? PRIOR APPLICATION NUMBER: US 60/335,936
 ? PRIOR FILING DATE: 2001-11-14
 ? NUMBER OF SEQ ID NOS: 238
 ? SOFTWARE: FastSeq for Windows Version 4.0
 ? SEQ ID NO 186
 ? LENGTH: 603
 ? TYPE: PRT
 ? ORGANISM: Homo sapiens
 US-10-171-311-186

Query Match 87.8%; Score 41; DB 15; Length 603;
 Best Local Similarity 77.8%; Pred. No. 16;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LUGKPPPE 9
 DB 244 LUGKPPPE 252

RESULT 21
 US-09-898-837A-32
 ? Sequence 32, Application US/09898837A
 ? Publication No. US2003007697A:
 ? GENERAL INFORMATION:
 ? APPLICANT: Quinn, Kerry E.
 ? APPLICANT: Spytex, Kimberly A.
 ? APPLICANT: Majumder, Kumud
 ? APPLICANT: Vernet, Corine
 ? APPLICANT: Herrmann, John E.
 ? APPLICANT: Burgess, Catherine
 ? APPLICANT: Fernandes, Elma
 ? APPLICANT: Taupier, Jr., Raymond
 ? APPLICANT: Rastelli, Luca
 ? APPLICANT: Curaden Corporation
 ? APPLICANT: Gerlach, Valerie L.
 ? APPLICANT: MacDougall, John R.
 ? TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN KINASE LIKE PROTEINS AND
 ? TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THE SAME
 ? FILE REFERENCE: 15966-598 CIP
 ? CURRENT APPLICATION NUMBER: US/03/098,837A
 ? CURRENT FILING DATE: 2001-07-03
 ? PRIOR APPLICATION NUMBER: U.S.S.N. 60/155,986
 ? PRIOR FILING DATE: 1999-11-17
 ? PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,819
 ? PRIOR FILING DATE: 2000-04-05
 ? PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,631
 ? PRIOR FILING DATE: 2000-04-07
 ? PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,730
 ? PRIOR FILING DATE: 2000-04-13
 ? PRIOR APPLICATION NUMBER: U.S.S.N. 60/214,672
 ? PRIOR FILING DATE: 2000-09-15
 ? PRIOR APPLICATION NUMBER: U.S.S.N. 60/191,347
 ? PRIOR FILING DATE: 2000-02-09
 ? PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195
 ? PRIOR FILING DATE: 2000-04-03
 ? PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,926
 ? PRIOR FILING DATE: 2000-07-03
 ? PRIOR APPLICATION NUMBER: U.S.S.N. 09/715,427
 ? PRIOR FILING DATE: 2000-11-16
 ? NUMBER OF SEQ ID NOS: 53
 ? SOFTWARE: PatentIn Ver. 2.1
 ? SEQ ID NO 32
 ? LENGTH: 256
 ? TYPE: PRT
 ? ORGANISM: Saccharomyces cerevisiae
 US-09-898-837A-32

Query Match 83.7%; Score 41; DB 15; Length 256;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 LUGKPPPE 9

Db 193 LUGKPPFQ 201
 RESULT 22
 US-09-012-135A-4
 ? Sequence 4, Application US/09012135A
 ? Patent No. US20020081578A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Plowman, Gregory
 ? APPLICANT: Mossie, Kevin
 ? TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
 ? TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
 ? NUMBER OF SEQUENCES: 39
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Lyon & Lyon
 ? STREET: 633 West Fifth Street
 ? STREET: Suite 4700
 ? CITY: Los Angeles
 ? STATE: California
 ? COUNTRY: U.S.A.
 ? ZIP: 90071-2066
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ? MEDIUM TYPE: storage
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: IBM P.C. DOS 5.0
 ? SOFTWARE: FastSeq for Windows 2.0
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/012,135A
 ? FILING DATE: January 22, 1998
 ? CLASSIFICATION: 435
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 09/005,268
 ? FILING DATE: January 9, 1998
 ? APPLICATION NUMBER: 08/755,728
 ? FILING DATE: No. US20020081578A1ember 25, 1996
 ? APPLICATION NUMBER: 60/023,943
 ? FILING DATE: August 14, 1996
 ? APPLICATION NUMBER: 60/008,809
 ? FILING DATE: December 18, 1995
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Warburg, Richard J.
 ? REGISTRATION NUMBER: 32,327
 ? REFERENCE/DOCKET NUMBER: 231/282
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (213) 499-1600
 ? TELEFAX: (213) 955-0440
 ? TELEX: 67-3510
 ? INFORMATION FOR SEQ ID NO: 4:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 433 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: protein
 ? HYPOTHETICAL: NO
 ? ANTI-SENSE: NO
 US-09-012-135A-4

Query Match 83.7%; Score 41; DB 9; Length 403;
 Best Local Similarity 87.5%; Pred. No. 23;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LUGKPPPE 9
 DB 323 LUGKPPPE 330

RESULT 23
 US-10-026-021-7
 ? Sequence 7, Application US/10026021
 ? Publication No. US2003002776A1

GENERAL INFORMATION:
APPLICANT: Hitoshi, Yasumichi
APPLICANT: Dero, Susan
APPLICANT: Jenkins, Yonchu
APPLICANT: Rigel Pharmaceuticals, Inc.
TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
TREATMENT OF CANCER
FILE REFERENCE: C2:044-001213US
CURRENT APPLICATION NUMBER: US/07/026,021
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/309,632
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 7
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human ARK mitotic kinase
US-10-026-021-7

Query Match 83.7%; Score 41; DB 15; Length 403;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LIGKPPFE 9
|:|||||
DB 323 LVGKPPFE 330

RESULT 24
US-10-059-585-33
Sequence 23, Application US/10059585
Publication No. US20030082776A1
GENERAL INFORMATION:
APPLICANT: Ota, Toshio
APPLICANT: Isogai, Takao
APPLICANT: Nishikawa, Tetsuo
APPLICANT: Hayashi, Koji
APPLICANT: Otsuka, Kaoru
APPLICANT: Yamamoto, Jun-ichi
APPLICANT: Ishii, Shizuko
APPLICANT: Sugiyama, Tomoyasu
APPLICANT: Wakamatsu, Ai
APPLICANT: Nagai, Keiichi
APPLICANT: Otsuki, Tetsuji
APPLICANT: Funahashi, Shin-ichi
APPLICANT: Senoo, Chiaki
APPLICANT: Nezu, Jun-ichi
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-098001
CURRENT APPLICATION NUMBER: US/10/059,585
PRIOR FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: PCT/JPO00/05060
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: US 60/159,590
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 11-248036
PRIOR FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens

US-10-059-585-33

Query Match 83.7%; Score 41; DB 15; Length 403;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LIGKPPFE 9
|:|||||
DB 323 LVGKPPFE 330

RESULT 25
US-10-209-324-2
Sequence 2, Application US/10209324
Publication No. US20030108910A1
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF CALIFORNIA SAN FRANCISCO
APPLICANT: TOLAND, Amanda E.
APPLICANT: BALMAIN, Allan
TITLE OF INVENTION: STK15 (STK6) GENE POLYMORPHISM AND METHODS OF DETERMINING CANCER
FILE REFERENCE: UCSF1120-2
CURRENT APPLICATION NUMBER: US/10/209,324
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/334,146
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/308,911
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patent in version 3.1
SEQ ID NO 2
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (31)-(31)
OTHER INFORMATION: Xaa is Ile or Phe
US-10-209-324-2

Query Match 83.7%; Score 41; DB 15; Length 403;
Best Local Similarity 87.5%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LIGKPPFE 9
|:|||||
DB 323 LVGKPPFE 330

RESULT 26
US-C9-842-582-9
Sequence 9, Application US/C9842582
Patent No. US20020155570A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: 2246, NOVEL PROTEIN KINASE MOLECULES AND
METHODS OF INVENTION: USES THEREFOR
FILE REFERENCE: 38155-20054.00
CURRENT APPLICATION NUMBER: US/C9/842,582
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,391
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Consensus amino acid
US-09-842-582-9

Query Match 79.6%; Score 39; DB 10; Length 40;

Best Local Similarity 87.58; Pred. No. 5.3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLGKPPF 8
 |||||
Db 33 MLTGKPPF 40

RESULT 27

US-09-515-806-24
; Sequence 24, Application US/09515806
; Patent No. US2002032321A1
; GENERAL INFORMATION:
; APPLICANT: COOK, WILLIAM J.
; TITLE OF INVENTION: KAPELER-SIBERMANN, ROSANA
; FILE REFERENCE: 14790, NOVEL PROTEIN KINASE MOLECULE AND USES THEREFOR
; CURRENT APPLICATION NUMBER: US/09/515,806
; CURRENT FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: Kinase sequence
US-09-515-806-24

Query Match 79.64; Score 39; DB 10; Length 122;
Best Local Similarity 87.58; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLGKPPF 8
 |||||
Db 30 MLTGKPPF 37

RESULT 28

US-10-172-088-12
; Sequence 12, Application US/10172088
; Publication No. US2003000837CA1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 13295 NOVEL PROTEIN KINASE MOLECULES AND
; FILE REFERENCE: 38155-2001.01
; CURRENT APPLICATION NUMBER: US/10/172,088
; CURRENT FILING DATE: 2002-09-18
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/199,391
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-10-172-088-12

Query Match 79.64; Score 39; DB 15; Length 183;
Best Local Similarity 87.58; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLGKPPF 8
 |||||
Db 176 MLTGKPPF 183

RESULT 29

US-09-736-076-55
; Sequence 55, Application US/C9736076
; Patent No. US2002049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/C9/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(10)
; NAME/KEY: AMIDATION
; LOCATION: (0)...(8)
; OTHER INFORMATION: Plk
US-09-736-076-55

Query Match 77.64; Score 38; DB 9; Length 8;
Best Local Similarity 75.04; Pred. No. 5.9e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGKPPF 8
 |||||
Db 1 LLVGKPPF 8

RESULT 30

US-09-012-135A-3
; Sequence 3, Application US/09012135A
; Patent No. US20020381578A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,135A
; FILING DATE: January 22, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,268
; FILING DATE: January 9, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: NO. US20020381578A1ember 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809

FILING DATE: December 18, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 231/282
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 344 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-C9-012-135A-3

Query Match 77.6%; Score 38; DB 9; Length 344;
 Best Local Similarity 66.7%; Pred. No. 68;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPEFE 9
 Db 266 LLVGNPPE 274

RESULT 31

US-10-059-585-34
 Sequence 34, Application US/10053585
 Publication No. US2003008276A1
 GENERAL INFORMATION:
 APPLICANT: Cda, Toshio
 APPLICANT: Isogai, Takao
 APPLICANT: Nishikawa, Tetsuo
 APPLICANT: Hayashi, Koji
 APPLICANT: Otsuka, Kaoru
 APPLICANT: Yamamoto, Jun-ichi
 APPLICANT: Ishii, Shizuko
 APPLICANT: Sugiyama, Tomoyasu
 APPLICANT: Wakamatsu, Ai
 APPLICANT: Nagai, Keiichi
 APPLICANT: Otsuki, Tetsuji
 APPLICANT: Funahashi, Shin-ichi
 APPLICANT: Senoo, Chiaki
 APPLICANT: Nezu, Jun-ichi

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
 TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
 FILE REFERENCE: 06501-098021
 CURRENT APPLICATION NUMBER: US/10/059,595
 PRIOR FILING DATE: 2002-01-29
 PRIOR APPLICATION NUMBER: PCT/JP00/05060
 PRIOR FILING DATE: 2000-07-28
 PRIOR APPLICATION NUMBER: US 60/183,322
 PRIOR FILING DATE: 2000-02-17
 PRIOR APPLICATION NUMBER: US 60/159,590
 PRIOR FILING DATE: 1999-10-18
 PRIOR APPLICATION NUMBER: JP 2000-118776
 PRIOR FILING DATE: 2000-01-11
 PRIOR APPLICATION NUMBER: JP 2000-181767
 PRIOR FILING DATE: 2000-05-02
 PRIOR APPLICATION NUMBER: JP 11-248016
 PRIOR FILING DATE: 1999-07-29
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 34
 LENGTH: 344
 TYPE: PRT
 ORGANISM: Homo sapiens

US-10-059-585-34

Query Match 77.6%; Score 38; DB 15; Length 344;
 Best Local Similarity 66.7%; Pred. No. 68;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPEFE 9
 Db 266 LLVGNPPE 274

RESULT 32

US-10-171-311-214
 Sequence 214, Application US/10171311
 Publication No. US20030087270A1
 GENERAL INFORMATION:
 APPLICANT: Schlegel, Robert
 APPLICANT: Chen, Yan
 APPLICANT: Zhao, Xumei
 APPLICANT: Monahan, John
 APPLICANT: Kamatkar, Shubhangi
 APPLICANT: Glatt, Karen
 APPLICANT: Gannavarapu, Manjula
 APPLICANT: Hoerish, Sebastian
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
 TITLE OF INVENTION: OF CERVICAL CANCER
 FILE REFERENCE: MRI-035
 CURRENT APPLICATION NUMBER: US/10/171,311
 CURRENT FILING DATE: 2002-06-12
 PRIOR APPLICATION NUMBER: US 60/298,159
 PRIOR FILING DATE: 2001-06-13
 PRIOR APPLICATION NUMBER: US 60/298,155
 PRIOR FILING DATE: 2001-06-13
 PRIOR APPLICATION NUMBER: US 60/335,936
 PRIOR FILING DATE: 2001-11-14
 NUMBER OF SEQ ID NOS: 238
 SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 214
 LENGTH: 344
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-171-311-214

Query Match 77.6%; Score 38; DB 15; Length 344;
 Best Local Similarity 66.7%; Pred. No. 68;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPEFE 9
 Db 266 LLVGNPPE 274

RESULT 33

US-09-974-298-136
 Sequence 136, Application US/09974298
 Patent No. US20020156263A1
 GENERAL INFORMATION:
 APPLICANT: Chen, Huel-Mei
 TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
 FILE REFERENCE: PA-0037 P
 CURRENT APPLICATION NUMBER: US/09/974,298
 CURRENT FILING DATE: 2001-10-04
 PRIOR APPLICATION NUMBER: 60/238,331
 PRIOR FILING DATE: 2000-05-10
 NUMBER OF SEQ ID NOS: 194
 SOFTWARE: PERL Program
 SEQ ID NO 136
 LENGTH: 347
 TYPE: PRT
 ORGANISM: Homo sapiens

FEATURE:
 NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. US20020156263A1 002940CD1
 US-09-974-298-136

Query Match 77.6% Score 38; DB 10; Length 347;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPFE 9
:|:|:|:
Db 269 LUVNPPFE 277

RESULT 34
US-10-291-253A.16
; Sequence 16, Application US/10291253A
; Publication No. US20030150017A1
; GENERAL INFORMATION:
; APPLICANT: Botella, Jose
; APPLICANT: Graham, Michael
; APPLICANT: Fairbairn, David
; TITLE OF INVENTION: A Method for Facilitating Pathogen Resistance
; FILE REFERENCE: nematode
; CURRENT APPLICATION NUMBER: US/10/291.253A
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: PR8706
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: PR8802
; PRIOR FILING DATE: 2001-11-12
; PRIOR APPLICATION NUMBER: US60/341404
; PRIOR FILING DATE: 2001-12-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 16
; TYPE: PRT
; LENGTH: 348
; ORGANISM: Meloidogyne incognita
US-10-291-253A.16

Query Match 77.6% Score 38; DB 12; Length 348;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPFE 9
:|:|:|:
Db 210 MYAGKPPFE 218

RESULT 35
US-10-026-021.3
; Sequence 1, Application US/100260.1
; Publication No. US2003027756A;
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasunichi
; APPLICANT: Demo, Susan
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; FILE REFERENCE: Treatment of Cancer
; FILE REFERENCE: 021044-0012-00S
; CURRENT APPLICATION NUMBER: US/10/026.021
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1...379)
; OTHER INFORMATION: SAK serine/threonine kinase kinase domain
US 10-026-021.3

Query Match 77.6% Score 38; DB 15; Length 379;
Best Local Similarity 55.6%; Pred. No. 74;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPFE 9
:|:|:|:
Db 204 LUGRPFFD 212

RESULT 36
US-09-893-737-106
; Sequence 106, Application US/09893737
; Patent No. US2002011085A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul C.
; APPLICANT: Presnell, Scott R.
; TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
; FILE REFERENCE: 00-41
; CURRENT APPLICATION NUMBER: US/09/893.737
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/215,446
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-737-106

Query Match 77.6% Score 38; DB 10; Length 419;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPP 7
|||:|:
Db 170 MLGKPP 176

RESULT 37
US-09-949-970-2
; Sequence 2, Application US/09949370
; Patent No. US20020042105A1
; GENERAL INFORMATION:
; APPLICANT: BATHE, BRIGITTE
; APPLICANT: HANS, STEPHAN
; APPLICANT: FARMICK, MIKE
; APPLICANT: HERMANN, THOMAS
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE PCNB GENE
; FILE REFERENCE: 213734USX
; CURRENT APPLICATION NUMBER: US/09/949.970
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: DE 10044912.3
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: DE 10120095.1
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/297,250
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 2
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-949-970-2

Query Match 77.6% Score 38; DB 9; Length 627;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPFE 9
:|:|:|:
Db 188 LVTGPPFE 196

```

RESULT 38
US-09-949-970-4
: Sequence 4, Application US/09349970
: Patent No. US2002034205A1
: GENERAL INFORMATION:
: APPLICANT: BATHE, BRIGITTE
: APPLICANT: HANS, STEPHAN
: APPLICANT: FARWICK, M-KE
: APPLICANT: HERMANN, THOMAS
: TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE PENH GENE
: FILE REFERENCE: 213734USX
: CURRENT APPLICATION NUMBER: US/09/949,970
: PRIOR FILING DATE: 2001-09-12
: PRIOR APPLICATION NUMBER: DE 10044912.3
: PRIOR FILING DATE: 2000-09-12
: PRIOR APPLICATION NUMBER: DE 10120395.1
: PRIOR FILING DATE: 2001-04-25
: PRIOR APPLICATION NUMBER: US 60/297,250
: PRIOR FILING DATE: 2001-06-12
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: Patent in version 3.1
: SEQ ID NO 4
: LENGTH: 627
: TYPE: PRT
: ORGANISM: Corynebacterium glutamicum
: NAME/KEY: misc feature
: LOCATION: (2343)..(2343)
: OTHER INFORMATION: C-T transition
US-09-949-970-4

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Query Match 77.6%; Score 38; DB 9; Length 627;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPE 9
DB 188 LVTKPPE 196

```

```

RESULT 39
US-09-738-626-3546
: Sequence 3546, Application US/09738626
: Publication No. US20020197435A1
: GENERAL INFORMATION:
: APPLICANT: NAKAGAWA, SATOSHI
: APPLICANT: MIZOGUCHI, HIROSHI
: APPLICANT: ANDO, SEIKO
: APPLICANT: HAYASHI, MIKIRO
: APPLICANT: OCHIAI, KEIKO
: APPLICANT: YOKOI, HARUHIKO
: APPLICANT: TATEISHI, NAOKO
: APPLICANT: SENOH, AKIHIRO
: APPLICANT: IKEDA, MASATO
: APPLICANT: OZAKI, AKIO
: TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
: FILE REFERENCE: 249-125
: CURRENT APPLICATION NUMBER: US/09/738,626
: CURRENT FILING DATE: 2000-12-18
: PRIOR APPLICATION NUMBER: JP 99/377494
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: JP 00/159162
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: JP 03/280928
: PRIOR FILING DATE: 2000-08-03
: NUMBER OF SEQ ID NOS: 7059
: SOFTWARE: Patent in ver. 3.0
: SEQ ID NO 3546
: LENGTH: 646
: TYPE: PRT
: ORGANISM: Corynebacterium glutamicum

```

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US-09-738-626-3546
Query Match 77.6%; Score 38; DB 10; Length 646;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPE 9
DB 207 LVTGKPPE 215

RESULT 40
US-09-771-161A-195
: Sequence 195, Application US/09771161A
: Patent No. US20020110811A1
: GENERAL INFORMATION:
: APPLICANT: LEVINE, et al.
: TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
: FILE REFERENCE: 802623-2005.1
: CURRENT APPLICATION NUMBER: US/09/771,161A
: PRIOR FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: 09/724,676
: PRIOR FILING DATE: 2000-11-28
: PRIOR APPLICATION NUMBER: 136776
: PRIOR FILING DATE: 2000-06-15
: PRIOR APPLICATION NUMBER: 135619
: PRIOR FILING DATE: 2000-04-12
: NUMBER OF SEQ ID NOS: 273
: SOFTWARE: Patent in version 3.0
: SEQ ID NO 195
: LENGTH: 737
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-771-161A-195

```

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Query Match 77.6%; Score 38; DB 10; Length 737;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPE 9
DB 600 MXAGQPPE 608

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Search completed: November 14, 2003, 13:43:27
Job time : 22.3714 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: November 14, 2003, 13:20:05 ; Search time 10.9 Seconds
(without alignments)
80.14: Million cell updates/sec

Title: US-09-736-076-17

Perfect score: 49

Sequence: 1 MLGKPPFE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283108 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283108

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.76:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	45	92.9	682	2 A44493	serum-inducible kinase
2	43	87.8	603	2 S34130	serine/threonine kinase
3	43	87.8	603	2 A47545	protein kinase EC
4	43	87.8	603	2 A54596	protein kinase - m
5	41	83.7	305	2 T43221	serine/threonine kinase
6	41	83.7	329	2 B87750	protein B8207.4 [i
7	41	83.7	389	2 S52242	protein kinase EC
8	41	83.7	403	2 JCS974	aurora-related kin
9	41	83.7	407	2 S52243	p46Eg245 protein -
10	41	83.7	683	2 T38254	serine/threonine kinase
11	41	83.7	705	2 A48144	protein kinase CDC
12	40	81.6	766	2 S69657	hypothetical prote
13	39	79.6	371	2 T16391	hypothetical prote
14	39	79.6	465	2 S68462	protein kinase ATP
15	39	79.6	471	2 S68463	protein kinase ATP
16	39	79.6	480	2 S68639	ribosomal protein
17	39	79.6	576	2 S22127	protein kinase po
18	39	79.6	592	2 T43402	probable protein k
19	39	79.6	639	2 A32545	protein kinase C
20	38	77.6	465	2 B55749	protein kinase EC
21	38	77.6	521	2 D88640	protein F55A8.2 [i
22	38	77.6	525	2 S45884	probable serine/th
23	38	77.6	547	2 S44841	K06H7.1 protein -
24	38	77.6	547	2 T22856	hypothetical prote
25	38	77.6	634	1 B32392	protein kinase C
26	38	77.6	648	2 T43337	polo-like kinase-1
27	38	77.6	707	1 A53532	protein kinase C
28	38	77.6	736	2 KIRBCE	protein kinase C
29	38	77.6	737	1 S28942	protein kinase C

30	38	77.6	737	1 KIRTC	protein kinase C
31	38	77.6	737	1 KIMSC	protein kinase C
32	38	77.6	925	2 A55748	protein kinase EC
33	38	77.6	1081	2 S51899	probable protein k
34	37	75.5	615	2 T29223	hypothetical prote
35	37	75.5	664	2 G89894	protein kinase [m
36	37	75.5	672	1 KIRUCA	protein kinase C
37	37	75.5	672	1 KIRTC	protein kinase C
38	37	75.5	672	1 KIMSCA	protein kinase C
39	37	75.5	672	1 KIRBC	protein kinase C
40	37	75.5	672	1 KIRBC	protein kinase C
41	37	75.5	676	2 A32337	protein kinase C
42	37	75.5	682	2 KIBOGC	protein kinase C
43	37	75.5	697	1 KIRTC	protein kinase C
44	37	75.5	697	1 KIRBGC	protein kinase C
45	37	75.5	697	2 JN0548	protein kinase C

ALIGNMENTS

RESULT 1

A44493
serum-inducible kinase - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 10-Sep-1997
C:Accession: A44493
R:Simmons, D.L.; Neel, B.G.; Stevens, R.; Evelt, G.; Erikson, R.L.
Mol. Cell. Biol. 12, 4164-4169, 1992
A:Title: Identification of an early-growth-response gene encoding a novel putative pr
A:Reference number: A44493; MUID:92375085; PMID:508211
A:Accession: A44493
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-682 <SIM>
A:Experimental source: F-2 cells
A>Note: sequence extracted from NCBI; backbone (NCBI:111721, NCBIP:111722)
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho
C:Keywords: Arp
F:77-331/Domain: protein kinase homology <KIN>

Query Match 93.9%; Score 46; DB 2; Length 682;
Best Local Similarity 88.9%; Pred. No. 0.86;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPFE 9
DB 270 MLGKPPFE 278

RESULT 2

S34130
serine/threonine-specific protein kinase PLK (EC 2.7.1.1) - human
A:Alternate names: polo-like protein kinase; protein kinase plk-1
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C:Accession: S34130; I38123; S61543
R:Golsteyn, R.M.; Schultz, S.J.; Bartek, J.; Ziemiecki, A.; Ried, T.; Nigg, E.A.
submitted to the EMBL Data Library, June 1993
A:Description: Cloning and characterization of a novel human protein kinase plk-1 a F
through mitosis.
A:Reference number: S34130
A:Accession: S34130
A:Molecule type: mRNA
A:Residues: 1-603 <GOL>
A:Cross-references: EMBL:X73458; NID:g312997; PID:CAA51837.1; PID:g312998
A:Experimental source: nasopharyngeal carcinoma
R:Holtrich, U.; Wolf, G.; Brauning, A.; Karn, T.; Bohme, B.; Rubsamen-Waigmann, H.,
Proc. Natl. Acad. Sci. U.S.A. 91, 1736-1740, 1994
A:Title: Induction and down-regulation of PLK, a human serine/threonine kinase expres
A:Reference number: A53134; MUID:94173904; PMID:8127874
A:Accession: I38123
A>Status: preliminary; nucleic acid sequence not shown

```

A:Molecule type: mRNA
A:Residues: 1-140, P', 142-226, E', 228-603 <RES>
A:Cross-references: EMBL:X75932; NID:g460768; PIDN:CAA53536.1; PID:g460769
A:Experimental source: lung tumor
R:Brauninger, A.; Strebhardt, K.; Ruebsaenen-Waigmann, H.
Oncogene 11, 1793-1800, 1995
A:Title: Identification and functional characterization of the human and murine polo-like
kinase 1
A:Reference number: S61543; MUID:96068906; PMID:7478607
A:Accession: S61543
A:Molecule type: DNA
A:Residues: 1-122, T', 124-136 <BRA>
A:Cross-references: EMBL:X90725; NID:gl061143; PIDN:CAA62263.1; PID:gl061144
A:Experimental source: placenta
A:Note: the authors translated the codon AGC for residue 107 as Met
C:Genetics:
A:Gene: GDB:PLK
A:Cross-references: GDB:331003
A:Map position: 17pter-17p12
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:51-305/Domain: protein kinase homology <KIN>

Query Match 87.8%; Score 43; DB 2; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
   ||| |||
Db 244 LLVGKPPPE 252

RESULT 5
T43221
serine/threonine-specific protein kinase (EC 2.7.1.1) 2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C:Accession: T43221
R:Schumacher, J.M.; Golden, A.; Donovan, P.J.
J. Cell Biol. 143, 1635-1646, 1998
A:Title: AIR-2: An aurora/Ipl1-related protein kinase associated with chromosomes an
A:Reference number: 222347; MUID:99069487; PMID:9852156
A:Accession: T43221
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-305 <SCH>
A:Cross-references: EMBL:AF071207; PIDN:AAC70945.1
C:Genetics:
A:Gene: AIR-2
A:Map position: 1
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: phosphotransferase

Query Match 83.7%; Score 41; DB 2; Length 305;
Best Local Similarity 87.5%; Pred. No. 3.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPPE 9
   ||| |||
Db 220 LVGKPPPE 227

RESULT 6
B87790
protein B0207.4 (imported) - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: B87790
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bi
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999,
A:Accession: B87790
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-329 <STO>
A:Cross-references: GB:chr_1; PIDN:AAB52459.1; PID:gl943805; GSPDB:GN00019; CESP:B02
C:Genetics:
A:Gene: B0207.4
A:Map position: 1
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 83.7%; Score 41; DB 2; Length 329;
Best Local Similarity 87.5%; Pred. No. 3.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPPE 9
   ||| |||
Db 244 LVGKPPPE 25;

A:Molecule type: mRNA
A:Residues: 1-140, P', 142-226, E', 228-603 <RES>
A:Cross-references: EMBL:X75932; NID:g460768; PIDN:CAA53536.1; PID:g460769
A:Experimental source: lung tumor
R:Brauninger, A.; Strebhardt, K.; Ruebsaenen-Waigmann, H.
Oncogene 11, 1793-1800, 1995
A:Title: Identification and functional characterization of the human and murine polo-like
kinase 1
A:Reference number: S61543; MUID:96068906; PMID:7478607
A:Accession: S61543
A:Molecule type: DNA
A:Residues: 1-122, T', 124-136 <BRA>
A:Cross-references: EMBL:X90725; NID:gl061143; PIDN:CAA62263.1; PID:gl061144
A:Experimental source: placenta
A:Note: the authors translated the codon AGC for residue 107 as Met
C:Genetics:
A:Gene: GDB:PLK
A:Cross-references: GDB:331003
A:Map position: 17pter-17p12
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:51-305/Domain: protein kinase homology <KIN>

Query Match 87.8%; Score 43; DB 2; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
   ||| |||
Db 244 LLVGKPPPE 252

RESULT 2
A47545
protein kinase (EC 2.7.1.37) Plk - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C:Accession: A47545
R:Clay, F.J.; McEwen, S.J.; Bertoncello, T.; Wilks, A.F.; Dunn, A.R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4882-4886, 1993
A:Title: Identification and cloning of a protein kinase encoding mouse gene, Plk, relate
A:Reference number: A47545; MUID:91281660; PMID:8099445
A:Accession: A47545
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-603 <CLA>
A:Cross-references: GB:L06144; NID:g909461; PIDN:AAA33046.1; PID:gl93462
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; phosphotransferase
F:51-305/Domain: protein kinase homology <KIN>

Query Match 87.8%; Score 43; DB 2; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
   ||| |||
Db 244 LLVGKPPPE 252

RESULT 4
A54596
protein kinase - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: A54596
R:Lake, R.J.; Gelinek, W.R.
Mol. Cell. Biol. 13, 7793-7801, 1993
A:Title: Cell cycle- and terminal differentiation-associated regulation of the mouse mRN
A:Reference number: A54596; MUID:94067140; PMID:7502533
A:Accession: A54596
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-603 <RES>

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RESULT 7
S52242
Protein kinase (EC 2.7.1.1) p46Xleg22 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 18-Jun-1999
C:Accession: S52242
R:Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A:Description: Eg2, selected by differential screening encodes a new Xenopus protein kin
A:Reference number: S52242
A:Accession: S52242
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-389 <ROG>
A:Cross-references: EMBL:Z17206; NID:G609279; PIDN:CAA79314.1; PID:G609280
C:Superfamily: Kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase
F:119-371/Domain: protein kinase homology <KIN>
F:127-135/Region: protein kinase ATP-binding motif

Query Match      83.7%   Score 41; DB 2; Length 389;
Best Local Similarity 87.5%   Pred. No. 4.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  2 LLGKPPFE 9
Db  311 LVGKPPFE 118

RESULT 8
JC5974
aurora-related kinase 1 (EC 2.7.1.1) - human
C:Species: Homo sapiens (man)
C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jan-2000
C:Accession: JC5974
R:Shindo, M.; Nakano, H.; Kuroyanagi, H.; Shitazawa, T.; Mihata, M.; Gilbert, D.J.; Jenk
B:Ochem, Bicipys Res. Commun. 244, 285-292, 1998
A:Title: cDNA cloning, expression, subcellular localization, and chromosomal assignment
A:Reference number: JC5974; MUID:98183439; PMID:9514926
A:Accession: JC5974
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-403 <SHI>
A:Cross-references: GB:AF08551
C:Superfamily: Unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolo
C:Keywords: phosphotransferase
F:131-383/Domain: protein kinase homology <KIN>

Query Match      83.7%   Score 41; DB 2; Length 403;
Best Local Similarity 87.5%   Pred. No. 4.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  2 LLGKPPFE 9
Db  323 LVGKPPFE 130

RESULT 9
S52243
p46eg265 protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 24-Sep-1999
C:Accession: S52243; S34642; I51695
R:Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A:Description: Eg2, selected by differential screening encodes a new Xenopus protein kin
A:Reference number: S52242
A:Accession: S52243
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-407 <ROG>
A:Cross-references: EMBL:Z17207; NID:G609281; PIDN:CAA79315.1; PID:G609282

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R:Bouvet, P.; Omilli, F.; Ariot-Bonnemain, Y.; Legagneux, V.; Roghi, C.; Basset, T.;
submitted to the EMBL Data Library, June 1993
A:Description: Targetted deadenylation of specific mRNAs in Xenopus embryos by a mech
A:Reference number: S34642
A:Accession: S34642
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 328-407 <BOU>
A:Cross-references: EMBL:Z24453; NID:G394756; PIDN:CAA80826.1; PID:G394757
R:Bouvet, P.; Omilli, F.; Ariot-Bonnemains, Y.; Legagneux, V.; Roghi, C.; Bassez, T.;
Mol. Cell. Biol. 14, 1993-1900, 1994
A:Title: The deadenylation conferred by the 3' untranslated region of a developmental
A:Reference number: I51695; MUID:94158861; PMID:8114721
A:Accession: I51695
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 328-407 <BO2>
A:Cross-references: EMBL:Z24453; NID:G394756; PIDN:CAA80826.1; PID:G394757
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: ATP; phosphotransferase; protein kinase
F:138-390/Domain: protein kinase homology <KIN>
F:146-154/Region: protein kinase ATP-binding motif

Query Match      83.7%   Score 41; DB 2; Length 407;
Best Local Similarity 87.5%   Pred. No. 4.5;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  2 LLGKPPFE 9
Db  330 LVGKPPFE 337

RESULT 10
T38254
serine/threonine-specific protein kinase p101 (EC 2.7.1.1) - fission yeast (Schizosac
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T38254; T45128
R:Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z21781
A:Accession: T38254
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-683 <BRC>
A:Cross-references: EMBL:Z98559; PIDN:CAB11167.1; GSPDB:GN00066; SPDB:SPAC23C11.16
A:Experimental source: strain 972h; cosmid c23C11
R:Ohkura, H.; Hagan, I.M.; Glover, D.M.
Genes Dev. 9, 1059-1073, 1995
A:Title: The conserved Schizosaccharomyces pombe kinase p101, required to form a bipo
A:Reference number: Z2921; MUID:95262899; PMID:7744248
A:Accession: T45128
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-683 <OHK>
A:Cross-references: EMBL:X85758; NID:G887640; PIDN:CAA59766.1; PID:G887641
A:Experimental source: strain 972 derivative
C:Genetics:
A:Gene: p101; SPAC23C11.16
A:Map position: 1
C:Function:
A:Description: required to form a bipolar spindle and early in the regulatory cascade
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: phosphotransferase; protein kinase

Query Match      83.7%   Score 41; DB 2; Length 683;
Best Local Similarity 66.7%   Pred. No. 7.8;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy  1 MLGKPPFE 9
Db  233 LLGKPPFQ 241

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RESULT 11
A48144
protein kinase CDC5 (EC 2.7.1.1) - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein kinase PKX2; protein YMR270.03C; protein YMR001C
C:Species: Saccharomyces cerevisiae
C>Date: 30-Jun-1995 #sequence_revision 10-Jun-1995 #text_change 24-Sep-1999
C:Accession: A48144; S53030; S27445
R:Kitada, K.; Johnson, A.L.; Johnston, L.H.; Sugino, A.
MOL: Cell. Biol. 13, 4445-4457, 1993
A:Title: A multicopy suppressor gene of the Saccharomyces cerevisiae G1 cell cycle mutant
A:Reference number: A48144; MUID:93309479; PMID:8321244
A:Accession: A48144
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-705 <KIT>
A:Cross-references: EMBL:M84220; NID:gl72186; FIDN:AAA2576.1; PID:gl72187
R:Devlin, K.; Churcher, C.M.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53028
A:Accession: S53030
A:Molecule type: DNA
A:Residues: 1-705 <DEV>
A:Cross-references: EMBL:748613; NID:g728645; PIDN:CAA8516.1; PID:g728648; MIPS:YMR001C
A:Experimental source: strain AB972
C:Genetics:
A:Gene: SGD:CDC5; PKX2
A:Cross-references: SGD:S0004603; MIPS:YMR001C
A:Map position: 13R
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; cell cycle control; phosphotransferase; protein kinase
F:82-337/Domain: protein kinase homolog <KIN>

Query Match 83.7%; Score 41; DB 2; Length 705;
Best Local Similarity 66.7%; Pred. No. 8;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGKPPF 9
DB 274 MLGKPPFQ 282

RESULT 12
S69657
Hypothetical protein YMR490C - Yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C>Date: 22-Aug-1996 #sequence_revision 10-Jun-1995 #text_change 13-Apr-2002
C:Accession: S69657
R:Pietrich, F.S.
submitted to the EMBL Data Library, August 1995
A:Description: The sequence of S. cerevisiae cosmid 9410, 803b, 816b, and 9787.
A:Reference number: S69554
A:Accession: S69657
A:Molecule type: DNA
A:Residues: 1-766 <DIE>
A:Cross-references: EMBL:U33050; NID:g927266; PIDN:AA564917.1; PID:g927745; MIPS:YDR490C
C:Genetics:
A:Gene: SGD:PKH1
A:Cross-references: SGD:S0002098
A:Map position: 4R
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
F:123-391/Domain: protein kinase ATP-binding motif

Query Match 81.6%; Score 40; DB 2; Length 766;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGKPPF 9
DB 330 MLGKPPF 339

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RESULT 13
T16391
Hypothetical protein F47F2.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000
C:Accession: T16391
R:Bentley, D.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid F47F2.
A:Reference number: Z18506
A:Accession: T16391
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-371 <BEN>
A:Cross-references: EMBL:U40943; NID:gl072202; PID:gl072204; PIDN:AAA8716.1; CESP:F
C:Genetics:
A:Gene: CESP:F47F2.1
A:Introns: 39/3; 70/1; 126/2; 156/2; 182/3; 214/2; 286/2; 331/3
C:Superfamily: kinase-related transforming protein; protein kinase homolog
F:61-317/Domain: protein kinase homolog <KIN>

Query Match 79.6%; Score 39; DB 2; Length 371;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGKPPF 8
DB 251 MMVGKPPF 258

RESULT 14
S68462
protein kinase ATPK6/ATPK1 (EC 2.7.1.1) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 24-Sep-1999
C:Accession: S68462; A54141
R:Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 358, 199-204, 1995
A:Title: Two genes that encode ribosomal protein S6 kinase homologs are induced by ca
A:Reference number: S68462; MUID:95129712; PMID:7828736
A:Accession: S68462
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-465 <MLZ>
A:Cross-references: EMBL:D42056; NID:g867996; PIDN:BA007656.1; PID:di008238; PID:g86
R:Zhang, S.H.; Lawton, M.A.; Hunter, T.; Lamb, C.J.
J. Biol. Chem. 269, 17586-17592, 1994
A:Title: atpk1, a novel ribosomal protein kinase gene from Arabidopsis. I. Isolation
A:Reference number: A54141; MUID:94292519; PMID:7912697
A:Contents: ecotype Landsberg erecta
A:Accession: A54141
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-465 <ZHA>
A:Cross-references: GB:L29030; NID:g508307; PIDN:AAA21142.1; PID:g508308
A>Note: sequence extracted from NCBI backbone (NCBIN:149344, NCBIPI:149415)
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:132-389/Domain: protein kinase homolog <KIN>
F:140-148/Region: protein kinase ATP-binding motif

Query Match 79.6%; Score 39; DB 2; Length 465;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 MLGKPPF 8
DB 324 MLGKPPF 331

RESULT 15
S68463

```

protein kinase ATPK19 [EC 2.7.1.1] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 05-Dec-1996 #sequence_revision 27-Feb-1997 #text_change 24-Sep-1999
 C:Accession: S68463
 R:Mizoguchi, T.; Hayashida, N.; Yamauchi Shinozaki, K.; Kamada, H.; Shinozaki, K.
 FEBS Lett. 358, 199-204, 1995
 A:Title: Two genes that encode ribosomal-protein S6 kinase homologs are induced by cold
 A:Reference number: S68462; MUID:95129742; PMID:7828736
 A:Accession: S68463
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-471 <M2>
 A:Cross-references: EMBL:D42661; MIM:6152642; PIRN:BAAT7661.1; PID:d1038243; PID:g86799
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:138-195/Domain: protein kinase homology <KIN>
 F:146-154/Region: protein kinase ATP-binding motif

Query Match 79.6%; Score 39; DB 2; Length 471;
 Best Local Similarity 87.5%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 |||||
 DB 310 MLGKPPF 337

RESULT 16
 S6639
 Ribosomal protein S6 kinase homolog (clone Aspk1) - oat
 N:Alternate names: mitogen-activated protein kinase pp7; homolog
 C:Species: Avena sativa (oat)
 C>Date: 27-Oct-1995 #sequence_revision 23-Nov-1995 #text_change 24-Sep-1999
 C:Accession: S6639
 R:Butt, A. K.; Phillips, A. L.
 Plant Mol. Biol. 27, 1043-1052, 1995
 A:Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that show
 A:Reference number: S6638; MUID:9528434; PMID:7766874
 A:Accession: S6639
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-480 <HUT>
 A:Cross-references: EMBL:X79992; MIM:6871945; PIRN:CAAS6313.1; PID:g871996
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 C:Keywords: ATP; phosphotransferase; protein kinase
 F:143-407/Domain: protein kinase homology <KIN>
 F:157-165/Region: protein kinase ATP-binding motif

Query Match 79.6%; Score 39; DB 2; Length 480;
 Best Local Similarity 87.5%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 |||||
 DB 341 MLGKPPF 348

RESULT 17
 S22127
 protein kinase pco [EC 2.7.1.1] - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Sep-1999
 C:Accession: S22127
 R:Sunkel, C. E.
 Submitted to the EMBL Data Library, November 1991
 A:Reference number: S22127
 A:Accession: S22127
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-576 <SN>
 A:Cross-references: EMBL:X63361; MIM:683361; PIRN:CAAA44963.1; PID:g9356
 C:Superfamily: protein kinase C alpha; protein kinase C2 region homology; protein k
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 A:Gene: FlyBase:pco

A:Cross-references: FlyBase:FBgn0001124
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
 C:Keywords: ATP; phosphotransferase
 F:23-277/Domain: protein kinase homology <KIN>

Query Match 79.6%; Score 39; DB 2; Length 576;
 Best Local Similarity 66.7%; Pred. No. 16;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 9
 |||||
 DB 216 MLGKPPF 224

RESULT 18
 T43402
 probable protein kinase (EC 2.7.1.1) - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
 C:Accession: T43402; T41425
 R:Niederberger, C.
 submitted to the EMBL Data Library, July 1998
 A:Reference number: 222486
 A:Accession: T43402
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-592 <NIE>
 A:Cross-references: EMBL:X99280; PIRN:CAA67672.1
 A:Experimental source: strain h90
 R:Wood, V.; Rajandream, M. A.; Barrell, B. G.; Murphy, L.; Harris, D.
 submitted to the EMBL Data Library, September 1998
 A:Reference number: 221954
 A:Accession: T41425
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-592 <WOO>
 A:Cross-references: EMBL:AL031798; PIRN:CAA211194.1; GSPDB:GN00068; SPDB:SPCC576.15c
 A:Experimental source: strain 972h; cosmid c576
 C:Genetics:
 A:Gene: KSG1; SPCC576.15c
 A:Map position: 3
 A:Introns: 191/3
 C:Keywords: phosphotransferase

Query Match 79.6%; Score 39; DB 2; Length 592;
 Best Local Similarity 87.5%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 |||||
 DB 305 MLGKPPF 312

RESULT 19
 A32545
 protein kinase C (EC 2.7.1.1) - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1999
 R:Accession: A32545
 R:Rosenthal, A.; Rhee, L.; Yadegari, R.; Paro, R.; Ullrich, A.; Goeddel, D. V.
 EMBO J. 6, 433-441, 1987
 A:Title: Structure and nucleotide sequence of a Drosophila melanogaster protein kinase
 A:Reference number: A32545; MUID:87218499; PMID:3107983
 A:Accession: A32545
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-639 <ROS>
 A:Cross-references: GB:X05076; MIM:68352; PIRN:CAA28736.1; PID:g8353; GB:Y00042
 C:Genetics:
 A:Gene: FlyBase:PKc53e
 A:Cross-references: FlyBase:FBgn0003091
 C:Superfamily: protein kinase C alpha; protein kinase C2 region homology; protein k
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F:46-95/Domain: protein kinase C zinc-binding repeat homology <KZ1>
 F:111-160/Domain: protein kinase C zinc-binding repeat homology <KZ2>
 F:161-273/Domain: protein kinase C C2 region homology <KC2>
 F:339-599/Domain: protein kinase homology <KN>
 F:347-355/Region: protein kinase ATP-binding motif

Query Match 79.6%; Score 39; DB 2; Length 613;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFF 9
 |||||
 DB 533 MLVGKPPFD 541

RESULT 20

B55748

protein kinase (EC 2.7.1.37) Sak.b - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 19-Dec-1997

C:Accession: B55748

R:Podet, C.; Motte, B.; Yousefi, S.; Heffernan, M.; Dennis, J.W.

Proc. Natl. Acad. Sci. U.S.A. 91: 6388-6392, 1994

A:Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosophila

A:Reference number: A55748; MUID:94294457; PMID:802279.

A:Accession: B55748

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-465 <F0D>

A:Cross-references: GB:U29483

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol

C:Keywords: ATP; phosphotransferase

F:1-265/Domain: protein kinase homology <KIN>

F:18-26/Region: protein kinase ATP-binding motif

Query Match 77.6%; Score 38; DB 2; Length 465;
 Best Local Similarity 55.6%; Pred. No. 20;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFF 9
 |||||
 DB 204 LLLGKPPFD 212

RESULT 21

D88640

protein kinase (EC 2.7.1.37) Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 10-May-2001 #sequence_revision 1 May 2001 #text_change 17-May-2002

C:Accession: D88640

R:Antonys, The C. elegans Sequencing Consortium

Science 282, 2012-2018, 1998

A:Title: genome sequence of the nematode C. elegans: a platform for investigating biolog

A:Reference number: A75000; MUID:99069613; PMID:985191

A>Note: see websites genome.wustl.edu/gsc/C.elegans/ at 1 www.sanger.ac.uk/Projects/C.ele

A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: D88640

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-521 <STO>

A:Cross-references: GB:chr_IV; PIDN:AAC19146.1; PID:G3193148; GSPDB:GN00022; CESP:F55A8.

C:Genetics:

A:Gene: F55A8.2

A:Map position: 4

C:Superfamily: cGMP-dependent protein kinase; cAMP receptor protein cyclic nucleotide-bi

Query Match 77.6%; Score 38; DB 2; Length 521;

Best Local Similarity 55.6%; Pred. No. 22;

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFF 9
 |||||
 DB 401 LMLGKPPFD 403

RESULT 22

S45884

probable serine/threonine specific protein kinase (EC 2.7.1.1.-) YBR028C - yeast (Saccl

N:Alternate names: protein YBR0312

C:Species: Saccharomyces cerevisiae

C>Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002

C:Accession: S45884; S46558

R:Grivell, L.A.; de Haan, M.; Maat, M.J.; Smits, P.H.M.

submitted to the Protein Sequence Database, August 1994

A:Reference number: S45875

A:Accession: S45884

A:Molecule type: DNA

A:Residues: 1-525 <GR>

A:Cross-references: EMBL:Z35697; NID:G536370; PIDN:CAA84970.1; PID:G536371; MIPS:YBR1

A:Experimental source: strain S288C

R:Smits, P.H.M.; de Haan, M.; Maat, C.; Grivell, L.A.

Yeast 10 (Suppl. A), S75-S80, 1994

A:Title: The complete sequence of a 33 kb fragment on the right arm of chromosome II

ly identified genes and a homologue of the SCO1 gene.

A:Reference number: S46551; MUID:94378725; PMID:8091864

A:Accession: S46558

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-525 <SM1>

A:Cross-references: EMBL:X76078; NID:G498748; PIDN:CAA53684.1; PID:G498756

A:Experimental source: strain S288C

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 199

C:Genetics:

A:Cross-references: SGD:S0000232

A:Map position: 2R

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho

C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F:126-423/Domain: protein kinase homology <KIN>

F:134-142/Region: protein kinase ATP-binding motif

F:277/Active site: Asp #status predicted

Query Match 77.6%; Score 38; DB 2; Length 525;
 Best Local Similarity 75.0%; Pred. No. 22;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
 |||||
 DB 355 MLVGKPPF 362

RESULT 23

S44841

K06H7.1 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar 2001

C:Accession: S44841

R:Favella, A.D.

submitted to the EMBL Data Library, May 1993

A:Description: Sequence of the C. elegans cosmid K06H7.

A:Reference number: S44620

A:Accession: S44841

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-547 <FAV>

A:Cross-references: EMBL:L15314; NID:G289690; PIDN:AAA28084.1; PID:G289691

C:Genetics:

A:Introns: 25/3; 36/3; 80/3; 149/3; 186/2; 229/3; 311/3

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase ho

C:Keywords: ATP; serine/threonine-specific protein kinase

F:265-518/Domain: protein kinase homology <KIN>

Query Match 77.6%; Score 38; DB 2; Length 547;
 Best Local Similarity 66.7%; Pred. No. 23;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPFF 9


```

Gb          1  MLGKPPFE 9
           1  :|||||
           495 MMAGQPPFE 503

RESULT 24
T22856
hypothetical protein F57F5.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Jun-2002
C:Accession: T22856
R:Harris, B.
submitted to the EMBL Data Library, July 1996
A:Reference number: Z19627
A:Accession: T22856
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-547 <N1>
A:Cross-references: EMBL:Z19627; PIDN:CA800101.1; GSPDB:GN00021; CESP:F57F5.5
A:Experimental source: Clone F57F5
C:Genetics:
A:Gene: CESP:F57F5.5
A:Map position: 5
A:Introns: 43/3; 129/2; 166/3; 187/1; 289/3; 341/2; 450/3; 499/3
F:1: 60/Domain: protein kinase C zinc-binding repeat homology <K2N1>
F:89-139/Domain: protein kinase C zinc-binding repeat homology <K2N2>

Query Match 77.6%; Score 38; DB 2; Length 547;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy          1  MLGKPPFE 9
           1  :|||||
           495 MMAGQPPFE 419

RESULT 25
B23392
protein kinase C (EC 2.7.1.1) epsilon-related - fruit fly (Drosophila melanogaster)
N:Alternate names: protein kinase C 98F
C:Species: Drosophila melanogaster
C>Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 11-Jun-1999
C:Accession: B23392
R:Schaeffer, E.; Smith, D.; Mardon, G.; Quinn, W.; Zuker, C.
J. Biol. Chem. 269, 463-472, 1994
A:Title: Isolation and characterization of two new Drosophila protein kinase C genes, in
A:Reference number: B23392; MUID:87247301; PMID:7728775
A:Accession: B23392
A:Molecule type: mRNA
A:Residues: 1-634 <SCH>
A:Cross-references: GB:J04848; NID:g158128; PDB:1AAJ28614.1; PDB:G158129
C:Genetics:
A:Gene: FlyBase:PkC98F
A:Cross-references: FlyBase:FBgn0001003
C:Function:
A:Description: catalyzes the formation of peptidyl-serine phosphate or peptidyl-threonin
A:Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; pr
C:Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotransf
F:58-63/Region: pseudophosphorylation motif
F:72-121/Domain: protein kinase C zinc-binding repeat homology <K21>
F:147-196/Domain: protein kinase C zinc-binding repeat homology <K22>
F:309-317/Region: protein kinase ATP-binding motif
F:72-102,105,121/binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:85-88,110,113/binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:147,177,180,196/binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:160,163,185,198/binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:332,351,427,429/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 77.6%; Score 38; DB 1; Length 634;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Gb          1  MLGKPPFE 9
           1  :|||||
           495 MMAGQPPFE 503

RESULT 26
T43337
polo-like kinase-1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 01-Dec-2000
C:Accession: T43337; S44761
R:Chase, D.; Serafinas, C.; Ashcroft, N.; Kosinski, M.; Longo, D.; Ferris, D.K.; Gold
submitted to the EMBL Data Library, July 1998
A:Description: The polo-like kinase PLK-1 is required for nuclear envelope breakdown
A:Reference number: Z22438
A:Accession: T43337
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-648 <CHA>
A:Cross-references: EMBL:AF080581; PIDN:AAC34661.1
R:Favell, A.D.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid C14B9.
A:Reference number: S44617
A:Accession: S44761
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 'MKTL', 282-648 <FAV>
A:Cross-references: EMBL:L15188; NID:g289640; PID:g289648
C:Genetics:
A:Gene: plk-1
A:Map position: 3
A:Introns: 391/3; 540/3; 578/3
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

Query Match 77.6%; Score 38; DB 2; Length 648;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy          1  MLGKPPFE 9
           1  :|||||
           228 LLFQPPFE 236

RESULT 27
A53530
protein kinase C (EC 2.7.1.1) epsilon-related - Caenorhabditis elegans
N:Alternate names: protein kinase C PKCIB, neuronal
C:Species: Caenorhabditis elegans
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jun-1999
C:Accession: A53530
R:Land, M.; Islas-Trejo, A.; Freedman, J.H.; Rubin, C.S.
J. Biol. Chem. 269, 9234-9244, 1994
A:Title: Structure and expression of a novel, neuronal protein kinase C (PKCIB) from
A:Reference number: A53530; MUID:94179345; PMID:8132661
A:Accession: A53530
A:Molecule type: mRNA
A:Residues: 1-707 <LAN>
A:Cross-references: GB:U00181; NID:g484065; PIDN:AAA18259.1; PID:g392435
C:Genetics:
A:Gene: kin-13
A:Map position: V
A:Note: located near myo-3, col-1, and CPROT/2 genes
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threos
A:Note: activity is calcium-independent, phospholipid-dependent, and activated by dia
C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology;
C:Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotra
F:157-162/Region: pseudophosphorylation motif
F:171-220/Domain: protein kinase C zinc-binding repeat homology <K21>
F:249-298/Domain: protein kinase C zinc-binding repeat homology <K22>
F:376-638/Domain: protein kinase homology <KIN>

```

F:194-392/Region: protein kinase ATP-binding motif
 F:171-201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:184,187,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:249,279,282,298/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:262,265,287,290/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:467,426,502,504/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 77.6%; Score 38; DB 1; Length 707;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLCKPPPE 9
 : : : : :
 Db 570 MMAGQPPPE 578

RESULT 28
 KIR3CE
 C:Species: *Oryctolagus cuniculus* (domestic rabbit)
 C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 21-Nov-1997
 C:Accession: A29880
 C:GlnO, S.; Akita, Y.; Komno, Y.; Imaoh, S.; Suzuki, K.
 Cell 53, 731-741, 1998
 A:Title: A novel phorbol ester receptor/protein kinase, nPKC, distantly related to the P
 A:Reference number: A29880; MUID:8623367; PMID:9370672
 A:Accession: A29880
 A:Molecule type: mRNA
 A:Residues: 1-736 <CHN>
 A:Cross-references: GB:M200:4
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
 A:Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
 C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; ph
 C:Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid B
 F:156-161/Region: pseudophosphorylation motif
 F:170-220/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:243-292/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:426-667/Domain: protein kinase homology <KIN>
 F:413-422/Region: protein kinase ATP-binding motif
 F:170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:436,455,531,533/Active site: Lys, Glu, Asp, Lys #status predicted
 F:702,709/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query Match 77.6%; Score 38; DB 1; Length 578;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLCKPPPE 9
 : : : : :
 Db 599 MMAGQPPPE 607

RESULT 29
 S28942
 C:Species: *Homo sapiens* (man)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jun-1999
 C:Accession: S28942
 C:Baista, P.; Strickland, M.B.; Holmes, W.; Iomris, C.A.; Ballas, L.M.; Burns, D.J.
 Biochim. Biophys. Acta 1132, 154-160, 1992
 A:Title: Sequence and expression of human protein kinase C-epsilon.
 A:Reference number: S28942; MUID:93003318; PMID:1362635
 A:Accession: S28942
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-737 <BAS>
 A:Cross-references: EMBL:X65293; NID:935494; PDB:CAA6368.1; PID:935495
 C:Comment: This is a calcium-independent, phospholipid-dependent, serine- and threonine-
 of inositol phospholipids. This protein is a receptor for tumor-promoting phorbol ester

C:Genetics:
 A:Gene: GDB:PRKCE
 A:Cross-references: GDB:128039; OMIM:175975
 A:Map position: 3pter-3qter
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
 A:Note: activity is calcium-independent, phospholipid-dependent, and activated by di
 C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology;
 C:Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphot
 F:156-161/Region: pseudophosphorylation motif
 F:170-220/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:243-292/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:406-668/Domain: protein kinase homology <KIN>
 F:414-422/Region: protein kinase ATP-binding motif
 F:170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted
 F:703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status

Query Match 77.6%; Score 38; DB 1; Length 737;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MLLCKPPPE 9
 : : : : :
 Db 600 MMAGQPPPE 608

RESULT 30
 KIR3CE
 C:Species: *Rattus norvegicus* (Norway rat)
 C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 C:Accession: B28163; B26408; S00216
 R:Ono, Y.; Fujii, T.; Ogita, K.; Kikkawa, U.; Igarashi, K.; Nishizuka, Y.
 J. Biol. Chem. 263, 6927-6932, 1988
 A:Title: The structure, expression, and properties of additional members of the prot
 A:Reference number: A92717; MUID:88198270; PMID:2834597
 A:Accession: B28163
 A:Molecule type: DNA
 A:Residues: 1-737 <ONG>
 A:Cross-references: GB:M8331; NID:9206182; PID:AAA1872.1; PID:9206183
 R:Huusey, G.M.; O'Brian, C.A.; Johnson, M.D.; Kirchmeier, P.; Weinstein, I.B.
 Proc. Natl. Acad. Sci. U.S.A. 84, 1065-1069, 1987
 A:Title: Isolation of cDNA clones encoding protein kinase C: evidence for a protein
 A:Reference number: A94145; MUID:87147193; PMID:3469647
 A:Accession: B26408
 A:Molecule type: mRNA
 A:Residues: 397-447; GORGLHDDREDFGSGAET, 467, 'LSNPITLLLPDQPPPLLRQ', 487-545, 'C', 547-
 A:Cross-references: GB:M5523; NID:9206192; PID:AAA1877.1; PID:9206193
 C:Comment: Protein kinase C epsilon and epsilon' appear to be encoded by the same ge
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-thre
 A:Note: activity is calcium-independent, phospholipid-dependent, and activated by di
 C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology
 C:Keywords: alternative splicing; ATP; autophosphorylation; duplication; phorbol est

Query Match 77.6%; Score 38; DB 1; Length 737;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      1 MLLGKPPPE 9
DB      600 MMAGQPPPE 608

RESULT 31
KIMSCE
Protein kinase C (EC 2.7.11.-) epsilon - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 21-Nov-1997
C:Accession: S02270
R:Schaap, D.; Parker, P.J.; Bristol, A.; Kriz, R.; Knopf, J.
FEBS Lett. 243, 351-357, 1989
A:Title: Unique substrate specificity and regulatory properties of PKC-epsilon: a rational
A:Reference number: S02270; MUID:93137541; PMID:2917656
A:Accession: S02270
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-737 <SCH>
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A:Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C:Superfamily: protein kinase C delta; protein kinase C zeta-binding repeat homology; p
C:Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid B
F:136-151/Region: pseudophosphorylation motif
F:170-220/Domain: protein kinase C zeta-binding repeat homology <Z1>
F:243-292/Domain: protein kinase C zeta-binding repeat homology <Z2>
F:406-668/Domain: protein kinase C zeta-binding repeat homology <K2>
F:414-422/Region: protein kinase ATP-binding motif
F:170, 201, 204, 220/Binding site: zinc (His, Cys, Cys) #status predicted
F:183, 166, 209, 212/Binding site: zinc (His, Cys, Cys) #status predicted
F:243, 273, 276, 292/Binding site: zinc (His, Cys, His, Cys) #status predicted
F:256, 259, 281, 284/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:437, 456, 532, 534/Active site: Cys, Glu, Asp, Lys #status predicted
F:703, 710/Binding site: phosphate (Thr) (covalent); by autophosphorylation) #status pred

Query Match 77.6%; Score 38; DB 1; Length 737;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 MLLGKPPPE 9
DB      600 MMAGQPPPE 608

RESULT 32
A55748
Protein kinase (EC 2.7.1.37) Sak-a - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 24-Sep-1999
C:Accession: A55748
R:Roder, C.; Notaro, S.; Yousefi, S.; Haffornan, M.; Dennis, J.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 6388-6392, 1994
A:Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosophila
A:Reference number: A55748; MUID:94294387; PMID:8422793
A:Accession: A55748
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-925 <FOO>
A:Cross-references: DB:129479; NID:9487869; PID:AA037648.1; PID:9487870
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP; phosphotransferase
F:10-265/Domain: protein kinase homology <KIN>
F:18-26/Region: protein kinase ATP-binding motif

Query Match 77.6%; Score 38; DB 2; Length 925;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGKPPPE 9
DB      204 LLIGRPFD 212

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RESULT 33
S51899
Probable protein kinase HRC1081 (EC 2.7.11.-) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein 00784; protein YOL100W
C:Species: Saccharomyces cerevisiae
C:Date: 05-May-1995 #sequence_revision 03-Aug-1995 #text_change 19-Apr-2002
C:Accession: S51899; S59175; S66796
R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, January 1995
A:Description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV includ
and a Delta.
A:Reference number: S51848
A:Accession: S51899
A:Molecule type: DNA
A:Residues: 1-1081 <VAN>
A:Cross-references: EMBL:248149; NID:9663234; PID:CAA88162.1; PID:9663254
R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Yeast 11, 1069-1075, 1995
A:Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including t
a delta element.
A:Reference number: S59156; MUID:96076631; PMID:7502582
A:Accession: S59175
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1081 <VAN>
A:Cross-references: EMBL:248149; NID:9663234; PID:CAA88162.1; PID:9663254
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
R:Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66791
A:Accession: S66796
A:Molecule type: DNA
A:Residues: 1-1081 <DUR>
A:Cross-references: EMBL:274842; NID:91419351; PID:CAA93113.1; PID:6251892; PID:9141
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:PKH2
A:Cross-references: SGD:S0005460
A:Map position: 15L
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: ATP; phosphotransferase
F:177-443/Domain: protein kinase homology <KIN>
F:185-193/Region: protein kinase ATP-binding motif

Query Match 77.6%; Score 38; DB 2; Length 1081;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 MLLGKPPPE 9
DB      382 MIAGKPPFK 390

RESULT 34
T29223
hypothetical protein F55G1.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C:Accession: T29223
R:Murray, J.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A:Description: The sequence of C. elegans cosmid F55G1.
A:Reference number: Z20591
A:Accession: T29223
A:Status: preliminary; translated from CB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-615 <MUR>
A:Cross-references: EMBL:U58750; PID:AA00642.1; GSPDB:GN00022; CESP:F55G1.8
A:Experimental source: strain Bristol N2; clone F55G1
C:Genetics:
A:Gene: CESP:F55G1.8

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F:345-353/Region: protein kinase ATP-binding motif
F:37,67,70,86/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:50,53,75,78/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:102,132,135,151/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:115,118,140,143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:368/Active site: Lys #status predicted
F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status: i

Query Match 75.5% Score 37; DB 1; Length 672;
Best Local Similarity 66.7% Pred. No. 45;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLIGKPPFE 9
   || :|||:
Db 531 MLAGQPPFD 539

RESULT 37
KIRTC
Protein kinase C (EC 2.7.1.1) alpha - rat
N:Alternate names: protein kinase C type III
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C:Accession: S02248; S02620
R:Ono, Y.; Fujii, T.; Igarashi, K.; Kikkawa, U.; Ogita, K.; Nishizuka, Y.
Nucleic Acids Res. 16, 5199-5200, 1988
A:Title: Nucleotide sequences of cDNAs for alpha and gamma subpecies of rat brain p.
A:Reference number: S02129; MUID:88262515; PMID:3387228
A:Accession: S02248
A:Molecule type: mRNA
A:Residues: 1-672 <ON>

```

C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane
C:Comment: Phosphatidylserine protein kinase receptor for cancer promoting phorbol ester
C:Comment: "The zinc-stabilized regions bind diacylglycerol and phorbol esters."
C:Superfamily: protein kinase C alpha; protein kinase C2 region homology; protein 'A'
C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester binding
F:19-29/Region: phospholipid binding #status experimental
F:22-27/Region: pseudophosphorylation motif
F:37-86/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F:102-151/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F:152-264/Domain: protein kinase C C2 region homology <KC2>
F:337-597/Domain: protein kinase homology <KIN>
F:345-353/Region: protein kinase ATP-binding motif
F:368/Active site: Lys #status predicted
F:631,638/Binding site: phosphate [Thr] (covalent) (by autophosphorylation) #status

Db 53: MLAGPPFD 539

jj j:lll:
53: MLAGPPFD 539

RESULT 38
KIMSCA
Protein kinase C (EC 2.7.11-) alpha - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C:Accession: S07104; J53G78
R: Megidish, T.; Mazurek, N.
Nature 342, 807-811, 1989
A:Title: A mutant protein kinase C that can transform fibroblasts.
A:Reference number: S07104; NUID:90098082; PMID:2601739
A:Accession: S07104
A:Molecule type: mRNA
A:Residues: 1-672 <MEG>
A:Cross-references: GB:X5:2685; GB:X5:603; NID:949938; PIDN:CAA36908.1; PID:949939
A:Experimental source: strain Ba,b/c
R: Rose-John, S.; Ullrich, A.; Marks, F.

Gene 74, 465-471, 1988
 A:Title: Molecular cloning of mouse protein kinase C (PKC) cDNA from Swiss 3T3 fibroblast
 A:Reference number: J00078; XUID:89242737; PMID:2469625
 A:Accession: J00078
 A:Molecule type: mRNA
 A:Residues: 1-146 'D', 148-217 'N', 219-276 'AH', 279-312 'V', 314 466 'N', 468-471 'N', 473-5
 A:Cross references: GB:M25811
 A:Note: The authors translated the codon AAC for residue 141 as Lys; the sequence shown
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-sp
 f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters,
 C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may
 C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
 C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kin
 C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bindin
 F:19-29/Region: pseudophosphorylation motif
 F:22-27/Region: protein kinase C zinc-binding repeat homology <K21>
 F:37-86/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:152-264/Domain: protein kinase C C2 region homology <K2>
 F:337-597/Domain: protein kinase homology <K1N>
 F:345-353/Region: protein kinase ATP-binding motif
 F:37,67,70,86/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:50,53,75,78/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:102,132,135,151/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:115,118,140,143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:368/Active site: Lys #status predicted
 F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query Match 75.5% Score 37; DB 1; Length 672;
 Best Local Similarity 66.7% Pred. No. 45;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGKPPFE 9
 DB 531 MLAGQPFED 539

RESULT 39
 KIRBC
 A:Title: Tissue specific expression of three distinct types of rabbit protein kinase C.
 A:Reference number: A26037; XUID:8114689; PMID:1616467
 A:Accession: C26037
 A:Molecule type: mRNA
 A:Residues: 1-672 <ORF>
 A:Cross references: FMBL:X04796; NID:q1632; PISN:CAA94943; PID:g1673
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-sp
 f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters,
 C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may
 C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
 C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kin
 C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bindin
 F:19-29/Region: pseudophosphorylation motif
 F:22-27/Region: protein kinase C zinc-binding repeat homology <K21>
 F:37-86/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:102-151/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:152-264/Domain: protein kinase C C2 region homology <K2>
 F:337-597/Domain: protein kinase homology <K1N>
 F:345-353/Region: protein kinase ATP-binding motif
 F:37,67,70,86/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:50,53,75,78/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:102,132,135,151/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:115,118,140,143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:368/Active site: Lys #status predicted
 F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status pred

Query Match 75.5% Score 37; DB 1; Length 672;
 Best Local Similarity 66.7% Pred. No. 45;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGKPPFE 9
 DB 531 MLAGQPFED 539

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGKPPFE 9
 DB 531 MLAGQPFED 539

RESULT 40
 KIRBC
 A:Title: The complete primary structure of protein kinase C - the major phorbol ester
 A:Reference number: A00621; XUID:86289425; PMID:3755547
 A:Accession: A00621
 A:Molecule type: mRNA
 A:Residues: 1-672 <PAR>
 A:Cross references: GB:M1373; NID:g163229; PISN:AAA30706.1; PID:g163530
 A:Experimental source: brain
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine
 f inositol phospholipids. This protein is a receptor for tumor-promoting phorbol este
 C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane
 C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
 C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein k
 C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bin
 F:19-29/Region: pseudophosphorylation motif
 F:22-27/Region: protein kinase C zinc-binding repeat homology <K21>
 F:37-86/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:102-161/Domain: protein kinase C C2 region homology <K2>
 F:152-264/Domain: protein kinase C C2 region homology <K2>
 F:337-597/Domain: protein kinase homology <K1N>
 F:345-353/Region: protein kinase ATP-binding motif
 F:37,67,70,86/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:50,53,75,78/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:102,132,135,151/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:115,118,140,143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:368/Active site: Lys #status predicted
 F:631,638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status p

Query Match 75.5% Score 37; DB 1; Length 672;
 Best Local Similarity 66.7% Pred. No. 45;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGKPPFE 9
 DB 531 MLAGQPFED 539

Search completed: November 14, 2003, 13:28:51
 Job time : 10.8 secs

GenCore version 5.1.6
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CV protein - protein search, using sw model

Run on: November 14, 2003, 12:56:44 ; Search time 6 6871 Seconds
(without alignment)
63.305 Million cell updates/sec

Title: US-09-736-076 17
Perfect score: 49
Sequence: 1 MLLXPPFE 9

Scoring table:
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41.*

Fred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	93.9	682	1	SNK_MOUSE
2	46	93.9	682	1	SNK_RAT
3	46	93.9	685	1	SNK_HUMAN
4	43	87.8	283	1	STK5_MOUSE
5	43	87.8	603	1	PLK1_HUMAN
6	43	87.8	603	1	PLK1_MOUSE
7	43	87.8	603	1	PLK1_RAT
8	41	83.7	403	1	STK6_HUMAN
9	41	83.7	407	1	STK6_XENLA
10	41	83.7	408	1	ST6L_XENLA
11	41	83.7	683	1	PI01_SCHPO
12	41	83.7	705	1	CEC5_YEAST
13	39	79.6	465	1	KPK1_ARATH
14	39	79.6	471	1	KP19_ARATH
15	39	79.6	576	1	POLO_DROME
16	39	79.6	679	1	KPC1_DROME
17	38	77.6	156	1	STKC_FIG
18	38	77.6	344	1	STKC_HUMAN
19	38	77.6	525	1	KEN8_YEAST
20	38	77.6	634	1	KPC3_DROME
21	38	77.6	646	1	PKN1_CGRL
22	38	77.6	649	1	PLK1_CAEEL
23	38	77.6	707	1	KPC2_CAEEL
24	38	77.6	736	1	KPCE_RAB7
25	38	77.6	737	1	KPCE_HUMAN
26	38	77.6	737	1	KPCE_MOUSE
27	38	77.6	737	1	KPCE_RAT
28	38	77.6	743	1	KPC2_APLCA
29	38	77.6	1081	1	KOKO_YEAST
30	37	75.5	615	1	P-K3_CAEEL
31	37	75.5	649	1	KPC1_APLCA
32	37	75.5	658	1	KPC1_LYTP1
33	37	75.5	672	1	KPCA_ECVIN

RESULT 1

ID	SNK_MOUSE	STANDARD	PRT	682 AA
AC	P53351			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Serine/threonine-protein kinase SNK (EC 2.7.1.-) (Serum inducible kinase).			
DE	kinase).			
GN	SNK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92375083; PubMed=1508211;			
RA	Simmons D.L., Neel B.G., Stevens R., Evett G., Eriksen R.L.;			
RT	"Identification of an early-growth-response gene encoding a novel putative protein kinase."			
RL	Mol. Cell. Biol. 12:4164-4169(1992).			
CC	FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS, WOUND HEALING OR NEOPLASIA.			
CC	TISSUE SPECIFICITY: BRAIN, LUNG AND HEART.			
CC	INDUCTION: BY SERUM AND PHORBOL ESTER.			
CC	SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	CDOS/POLO SUBFAMILY.			
CC	SIMILARITY: Contains 2 POLO box domains.			
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CC	EMBL; M96163; ; NOT ANNOTATED_CDS.			
DR	PIR; A44493; A44493.			
DR	MGI; MGI:1099790; Snk.			
DR	InterPro; IPR000959; POLO_box			
DR	InterPro; IPR000719; Prot_kinase			
DR	InterPro; IPR002290; Ser_thr_kinase			
DR	Pfam; PFC0069; pkinase; 1.			
DR	Pfam; PF00659; POLO_box; 2.			
DR	ProDom; PD000001; Prot_kinase; 1.			
DR	SMART; SM00220; S_TKc; 1.			
DR	PROSITE; PS50078; POLO_BOX; 2.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.			
FT	DOMAIN 54 59 POLY-HIS			
FT	DOMAIN 79 33; PROTEIN_KINASE			
FT	NP_BIND 85 93 ATP (BY SIMILARITY).			

P17252 homo sapien
P20444 mus musculus
P10102 oryctolagus
P05696 rattus norv
P05128 bos taurus
P05129 homo sapien
P05697 mus musculus
P10829 oryctolagus
Q00229 mytilus edu
Q9ub99 homo sapien
O55099 rattus norv
O70126 mus musculus

```
FT BINDING 108 108 ATP (BY SIMILARITY).
FT ACT SITE 202 202 BY SIMILARITY.
FT DOMAIN 507 570 POLO BOX 1.
FT DOMAIN 633 674 POLO BOX 2.
SQ SEQUENCE 682 AA: 77811 MW: 586DEA3FD238A9D CRC64;
Query Match 93.9% Score 46; DB 1; Length 682;
Best Local Similarity 88.9% Pred. No. 0.35;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
DB 270 MLLGRPPPE 278

RESULT 2
SNK_RAT STANDARD; PRT; 682 AA.
AC Q9R012;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Serine/threonine-protein kinase SNK (EC 2.7.1.1-) (Serum inducible kinase).
GN SNK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1].
RP MEDLINE=99452740; PubMed=10521327;
RA Kauselmann G., Weiler M., Wulff P., Jussberger S., Konietzko U.,
RA Scafield J., Staubli U., Beyerle-Hahn U., Streibhardt K., Kuhl D.;
RT "The polo-like protein kinases Pnk and Snk associate with a Cal(2+)-and
RT integrin-binding protein and are regulated dynamically with synaptic
RT plasticity."
RL EMBO J. 18:5528-5539(1999).
CC -!- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL
CC TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS,
CC WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 2 POLO BOX DOMAINS.
CC
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CC or send an email to license@sib-sib.ch)
CC
CC ENBL: AFI36583; AAF08366.1;
CC InterPro: IPR000959; POLO_BOX.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002280; Ser_thr_kinase.
CC Pfam: PF00069; Pkinase.1.
CC Pfam: PF00659; POLO_box.2.
CC ProDom: PD000001; Prot_kinase.1.
CC SMART: SMC220; S_TKc.1.
CC PROSITE: PS00079; POLO_BOX.2.
CC PROSITE: PS00187; PROTEIN_KINASE_ATF.1.
CC PROSITE: PS00011; PROTEIN_KINASE_DOM.1.
CC PROSITE: PS01008; PROTEIN_KINASE_ST.1.
CC Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
FT DOMAIN 54 59 POLY-HIS
FT DOMAIN 79 331 PROTEIN_KINASE
FT NP_BIND 85 93 ATP (BY SIMILARITY).
FT BINDING 108 108 ATP (BY SIMILARITY).
FT ACT_SITE 202 202 BY SIMILARITY.
FT DOMAIN 507 570 POLO BOX 1.
FT DOMAIN 603 674 POLO BOX 2.
```

```
SQ SEQUENCE 682 AA: 77919 MW: 58C50DBDE83D5F3 CRC64;
Query Match 93.9% Score 46; DB 1; Length 682;
Best Local Similarity 88.9% Pred. No. 0.35;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
DB 270 MLLGRPPPE 278

RESULT 3
SNK_HUMAN STANDARD; PRT; 685 AA.
AC Q9NYX3; O60679; Q96CV7; Q9UE61;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase SNK (EC 2.7.1.1-) (Serum inducible kinase).
GN SNK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1].
RP SEQUENCE FROM N.A.
RA Anderson K.M., Neturkar S.S., Hansbury M.J., Fornwald J., Scott G.,
RA Bourzyk M., Mui P., Inbrugia C.S., Carlson K., Marshall L.A.,
RA Roshak A.K.;
RT "Identification and characterization of human serum-inducible kinase
RT (SNK), a novel member of the polo-kinase family of cell cycle
RT regulators: potential implication for regulation of vascular smooth
RT muscle proliferation."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3].
RP SEQUENCE FROM N.A.
RA Tissue=Skin;
RX MEDLINE=2338257; PubMed=12477932;
RA Strausberg R.J., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustun T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4].
RP SEQUENCE OF 110-408 FROM N.A.
RA Fidler C., Boulwood J., Wang Jabs E., Waincoat J.S.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL
CC TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS,
CC WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
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CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -----
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CC -----
CC EMBL: AF059617; ARC14573.1;
CC EMBL: AF223574; AAF62397.1;
CC EMBL: U85755; AAD00575.1;
CC EMBL: BC013879; AAI13879.1;
CC MIM: 607023;
CC -----
CC InterPro: IPR000959; POLO box.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_Thr_kinase.
CC Pfam: PF00069; Pkinase; 1.
CC Pfam: PF00659; POLO box; 2.
CC SMART: SM00220; S_TKC; 1.
CC PROSITE: PS50078; POLO BOX; 2.
CC PROSITE: PS00157; PROTEIN KINASE ATP; 1.
CC PROSITE: PS50011; PROTEIN KINASE DOM; 1.
CC PROSITE: PS50010; PROTEIN KINASE ST; 1.
CC Transferrase: Serine/threonine-protein kinase; ATP binding; Repeat.
CC -----
CC DOMAIN 57 64 POLY-HIS.
CC FT DOMAIN 82 334 PROTEIN KINASE.
CC FT NP_BIND 88 96 ATP (BY SIMILARITY).
CC FT BINDING 111 111 ATP (BY SIMILARITY).
CC FT ACT_SITE 205 205 BY SIMILARITY.
CC FT DOMAIN 510 573 POLO BOX 1.
CC FT DOMAIN 606 677 POLO BOX 2.
CC FT CONFLICT 28 28 A -> G (IN REF. 1).
CC SEQUENCE 685 AA; 7823 MW; 6429666ED81CB333 CR^64;

Query Match 93.98; Score 46; DB 1; Length 685;
Best Local Similarity 88.99; Pred. NC. 0.35;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
|||..|
|..|..|
273 MLLGKPPFE 281

RESULT 4
STKC MOUSE STANDARD; PRT; 281 AA
AC O88445; O8JLC2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase 13 (EC 2.7.1.37) (Aurora/Ipl1/Eg2
DE protein 1) (Aurora-C).
GS STX13 OR AIE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=99025616; PubMed=9809744;

Tseng T.C., Chen S.H., Hsu Y.P., Tang T.K.
R Characterization of two novel testis-specific protein kinases (AIE1,
R AIE2) related to yeast and fly chromosome segregation regulators."
R CNA Cell Biol. 17:823-833(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=2555164; PubMed=11078217;

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RA Hu H.M., Chuang C.K., Lee M.J., Tseng T.C., Tang T.K.;
RA "Genomic organization, expression, and chromosome localization of a
RA third aurora-related kinase gene, Aie1."
RA DNA Cell Biol. 19:679-688(2000).
CC -!- FUNCTION: May play a part in organizing microtubules in relation
CC to the function of the centrosome/spindle pole during mitosis.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to spindle pole from anaphase to
CC cytokinesis (by similarity).
CC -!- TISSUE SPECIFICITY: Expressed only in testis.
CC -!- DEVELOPMENTAL STAGE: Expressed on day 14 dpc in prepubertal
CC testis, expression reached its plateau on day 21 dpc and remained
CC at a high level in adult.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC -----
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CC -----
CC EMBL: AF054620; AAC25954.1;
CC EMBL: AF195272; AAF25838.1;
CC HSP: Q63450; A06.
CC MGD: MGI:1321119; S:k13.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_Thr_kinase.
CC InterPro: IPR001245; Tyr_kinase.
CC Pfam: PF00069; Pkinase; 1.
CC PRINTS: PR00109; TYRKINASE.
CC PRODOM: PD000001; Prot_kinase; 1.
CC SMART: SM00220; S_TKC; 1.
CC PROSITE: PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE: PS00108; PROTEIN KINASE ST; 1.
CC PROSITE: PS50011; PROTEIN KINASE DOM; 1.
CC Cell cycle; Transferrase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 16 266 PROTEIN KINASE.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT CONFLICT 74 74 R -> P (IN REF. 2).
FT SEQUENCE 282 AA; 32907 MW; 7CB9AEC4984B7883 CR^64;

Query Match 87.88; Score 43; DB 1; Length 282;
Best Local Similarity 77.81; Pred. NC. 0.54;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
|||..|
|..|..|
205 MLLGKPPFE 213

RESULT 5
PLK1 HUMAN STANDARD; PRT; 603 AA.
ID PLK1 HUMAN
AC P53350;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase PLK (EC 2.7.1.-) (PLK-1) (Serine-
DE threonine protein kinase 13) (STPK13).
GS PLK OR PLK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94289293; PubMed=4018557;

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RC STRAIN=C57BL/6; TISSUE=Bone marrow;
 RX MEDLINE=93281660; PubMed=8099445;
 RA Clay F.J., McEwen S.J., Bertonecello I., Wilks A.F., Dunn A.R.;
 RT "Identification and cloning of a protein kinase-encoding mouse gene,
 Plx, related to the polo gene of *Drosophila*";
 RJ Proc. Natl. Acad. Sci. U.S.A. 90:4882-4886(1993).
 RN (2);
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
 RX MEDLINE=9428929; PubMed=8018557;
 RA Hamataka R., Yaloid S., Smith W.R., O'Connell C.D., Longo D.L.,
 RA Ferris C.K.;
 RT "Cloning and characterization of human and murine homologues of the
Drosophila polo serine-threonine kinase";
 RJ Cell Growth Differ. 5:249-257(1994).
 RN (3);
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=94067140; PubMed=7902533;
 RA Lake R.G., Jelinek W.R.;
 RT "Cell cycle- and terminal differentiation-associated regulation of
 the mouse RNA encoding a conserved mitotic protein kinase";
 RJ Mol. Cell. Biol. 13:7793-7801(1993).
 RN (1);
 RP FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
 DURING G1 OR S PHASE.
 CC -1: SUBCELLULAR LOCATION: Nuclear.
 CC -1: TISSUE SPECIFICITY: NEWBORN AND ADULT SPLEEN, FETAL AND NEWBORN
 CC KIDNEY, LIVER, BRAIN, THYMUS AND ADULT BONE MARROW, THYMUS,
 CC OVARY AND TESTES.
 CC -1: DEVELOPMENTAL STAGE: IN THE THYMUS, LEVELS INCREASED DURING FETAL
 CC DEVELOPMENT, WERE HIGHEST IN NEWBORN ANIMALS AND DECREASED IN THE
 CC ADULT. IN THE TESTES, THE PLX LEVELS WERE HIGHER IN THE ADULT THAN
 CC IN PREPUBESCENT MICE WHILE IN THE OVARY, THE LEVELS WERE HIGHER IN
 CC THE PREPUBESCENT MICE. ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
 CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
 CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
 CC DURING S PHASE.
 CC -1: SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1: SIMILARITY: Contains 2 POLO box domains.
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 CC -----
 CC EMBL: L06144; AAA39948.1;
 CC EMBL: U01263; AAA56635.1;
 CC EMBL: L19558; AAA18071.1;
 CC PIR: A47545; A47545;
 CC PIR: A54596; A54596;
 CC MGI: 97621; Plx.
 CC InterPro: IPR000399; POLO box.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR002290; Ser_thr_kinase.
 CC Pfam: PF00069; Pkinase.1.
 CC Pfam: PF00659; POLO box.2.
 CC ProDom: PD000031; Prot_kinase.1.
 CC SMART: SM00220; S_TKc.1.
 CC PROSITE: PS00078; POLO BOX.2.
 CC PROSITE: PS0107; PROTEIN_KINASE_ATP.1.
 CC PROSITE: PS0107; PROTEIN_KINASE_DOM.1.
 CC PROSITE: PS0108; PROTEIN_KINASE_ST.1.
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding; Repeat;
 CC Nuclear protein.
 CC DOMAIN 53 305 PROTEIN_KINASE.
 CC NP_BIND 59 67 ATP (BY SIMILARITY).
 CC BINDING 82 82 ATP (BY SIMILARITY).
 CC ACT_SITE 176 176 BY SIMILARITY.
 CC DOMAIN 417 490 POLO BOX 1.
 CC -----

FT DOMAIN 515 584 POLO BOX 2.
 FT CONFLICT 4 4
 FT CONFLICT 15 15 A -> V (IN REF. 1).
 FT CONFLICT 23 23 A -> T (IN REF. 1).
 FT CONFLICT 27 27 P -> L (IN REF. 1).
 FT CONFLICT 29 29 V -> L (IN REF. 1).
 FT CONFLICT 29 29 G -> S (IN REF. 1).
 FT CONFLICT 41 41 P -> L (IN REF. 1).
 FT CONFLICT 54 54 V -> I (IN REF. 1).
 FT CONFLICT 495 495 A -> R (IN REF. 1).
 SQ SEQUENCE 603 AA; 68300 MW; 1B980646366EPA10 CRC64;
 Query Match 87.8%; Score 43; DB 1; Length 603;
 Best Local Similarity 77.8%; Pred. No. 1.2;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGKPPPE 9
 DB 244 LLVGKPPPE 252
 RESULT 7
 PLK1 RAT
 ID PLK1 RAT STANDARD; PRT; 603 AA.
 AC Q62673;
 DT 16-OCT-2001 (Rel. 40, Created);
 DT 16-OCT-2001 (Rel. 40, Last sequence update);
 DT 16-OCT-2001 (Rel. 40, Last annotation update);
 DE Serine/threonine-protein kinase PLK (EC 2.7.1.1-) (PLK-1).
 GN PLK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RA Amstrup J., Hansen J.A., Hxarlis Nielsen J.;
 RA Submitted (May 1994) to the EMBL/GenBank/DBJ databases.
 CC -1: FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
 CC DURING G1 OR S PHASE (BY SIMILARITY).
 CC -1: SUBCELLULAR LOCATION: Nuclear (BY SIMILARITY).
 CC -1: SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1: SIMILARITY: Contains 2 POLO box domains.
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 CC -----
 CC EMBL: U0188; AAA18885.1;
 CC InterPro: IPR000959; POLO box.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR002290; Ser_thr_kinase.
 CC Pfam: PF00069; Pkinase.1.
 CC Pfam: PF00659; POLO box.2.
 CC ProDom: PD000001; Prot_kinase.1.
 CC SMART: SM00220; S_TKc.1.
 CC PROSITE: PS00078; POLO BOX.2.
 CC PROSITE: PS0107; PROTEIN_KINASE_ATP.1.
 CC PROSITE: PS0107; PROTEIN_KINASE_DOM.1.
 CC PROSITE: PS0108; PROTEIN_KINASE_ST.1.
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding; Repeat;
 CC Nuclear protein.
 CC DOMAIN 53 305 PROTEIN_KINASE.
 CC NP_BIND 59 67 ATP (BY SIMILARITY).
 CC BINDING 82 82 ATP (BY SIMILARITY).
 CC ACT_SITE 176 176 BY SIMILARITY.
 CC DOMAIN 417 480 POLO BOX 1.
 CC DOMAIN 515 584 POLO BOX 2.

SQ SEQUENCE 503 AA; 68313 MW; 107AFB3B7EDCC02 CHK64;
 Query Match 67.8%; Score 43; DB 1; Length 603;
 Best local Similarity 77.8%; Pred. No. 1.2;
 Matches 7; Conservative 2; Mismatches 0; Gaps 0;
 QY : MLGKPPFE 9
 DB 244 LLVGKPPFE 252
 RESULT 8
 STK6 HUMAN
 ID STK6 HUMAN STANDARD; PRT; 403 AA.
 AC Q14945; O63445; O75873; Q9B0C6; Q9UPQ5;
 DT 28-FEB-2003 (Rel. 41, Created;
 DT 28-FEB-2003 (Rel. 41, Last sequence update;
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Serine/threonine kinase 6 (EC 2.7.1.37) (Serine/threonine kinase 15)
 DE (Aurora/TPK-related kinase 1) (Aurora-related kinase 1) (ARK1)
 DE (Aurora-A) (Breast-tumor-amplified kinase)
 DN STK6 OR STK15 OR AIK OR ARK1 OR AURA OR BTK.
 OS Homo sapiens (Human)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=97298083; PubMed=915323;
 RA Kimura M., Kotani S., Hattori T., Suji N., Yoshioka T., Todokoro K.,
 RA Okano Y.;
 PT "Cell cycle-dependent expression and spindle pole localization of a
 PT novel human protein kinase, Ark, related to Aurora of Drosophila and
 ST yeast Ipl1";
 RT J. Biol. Chem. 272:13766-13771(1997);
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98183439; PubMed=9514916;
 RA Shindo N., Nakano H., Kuroyanagi H., Shirasawa T., Mahara M.,
 RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
 PT "cDNA cloning, expression, subcellular localization, and chromosomal
 ST assignment of mammalian aurora homologues, aurora-related kinase (ARK)
 RT 1 and 2";
 RT Biochem. Biophys. Res. Commun. 244:1544-1548(1998);
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast;
 RX MEDLINE=98442657; PubMed=9771714;
 RA Zhou H., Kuang C., Zhong L., Kuo W., Gray J.W., Sahin A.;
 RA Brinkley B.R., Sen S.;
 PT "Tumour amplified kinase STK15/ATK induces centrosome amplification,
 RT aneuploidy and transformation";
 RT Nat. Genet. 20:189-193(1998);
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Wang L., Thibodeau S.N.;
 PT "Mutational analysis of the STK15 gene in human tumors";
 RT Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA DeCukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley C.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhari P.D., Dunn P.,
 RA Ellington A.G., Frankland J.A., Fraser A., French Z., Garner P.,
 RA Graffan D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharshaino M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McEwan J.C., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RT Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20";
 RL Nature 414:865-871(2001);
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cervix, Colon, Kidney, and Muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Boudreau M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.J., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002);
 RN [7]
 RP CELL-CYCLE REGULATION.
 RX MEDLINE=21895866; PubMed=11790771;
 RA Tanaka M., Ueda A., Kanamori H., Ideguchi H., Yang J., Kitajima S.,
 RA Ishiguro Y.;
 RT "Cell-cycle-dependent regulation of human aurora A transcription is
 RT mediated by periodic repression of E4TF1";
 RJ J. Biol. Chem. 277:10719-10726(2002);
 RN [8]
 RP REVIEW.
 RX MEDLINE=21306577; PubMed=11413462;
 RA Nigg E.A.;
 RT "Mitotic kinases as regulators of cell division and its checkpoints";
 RL Nat. Rev. Mol. Cell Biol. 2:21-32(2001).
 CC -!- FUNCTION: May play a role in cell cycle regulation during anaphase
 CC and/or telophase, in relation to the function of the
 CC centrosome/spindle pole region during chromosome segregation.
 CC Maybe involved in microtubule formation and/or stabilization. May
 CC play a key role during tumor development and progression.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBCELLULAR LOCATION: Localizes on centrosomes in interphase cells
 CC and at each spindle pole in mitosis.
 CC -!- TISSUE SPECIFICITY: Highly expressed in testis and weakly in
 CC skeletal muscle, thymus and spleen. Also highly expressed in
 CC colon, ovarian, prostate, neuroblastoma, breast and cervical
 CC cancer cell lines. Expression is cell-cycle regulated, low in
 CC G1/S, accumulates during G2/M, and decreases rapidly after.
 CC -!- PTM: Phosphorylated.
 CC -!- DISEASE: Defects in STK6 are responsible for numerical centrosome
 CC aberrations including aneuploidy.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC AURORA SUBFAMILY.
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts

CC in positions 155, 125, 129, 235 and 241.
 CC -!- CAUTION: Although authors have considered STK6 and STK15 as two
 CC different proteins, it is clear that they are the same protein.
 CC -----
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 CC -----
 DP EMBL: D84212; SRA23532.1; AL1_FRAVE
 DR EMBL: AF038551; AA12708.1;
 DR EMBL: AF011467; AAC23448.1;
 CR EMBL: AF011467; AAC23448.1;
 DR EMBL: AF011468; AAC63902.1;
 DR EMBL: AF195947; AAF29508.1;
 DR EMBL: AF195942; AAF29508.1; JOINED.
 UR EMBL: AF195943; AAF29508.1; JOINED.
 DR EMBL: AF195944; AAF29508.1;
 DR EMBL: AF195945; AAF29508.1; JOINED.
 DR EMBL: AF195946; AAF29508.1; JOINED.
 DR EMBL: AL212914; CAC12717.1;
 DR EMBL: BC011280; AAH01280.1;
 DR EMBL: BC022499; AAH02499.1;
 DR EMBL: BC056423; AAH06423.1;
 DR EMBL: BC074644; AAH27464.1;
 DR GX: O14965;
 DR MIM: 602687;
 DR MIM: 603072;
 DR HSP: P24941; 1B0H.
 DR Genew: HGNC:11409; STK6.
 DR Genew: HGNC:11393; STK15.
 DR GO: GO:0005634; Cytoplasm; TAS.
 DR GO: GO:0005819; Cytoplasm; TAS.
 DR GO: GO:0007087; Mitosis; TAS.
 DR GO: GO:0006468; P-protein amino acid phosphorylation; TAS.
 DR InterPro: IPR000719; Prot kinase.
 DR InterPro: IPR02290; Ser Thr_pkinase.
 DR InterPro: IPR01245; Tyr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TK; 1.
 DR SMART: SM02197; Tyrc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
 KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 133 383 PROTEIN KINASE.
 FT NP_BIND 139 147 ATP (BY SIMILARITY).
 FT BINDING 162 162 ATP (BY SIMILARITY).
 FT ACT_SITE 256 256 BY SIMILARITY.
 FT ACT_SITE 31 31 F -> I (IN REF. 2).
 FT CONFLICT 57 57 V -> I (IN REF. 2).
 FT CONFLICT 57 57 V -> I (IN REF. 2).
 SQ SEQUENCE 453 AA: 45809 MW: 12541594834CD157 CRN4;
 Query Match 83.7%; Score 41; DB 1; Length 403;
 Best Local Similarity 87.5%; Pred. No. 1.9;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LLGKPPFE 9
 DB 323 LVGKPPFE 330
 RESULT 5
 STK6 XENLA
 ID STK6 XENLA STANDARD; PRT; 457 AA.
 AC Q91820.
 DT 28-FEB-2003 (rel. 41, Created).
 DT 28-FEB-2003 (rel. 41, Last sequence update).
 DT 28-FEB-2003 (rel. 41, Last annotation update).

DE Serine/threonine protein kinase Eg2 (EC 2.7.1.37) (p5g2) (p4659265).
 GN EG2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OC NCBI_TaxID=8395;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Egg;
 RX MEDLINE=98122855; PubMed=9454730;
 RA Roghi C., Giet R., Uzbekov R., Morin N., Chartrain I., Le Guellec R.,
 RA Couturier A., Doree M., Philippe M., Pigent C.,
 RT "The Xenopus protein kinase p5g2 associates with the centrosome in a
 RT cell cycle-dependent manner. Binds to the spindle microtubules and is
 RT involved in bipolar mitotic spindle assembly.";
 RL J. Cell Sci. 111:557-572(1998).
 CC -!- FUNCTION: Associates with the centrosome in a cell-cycle dependent
 CC manner and invades the microtubules at the poles of the spindle
 CC during mitosis suggesting that it may be involved in the correct
 CC formation of bipolar mitotic spindles.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis
 CC especially from prophase through anaphase. Partially colocalised
 CC with gamma tubulin in the centrosome, from S to M phase.
 CC -!- TISSUE SPECIFICITY: Highly expressed in ovary and testis.
 CC -!- PTM: Phosphorylated
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC AURORA SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: Z17267; CAA78915.1;
 DR PIR: S52243; S52243.
 DR HSP: P24941; 1A01.
 DR InterPro: IPR000719; Prot kinase.
 DR InterPro: IPR02290; Ser Thr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TK; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation.
 FT DOMAIN 140 390 PROTEIN KINASE.
 FT NP_BIND 146 154 ATP (BY SIMILARITY).
 FT BINDING 169 169 ATP (BY SIMILARITY).
 FT ACT_SITE 263 263 BY SIMILARITY.
 SQ SEQUENCE 407 AA: 46372 MW: DE1628A2C6D11277 CRC64;
 Query Match 83.7%; Score 41; DB 1; Length 407;
 Best Local Similarity 87.5%; Pred. No. 1.9;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LLGKPPFE 9
 DB 330 LVGKPPFE 337
 RESULT 10
 ST6L XENLA
 ID ST6L XENLA STANDARD; PRT; 408 AA.
 AC Q91819.
 DT 28-FEB-2003 (rel. 41, Created).
 DT 28-FEB-2003 (rel. 41, Last sequence update).
 DT 28-FEB-2003 (rel. 41, Last annotation update).

DE Serine/threonine protein kinase Eg2-like (EC 2.7.1.37) [p46X:Eg2].
OS Xenopus laevis (African clawed frog)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
CC Xeropodinae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
PC TISSUE=Egg;
RA Roghi C, Guillec R., Paris C., Couturier A., Philippe M.;
RT "Eg2, selected by differential screening encodes a new Xenopus protein
kinase family.";
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis,
CC especially from prophase through anaphase. Partially colocalised
CC with gamma tubulin in the centrosome, from S to M phase (By
CC similarity).
CC -!- PTM: Phosphorylated (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
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CC
DR EMBL: Z17256; CAA7891.4.1; ALT-INIT.
DR HSSP: P24941; IAQ1.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR022290; Ser_thr_kinase.
DR Pfam: PF00369; pk_kinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00223; S_TKc; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00157; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_TYR; 1.
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 142..192 PROTEIN KINASE
FT NP_BIND 142..164 ATP-BY-SIMILARITY
FT BINDING 169..169 ATP-BY-SIMILARITY
FT ACT_SITE 263 HY-SIMILARITY
SQ SEQUENCE 408 AA; 4646; MW: 97666.9235; AAEK QP64.

Query Match 83.7%; Score 41.09; Length 424;
Best Local Similarity 87.5%; Pred. No. 1.09;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LUCKPPE 9
DS 330 LVGKPPPE 337

RESULT 11
ID SCHPO
ID SCHPO STANDARD; PRT: 683 AA.
AC P5528; SCHPO
DT 01-OCT-1996 (Rel. 34, Created;
DT 01-OCT-1996 (Rel. 34, Last sequence update;
DT 15-SEP-2003 (Rel. 42, Last annotation update;
DE Serine/threonine-protein kinase p10; (EC 2.7.1.37).
GN PLQ; OR SPAC23C11.16
OS Schizosaccharomyces pombe (fission yeast).
CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
CC Schizosaccharomycetales; Schizosaccharomycetaceae;
CC Schizosaccharomycetes.
CX NCBI_TaxID=4896;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=95262899; PubMed=7744249;
RA Okura H., Hagan I.M., Glover D.M.;
RT "The conserved Schizosaccharomyces pombe kinase p10, required to
RT form a bipolar spindle, the actin ring, and septum, can drive septum
RT formation in G1 and G2 cells.";
RL Genes Dev. 9:1059-1073(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848403; PubMed=11859360;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras K., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Weljens I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Senito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Potaburg S.L.,
RA Cetrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Bartell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: REQUIRED TO FORM A BIPOLAR SPINDLE, THE ACTIN RING AND
CC SEPTUM. FUNCTIONS UPSTREAM OF THE WHOLE SEPTUM FORMATION PATHWAY,
CC INCLUDING ACTIN RING FORMATION (REGULATED BY LATE SEPTATION GENES)
CC AND SEPTAL MATERIAL DEPOSITION (REGULATED BY EARLY SEPTATION
CC GENES). BEHAVES AS A "SEPTUM-PROMOTING FACTOR", AND COULD ALSO BE
CC INVOLVED IN INDUCING OTHER LATE EVENTS OF CELL DIVISION
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- CDS/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC
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CC
DR EMBL: X85758; CAA59766.1; -;
DR EMBL: X85559; CAB11167.1; -;
DR PIR: T38254; T38254.
DR HSSP: O63450; 1A06.
DR GeneDB: Spombe; SPAC23C11.16; -;
DR InterPro: IPR000959; POLO_BOX.
DR InterPro: IPR00719; Prot_kinase.
DR InterPro: IPR02290; Ser_thr_kinase.
DR Pfam: PF00369; pk_kinase; 1.
DR Pfam: PF00659; POLO_BOX; 2.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00378; POLO_BOX; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

KW Transferase: Serine/threonine-protein kinase; ATP binding; Repeat.
 FT DOMAIN 41 296 PROTEIN KINASE.
 FT NP BIND 47 55 ATP (BY SIMILARITY).
 FT BINDING 69 69 ATP (BY SIMILARITY).
 FT ACT SITE 163 163 BY SIMILARITY.
 FT DOMAIN 502 567 POLO BOX 1.
 FT DOMAIN 604 670 POLO BOX 2.
 SC SEQUENCE 683 AA; 77301 MW; F1CUCF9B913927 CF 64;
 Query Match 83.7%; Score 41; DB 1; Length 63;
 Best Local Similarity 66.7%; Pred. No. 3.2;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY : MLGKPPFE 9
 : : : : :
 DB 233 LLIGKPPFQ 241
 : : : : :
 RESULT 12
 CDC5_YEAST
 ID CDC5_YEAST STANDARD; PR7; 705 AA.
 AC P34562;
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cell cycle protein kinase CDC5/MSD2 (EC 2.7.1.37).
 GN CDC5 OR PKX2 OR MSB2 OR YNR032C OR YN827C.03C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycus.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A64A;
 RA Kitada K., Sugino A., Johnston L.H., Johnson A.B.;
 RA MEDLINE=93309479; PubMed=8121244;
 RT "A multicopy suppressor gene of the Saccharomyces cerevisiae G1 cell
 cycle mutant gene dbf4 encodes a protein kinase and is identified as
 CDC5."
 RL Mol. Cell. Biol. 13:4445-4457(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Bowman S., Church C.M., Badcock K., Brown D., Chillingworth T.,
 RA Connor R., Dedman K., Devlin K., Genies S., Harlin N., Hunt S.,
 RA Jagers K., Iye G., Moule S., Odeh T., Pearson P., Wadsworth M.A.,
 RA Rice P., Skelton C., Walsh S., Whithead S., Barrett B.G.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
 XII."
 RL Nature 387:90-93(1997).
 RN [3]
 RP PHOSPHORYLATION OF SCC1.
 RA Alexandru G., Uhlmann F., Mechtler K., Poupard M.A., Nasmyth K.;
 RT "Phosphorylation of the cohesin subunit Scc1 by Polo/Cdc5 kinase
 regulates sister chromatid separation in yeast."
 RL Cell 105:459-472(2001).
 CC -!- FUNCTION: Protein kinase required for the cell cycle.
 CC Phosphorylates SCC1/MCD1.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein + ADP + a phosphoprotein.
 CC -!- SIMILARITY: BELONGS TO THE GSK/THR FAMILY OF PROTEIN KINASES.
 CC CDC5/POLO SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 POLO box domains.
 CC -----
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DR EMBL; M84220; AAA02576.1; -;
 DR EMBL; Z48613; CAAB8516.1; -;
 DR PIR; A48144; A48144.
 DR HSP; Q63450; IA06.
 DR SGD; S004601; CDC5.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0006261; P:DNA dependent DNA replication; IDA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
 DR InterPro; IPR000959; POLO box.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00659; POLO_Box; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS0078; POLO_BOX; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Cell cycle; Cell division; Serine/threonine-protein kinase;
 KW Transferase; ATP-binding; Repeat.
 FT DOMAIN 82 337 PROTEIN KINASE.
 FT NP BIND 88 96 ATP (BY SIMILARITY).
 FT BINDING 110 110 ATP (BY SIMILARITY).
 FT ACT SITE 204 204 BY SIMILARITY.
 FT DOMAIN 520 587 POLO BOX 1.
 FT DOMAIN 619 692 POLO BOX 2.
 SC SEQUENCE 705 AA; 81030 MW; B5A25F1BBEAA3DC CRC64;
 Query Match 83.7%; Score 41; DB 1; Length 705;
 Best Local Similarity 66.7%; Pred. No. 3.3;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY : MLGKPPFE 9
 : : : : :
 DB 274 LLIGKPPFQ 282
 : : : : :
 RESULT 13
 KPI1_ARATH
 ID KPI1_ARATH STANDARD; PR7; 465 AA.
 AC P42818;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serine/threonine-protein kinase AtPK1/AtPK6 (EC 2.7.1.-).
 GN AtPK1 OR AtPK6 OR At3G08730 OR F17014.20.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Landsberg erecta;
 RX MEDLINE=94292519; PubMed=7912697;
 RA Zhang S.-H., Lawton M.A., Hunter T., Lamb C.J.;
 RT "AtPK1, a novel ribosomal protein kinase gene from Arabidopsis. I.
 RT Isolation, characterization, and expression."
 RL J. Biol. Chem. 269:17586-17592(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=95129712; PubMed=7898736;
 RA Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,
 RA Shinozaki K.;
 RT "Two genes that encode ribosomal-protein S6 kinase homologs are
 RT induced by cold or salinity stress in Arabidopsis thaliana."
 RL FEBS Lett. 358:199-204(1995).
 RN [3]
 RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseid M.,
 RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA De Serey V., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
 RA De Simone V., Choisy N., Artiguenave F., Robert C., Brottier F.,
 RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Verzi A., D'Angelo V., Pallavicini A., Toppo S., Simonati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
 RA Reichert J., Scharfe M., Schoen C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
 RA Navarro P., Collado C., Berger-Llauro C., Purnelle B., Masuy D.,
 RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walte A., Utterback T., Fujii C.Y., Shea T.P.,
 RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
 RA Pai G., Miltischer C., Sellers P., Gill J.E., Feldblyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.,
 RA "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 thaliana";
 RL Nature 408:820-822(2000).
 RN [4].
 RP CHARACTERIZATION.
 RC STRAIN=cv. landsberg erecta;
 RX MEDLINE=94292520; PubMed=8021267;
 RA Zhang S.-H., Broome M.A., Lawton M.A., Hunter T., Lamb G.J.;
 RA "AtPK1, a novel ribosomal protein kinase gene from Arabidopsis. II.
 Functional and biochemical analysis of the encoded protein";
 RL J. Biol. Chem. 269:19593-19599(1994).
 CC 1- FUNCTION: COULD BE INVOLVED IN THE CONTROL OF PLANT GROWTH AND
 DEVELOPMENT. PHOSPHORYLATES TWO RIBOSOMAL PROTEINS, P14 AND P16.
 CC 2- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES.
 CC 3- DEVELOPMENTAL STAGE: PREDOMINATES DURING HIGH METABOLIC ACTIVITY
 IN GROWING BUDS, ROOT TIPS, LEAF MARGINS AND GERMINATING SEEDS.
 CC 4- PTM: UNDERGOES SERINE-SPECIFIC AUTOPHOSPHORYLATION.
 CC 5- SIMILARITY: BELONGS TO THE SER KINASE FAMILY OF PLANT KINASES.
 CC S6 KINASE SUBFAMILY.
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 CC -----
 ER EXEL: L29030; AAA21142.1;
 DR EM35: D42C56; BAA07656.1;
 DR EXBL: AC012562; AAG51351.1;
 DR PIR: S68462; S68462.
 DR HSSP: Q63450; 1A36.
 DR InterPro: IPR000961; Pkinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR022290; Ser_thr_kinase.
 DR Pfam: PF00369; Pkinase_1.
 DR Pfam: PF00433; Pkinase_C_1.
 DR ProDom: PD00001; Prot_kinase; 1.
 DR SMART: SM00133; S_TK_X1.
 DR SMART: SMC0220; S_TKX1.
 DR PROSITE: PS00107; PROTEIN_KINASE_AFP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 KW Transferase, Serine/threonine-protein kinase; ATP-binding;

KW Phosphorylation.
 FT DOMAIN 134 389 PROTEIN KINASE
 FT BP_BIND 140 148 ATP (BY SIMILARITY).
 FT BINDING 163 167 ATP (BY SIMILARITY).
 FT ACT_SITE 257 267 BY SIMILARITY.
 FT MUTAGEN 163 167 K->R: ACTIVITY SUBSTANTIALLY DIMINISHED.
 SQ SEQUENCE 455 AA; 52588 MW; 407133D674CA271F CRC64;
 Query Match 79.6%; Score 39; DB 1; Length 465;
 Best Local Similarity 87.5%; Pred.No. 5.3;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGKPPF 8
 DB 324 MLTGKPPF 331
 RESULT 14
 KP19_ARATH
 ID KP19_ARATH STANDARD; PRT; 471 AA.
 AC Q39030; Q949X5; Q9C5R1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Serine/threonine-protein kinase AtPK19 (EC 2.7.1.1-) (Ribosomal-protein
 S6 kinase homolog).
 GN ATPK19 OR AT3G08720 OR F7014.19.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_taxID=3702;
 RN [1].
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=95129712; PubMed=7829736;
 RA Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,
 RA Shinozaki K.;
 RT "Two genes that encode ribosomal-protein S6 kinase homologs are
 induced by cold or salinity stress in Arabidopsis thaliana";
 RL FEBS Lett. 358:199-204(1995).
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseid M.,
 RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA De Serey V., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
 RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Verzi A., D'Angelo V., Pallavicini A., Toppo S., Simonati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
 RA Reichert J., Scharfe M., Schoen C., Perez-Perez A., Ottenwaelder B.,
 RA Navarro P., Collado C., Berger-Llauro C., Purnelle B., Masuy D.,
 RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walte A., Utterback T., Fujii C.Y., Shea T.P.,
 RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
 RA Pai G., Miltischer C., Sellers P., Gill J.E., Feldblyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.,
 RA "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 thaliana";
 RT


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CC -----
CC EMBL: X63361; CAA44963.1;
CC EMBL: AE003514; AAF49036.1;
CC PIR: S22127; S22127.
CC HSP: G63450; LA06.
CC FlyBase: FBgn003124; polo.
CC GO: GO:0005813; C:centrosome; IDA.
CC GO: GO:0005819; C:spindle; IDA.
CC GO: GO:0004674; F:protein serine/threonine kinase activity; IDA.
CC GO: GO:0003140; P:male meiosis; IMP.
CC GO: GO:0007667; P:mitosis; IMP.
CC InterPro: IPR000959; POLO_BOX.
CC InterPro: IPR000719; Prot_Kinase.
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam: PFC0659; PKinase; 1.
CC Pfam: PFC0659; POLO_BOX; 2.
CC ProDom: PD000001; Prot_Kinase; 1.
CC SMART: SM00220; S_TKc; 1.
CC PROSITE: PS00078; POLO_BOX; 2.
CC PROSITE: PS00078; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE: PS00078; PROTEIN_KINASE_DCM; 1.
CC PROSITE: PS00078; PROTEIN_KINASE_ST; 1.
CC TRANSFERASE: Serine/threonine kinase; ATP-binding; Repeat.
CC DOMAIN 25 277
CC FT BINDING 31 39
CC FT BINDING 54 54
CC FT ACT_SITE 148 148
CC FT DOMAIN 398 461
CC FT DOMAIN 496 564
CC FT CONFLICT 187 187
CC FT CONFLICT 187 187
CC SEQUENCE 576 AA; 66973 MW; 522289AC9E889FAD Ck064;
Query Match 79.6%; Score 19, DP 1; Length 576;
Best Local Similarity 66.7%; Pred.No. 6.6; Mismatches 3; Indels 0; Gaps 0;
Matches 6; Conservative 3;
QY 1 MLLGXPFEE 9
DB 216 MLLGXPFEE 224
RESULT 16
ID KPC1 DROME STANDARD; FFT: 0.19 AA.
AC P01330; G9V7V6; G9V7V7.
CT 11-AUG-1987 (Ref: 25). Created.
CT 28-FEB-2003 (Ref: 41). Last sequence update.
DE Protein kinase C, brain isozyme (EC 2.7.11.1) (PKC) (dPKC53E:BR11).
GN PKC53E OR PKC1 OR CG6622.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephyroides; Ephyroididae; Drosophila.
CX EPHY_1; TaxID=7227;
RN [1]
SEQUENCE FROM N.A. (ISOFORM SHORT).
RC STRAIN=Canton-S, and Oregon-R;
RX MEDLINE=67218499; PubMed=3107983;
RA Rosenthal A., Rhee L., Yadegari R., Faro R., Ulrich A., Goeddel D.V.;
RT "Structure and nucleotide sequence of a Drosophila melanogaster
RT protein kinase C gene.";
RJ ENDO 5. 6:433-441(1987);
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196060; PubMed=10731132;
RA Adams M.D., Ceoliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Arantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Vandeil M.G., Zhang C., Chen L.X.,
RA Brandan R.C., Rogers Y.H.C., Blazek R.G., Champe M., Pfeiffer B.D.,

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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hoskin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Mortis J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spadling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskay R., Tector C., Turner B., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000);
RN [3]
SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=Berkley; Tissue=Ovary;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R.A., Gonzalez M., Guatin H., Kronmiller B., Li P.W., Liac G.,
RA Miranda A., Murgall C.J., Nunoo J., Paclet J.M., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
RA Celnik S.E.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P05130-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P05130-2; Sequence=VSP_004743;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: HEAD NEURAL TISSUE
CC -!- MISCELLANEOUS: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-
CC DEPENDENT, SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF OREGON-R.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. PKC
CC SUBFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X05076; CAA28736.1;
CC EMBL: X05279; CAA28890.2;

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RN SEQUENCE FROM N.A.
 RX MEDLINE=98193439; PubMed=9514916;
 RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mahara M.,
 RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.,
 RT "cDNA cloning, expression, subcellular localization, and chromosomal
 RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)
 RT 1 and 2.";
 RL Biochem. Biophys. Res. Commun. 244:284-292(1998).
 RN [2].
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99026855; PubMed=9829983;
 RA Tatsuka M., Katsuya H., Ota T., Tanaka T., Ohashi T., Suzuki F.,
 RA Terada Y.,
 RT "Multinuclearity and increased ploidy caused by overexpression of the
 RT aurora- and lpl-like midbody-associated protein mitotic kinase in
 RT human cancer cells.";
 RL Cancer Res. 58:4811-4816(1998).
 RN [3].
 RP SEQUENCE FROM N.A.
 RX TISSUE=Liver, and Spleen.
 RX MEDLINE=99077743; PubMed=9958806;
 RA Kimura M., Matsuda Y., Yoshiohka T., Sumi N., Okano Y.,
 RT "Identification and characterization of STK12/Aik2, a human gene
 RT related to aurora of Drosophila and yeast IPL1.";
 RL Oncogene. Cell Genet. 92:1147-152(1998).
 RN [4].
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21364697; PubMed=1171245;
 RA Prigent C., Gill R., Trower M., Sanson P.,
 RT "In silico cloning of a new protein kinase, Aik2, related to
 RT Drosophila aurora using the new tool: EST Blast.";
 RL In Silico Biol. 1:123-128(1999).
 RN [5].
 RP SEQUENCE FROM N.A.
 RA Zhang Q., Yu L., B. A.,
 RT "Cloning of a novel human gene homologous to mouse STK12.";
 RT Submitted (JUL 1997) to the EMBL/GenBank/DBJ databases.
 RN [6].
 RP SEQUENCE FROM N.A.
 RX TISSUE=lung, lymph, and muscle;
 RX MEDLINE=21388257; PubMed=12477972;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Liqun J.G.,
 RA Klausner R.D., Collins P.S., Wagner J., Scheu M., Schuler G.D.,
 RA Altschul S.F., Zeng B., Buetow K.H., Saeed A., Heath N.R.,
 RA Hopkins R.F., Jordan R., Moore T., Vaux S.J., Wang J., Wang J.,
 RA Datchenko B., Matsuda K., Fiume A., Chiu R., Hong L.,
 RA Stapleton M., Soares M.B., Schall D., Wang J., Scheraga T.B.,
 RA Brownstein Y.J., Udwin T.B., Tesnik P., Lathrop G., Franche C.,
 RA Raha S.S., Loquettano N.A., Peters M., Alkanon E., Mullan S.J.,
 RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Zeng R.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Jay S., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E., Lu X., Gibbs R.A.,
 RA Haney J., Heaton B., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green P.D., Dickson M.C.,
 RA Rodriguez A.C., Glimwood J., Schultz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywicki M.J., Skalska J., Smolius D.E.,
 RA Schnerch A., Schein J.E., Jones S.M., Xie M.A.,
 RT "Generation and initial analysis of more than 15,000 full length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12060-12065(2002).
 RN [7].
 RP REVIEW.
 RX MEDLINE=21306577; PubMed=11413442;
 RA Nigg E.A.,
 RT "Mitotic kinases as regulators of cell division and its checkpoints.";
 RL Nat. Rev. Mol. Cell Biol. 2:211-220(2001).
 CC FUNCTION: May be directly involved in regulating the cleavage of
 CC polar spindle microtubules and is a key regulator for the onset of
 CC cytokinesis during mitosis.
 CC CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated
 CC SUBCELLULAR LOCATION: Localized to the midzone of mitotic spindle

CC in late anaphase and concentrated into the midbody in telophase
 CC and cytokinesis. Colocalized with gamma tubulin in the mid-body.
 CC TISSUE SPECIFICITY: High level expression seen in the thymus. It
 CC is also expressed in the spleen, lung, testis, colon, placenta and
 CC fetal liver. Expressed during S and G2/M phase and expression is
 CC upregulated in cancer cells during M phase.
 CC DISEASE: Disruptive regulation of expression is a possible
 CC mechanism of the perturbation of chromosomal integrity in cancer
 CC cells through its dominant-negative effect on cytokinesis.
 CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC AURORA SUBFAMILY.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL; AF008552; AAC12709.1; -
 CC EMBL; AB011450; BAA32136.1; -
 CC EMBL; AB011446; BAA82709.1; -
 CC EMBL; AF004022; AAB65786.1; -
 CC EMBL; AF015254; AAC98891.1; -
 CC EMBL; BC000442; AAH00442.1; -
 CC EMBL; BC009751; AAH09751.1; -
 CC EMBL; BC013300; AAH13300.1; -
 CC HSSP; Q63430; 1A06.
 CC Genew; HGNC:11390; STK12.
 CC GK; Q96GD4; -
 CC MIM; 604970; -
 CC InterPro; IPR020552; N6_Mtase.
 CC InterPro; IPR000719; Prot_Kinase.
 CC InterPro; IPR022293; Ser_thr_kinase.
 CC InterPro; IPR01245; Tyr_kinase.
 CC Pfam; PF03069; pkinase; 1.
 CC ProDom; PDG30001; Prot_Kinase; 1.
 CC SMART; SM00220; S_TKc; 1.
 CC SMART; SM00219; TyrKc; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 CC Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-Binding.
 CC DMAP-N; 77 327 PROTEIN KINASE
 CC NP_BOND 83 91 ATP (BY SIMILARITY).
 CC BINDING 136 106 ATP (BY SIMILARITY).
 CC ACT_SITE 200 250 BY SIMILARITY.
 CC CONFLICT 14 15 RQ -> DK (IN REF. 5).
 CC CONFLICT 70 70 R -> RR (IN REF. 6; AAH13300).
 CC CONFLICT 167 161 E -> M (IN REF. 4 AND 5).
 CC CONFLICT 167 169 OKS -> HKT (IN REF. 4).
 CC CONFLICT 179 179 T -> TVPR (IN REF. 4).
 CC CONFLICT 160 180 I -> VRV (IN REF. 5).
 CC CONFLICT 226 226 P -> T (IN REF. 3).
 CC CONFLICT 249 253 MH -> ID (IN REF. 3).
 CC CONFLICT 271 271 MISSING (IN REF. 3).
 CC CONFLICT 298 298 T -> M (IN REF. 6; AAH09751/AAH13300).
 CC SEQUENCE 344 AA; 8325E3E5A1FB170 CRC64;
 SQ
 Query Match 77.6%; Score 38; DB 1; Length 344;
 Best Local Similarity 66.7%; Pred. No. 6.1;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLGKPPPE 9
 Db 266 LLVGNPPE 274
 RESULT 19
 KSN8 YEAST STANDARD; PRT; 525 AA.
 ID_KSN8 YEAST
 AC P39C70;

DT 01 OCT-1994 (Rel. 30, Created)
DT 01 OCT-1994 (Rel. 30, Last sequence update)
DT 16 OCT-2001 (Rel. 40, Last annotation update)
DE Probable serine/threonine-protein kinase YBR280C (EC 2.7.1.1).
GN YBR280C OR YBR0312.
OS Saccharomyces cerevisiae (Baker's yeast).
CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomycus.
OX NCBI_TaxID=4932.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C;
RC MEDLINE=89417825; PubMed=8091864.
RA Smith P.H.M., de Haan M., Maat C., Grivell L.A.;
RT "The complete sequence of a 33 kb fragment on the right arm of
RT chromosome 11 from Saccharomyces cerevisiae reveals 16 open reading
RT frames, including ten new open reading frames, five previously
RT identified genes and a homologue of the SCD1 gene".
RL Yeast 10:575-580 (1994).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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CC
CC EMBL; X76078; CAA53684.1;
CC PIR; S45684; S45684.
CC HSRP; P05132; CTP.
CC SCD1; S800232; YBR280C.
CC InterPro; IPR000961; Pkinase.C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC Pfam; PF00069; Pkinase; 1.
CC Pfam; PF00433; Pkinase; 1.
CC ProDom; PDC00001; Prot_kinase; 1.
CC SMART; SM00233; S_TK_X; 1.
CC SMART; SM02220; S_TK; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC Hypothetical; Kinase; Transferrase; Serine/threonine-protein kinase;
KW ATP-binding; 128 424 PROTEIN KINASE
FT DOMAIN 128 424
FT NP_BIND 134 142 ATP (BY SIMILARITY)
FT BINDING 157 157 ATP (BY SIMILARITY)
FT ACT_SITE 277 277 HY SIMILARITY
SC SEQUENCE 525 AA; 59591 MW; B8FF6E4A4367E77 CF=0.94;
Query Match 77.6%; Score 38; E-Value 525;
Best Local Similarity 75.0%; Pred. No. 3; Model 0;
Matches 6; Conservative 2; Mismatches 4; Gaps 0;
QY 1 MLGKPPF 8
DE 355 MLGKPPY 362
RESULT 20
XPCL_DROME
ID REC3_DROME STANDARD; PRT; 414 AA.
AC P13676; Q9VAG6;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein kinase C (EC 2.7.1.1) (PCK; PRKCBF);
GN PRKCBF OR PKC3 OR CG1934.
OS Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89429102; PubMed=2720775;
RC STRAIN=Berkley;
RC MEDLINE=20196006; PubMed=10731132.
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Arantes P.G., Scherer S.E., P.W. Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Shandari D., Solovokov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M., Pan
RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiaros T., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Teclor C., Turner E., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Ye R.F., Zaveri C.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster".
RL Science 287:2185-2195 (2000).
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- MISCELLANEOUS: THIS IS A CALCIUM-ACTIVATED.
CC -!- PHOSPHOLIPID-DEPENDENT, SERINE- AND THREONINE-SPECIFIC ENZYME.
CC binding domains.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC
CC EMBL; J04848; AA228818.1;
CC EMBL; A0003768; AA556946.1; ALT_NIT.

```

DR      FIR: B32392; B32392.
DR      HSP: P28867; IFTQ.
DR      FlyBase: FBgn030093; PKc98E.
DR      InterPro: IPR002219; DAG_PE_BIND.
DR      InterPro: IPR000961; Kinase C.
DR      InterPro: IPR000719; Prot_kinase.
DR      InterPro: IPR002290; Ser_thr_kinase.
DR      Pfam: PF00130; DAG_PE_bind_2.
DR      Pfam: PF00066; Kinase_1.
DR      Pfam: PF0433; Kinase_C_1.
DR      PRINTS: PD00008; DAGPEDOMAIN.
DR      ProDom: PD000001; Prot_kinase_1.
DR      SMART: SM00109; C_1_2.
DR      SMART: SM00133; S_TK_X_1.
DR      SMART: SM00220; S_TKC_1.
DR      PROSITE: PS00479; DAG_PE_BIND_DOM_1_2.
DR      PROSITE: PS50081; DAG_PE_BIND_DOM_2_2.
DR      PROSITE: PS50007; PROTEIN_KINASE_ATP_1.
DR      PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
DR      PROSITE: PS00109; PROTEIN_KINASE_S_T_1.
DR      Calcium-binding; Repeat; ATP-binding; Transferase;
DR      Serine/threonine-protein kinase; Multigene family; Zinc;
DR      Phorbol-ester binding.
DR      KEGG: 72 321 PHORBOL ESTER AND DAG BINDING 1.
DR      EC: 2.7.11.1 PHORBOL ESTER AND DAG BINDING 2.
DR      DOMAIN: 147 296 PROTEIN KINASE.
DR      DOMAIN: 303 560 ATP (BY SIMILARITY).
DR      NP_BIND: 329 317 ATP (BY SIMILARITY).
DR      BINDING: 332 332 ATP (BY SIMILARITY).
DR      ACT_SITE: 427 427 BY SIMILARITY.
DR      SEQUENCE: 634 AA; 7156 MW; 3AE3A3D6B7A276BA CDSR4;

Query Match 77.6%; Score 38; DB 1; Length 634;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

UY      : MLGGKPFFE 9
DB      495 MNAGQPFFE 503

RESULT 2:
ID      PKN1 CORGI STANDARD; PST; 446 AA.
CD      Q8N099;
CC      15-SEP-2003 (Ref: 42, Created:
CC      15-SEP-2003 (Ref: 42, Last sequence update:
CC      15-SEP-2003 (Ref: 42, Last annotation update:
CC      Probable serine/threonine protein kinase [GO:0004713] [EC:2.7.11.3].
CC      CG10041.
CC      Corynebacterium glutamicum (previbactor) flaxum
CC      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
CC      Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
CC      ACP_TaxID=1719;
CC      11;
CC      SEQUENCE FROM N.A.
CC      STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
CC      Nakagawa S.;
CC      "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
CC      Submitted (MAY-2002) to the EMBL/GenBank/EBI databases.
CC      -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC      -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC      -!- SIMILARITY: CONTAINS 3 PASTA DOMAINS.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to licenses@sb-sib.ch).
CC      EMBL: AF065274; BAB97434.1 ;
CC      InterPro: IPR004543; PASTA

```

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans".
 RT Nature 368:32-38(1994).
 RL [4]
 PN REVISIONS, AND ALTERNATIVE SPLICING.
 RA Waterston R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Required for oocyte nuclear envelope breakdown before
 CC entry of oocyte into spermatogenesis. In mitotic cells, plays a role
 CC in spindle organization and centrosome maturation. In meiotic
 CC cells, required for spindle dynamics and probably for spindle
 CC attachment to the chromosomes. Zygotic role in the development of
 CC the germline and nerve cord.
 CC -!- SUBCELLULAR LOCATION: In mitosis, remains associated with
 CC centrosomes entering prophase through to anaphase. During
 CC metaphase, found at the chromosomes of the metaphase plate. In
 CC meiosis, detected at centrosomes after pronuclear meeting in post-
 CC meiotic 1-cell embryos. Associated with chromatin during
 CC chromosome segregation of anaphase and in the region between the
 CC dividing chromosomes. Cytoplasmic in mature, unfertilized oocytes.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing. Named isoforms=2;
 CC Name=b;
 CC IsoId=bP4331-1; Sequence=0; splayed;
 CC Name=a;
 CC IsoId=bP4331-2; Sequence=VSP_004928;
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC GC/5/PCLO SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 PCLO box domains.
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 CC
 CC EMBL AF057165; AAC14129.1;
 CC EMBL AF080581; AAC34661.1;
 CC EMBL L15198; AAM27947.2;
 CC EMBL L15198; AAM22025.1;
 CC PIR T43337; T43337.
 CC RSP: C63450; 1A06.
 CC WormPep: C1499.43; CE26649.
 CC WormPep: C1499.43; CE32602.
 CC GO: GO:0005554; C:nucleus; IE:
 CC GO: GO:0005554; P:ATP binding activity; ISS.
 CC GO: GO:0004674; P:protein serine/threonine kinase activity; ISS.
 CC GO: GO:0007417; P:central nervous system development; IMP.
 CC GO: GO:0007098; P:centrosome cycle; IMP.
 CC GO: GO:0007077; P:mitotic nuclear envelope breakdown; IMP.
 CC GO: GO:0007052; P:mitotic spindle assembly; IMP.
 CC GO: GO:0006488; P:protein amino acid phosphorylation; ISS.
 CC InterPro: IPR000359; POLO_Box.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR002290; Ser_thr_kinase.
 CC Pfam: PF00659; POLO_Box_2.
 CC ProDom: PD000001; Prot_kinase; 1.
 CC SMART: SM00219; TyrKc; 1.
 CC PROSITE: PS00078; POLO_Box; 2.
 CC PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 CC PROSITE: PS00108; PROTEIN KINASE ST; 1.
 CC PROSITE: PS00111; PROTEIN KINASE DOM; 1.
 CC ATP-binding: Serine/threonine-protein kinase; Transferase; Repeat;
 KW Nuclear protein; Alternative splicing.
 FT DOMAIN 38 290 PROTEIN KINASE
 FT NP_BIND 45 52 ATP (BY SIMILARITY)
 FT BINDING 67 67 ATP (BY SIMILARITY)
 FT ACT_SITE 162 162 BY SIMILARITY
 FT DOMAIN 420 485 POLO_BOX_1
 FT DOMAIN 520 589 POLO_BOX_2

FT VARSPLIC 83 89 VDNERIL -> MTOEVO (in isoform a).
 FT /FTId=VSP_004928
 SQ SEQUENCE 649 AA: 73633 MW: 54D969F140D7A43B CRC64;
 Query Match 77.6%; Score 38; DB 1; Length 649;
 Best Local Similarity 66.7%; Pred. NO. 12;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLGKPPPE 9
 Db 229 LFGQPPPE 237
 RESULT 23
 KPC2_CABEL
 ID_KPC2_CABEL STANDARD; P87; 707 AA.
 AC P34895;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Protein kinase C-like 2 (EC 2.7.1.1) (PKC1B).
 GN KIN-13 OR PKC1B.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peleoderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=94179345; PubMed=8132661;
 RA Land M., Islas-Trejo A., Freedman J.H., Rubin C.S.;
 RT "Structure and expression of a novel neuronal protein kinase C
 RT (PKC1B) from Caenorhabditis elegans. PKC1B is expressed selectively
 RT in neurons that receive, transmit, and process environmental
 RT signals.";
 RL J. Biol. Chem. 269:9234-9244(1994).
 CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS. A CLASS OF TUMOR PROMOTERS.
 CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH MEMBRANES AND THE
 CC CYTOSKELETON.
 CC -!- TISSUE SPECIFICITY: EXPRESSED SELECTIVELY IN NEURONS THAT RECEIVE,
 CC TRANSMIT AND PROCESS ENVIRONMENTAL SIGNALS.
 CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC -!- SIMILARITY: Contains 1 C2 domain.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC
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 CC
 CC EMBL U00181; AAA18259.1;
 CC EMBL U00965; AAA17996.1;
 CC PIR A53530; A53530.
 CC HSP: P28867; IPTQ.
 CC InterPro: IPR000008; C2.
 CC InterPro: IPR002219; DAG_PS-bind.
 CC InterPro: IPR000961; Kinase_C.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR002290; Ser_thr_kinase.
 CC Pfam: PF00168; C2; 1.
 CC Pfam: PF00130; DAG_PS-bind; 2.
 CC Pfam: PF00069; kinase; 1.
 CC Pfam: PF00433; kinase_C; 1.
 CC PRINTS: PR00008; DAGPDOMAIN.
 CC ProDom: PD000001; Prot_kinase; 1.
 CC SMART: SM001C9; C1; 2.

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DR SMART; SMC0239; C2; 1.
DR SMART; SMC0333; S-TK_X; 1.
DR SMART; SMC0220; S-TK; 1.
DR PROSITE; PS00004; C2 DOMAIN 2; 1.
DR PROSITE; PS00479; DAG PE BIND DOM 1; 2.
DR PROSITE; PS00081; DAG PE BIND DOM 2; 2.
DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00109; C1; 2.
DR PROSITE; PS00109; C2; 1.
DR Transferase; Serine/threonine-protein kinase; ATP binding; Zinc;
KW Phorbol ester binding; Repeat; Membrane; Cytoskeleton.
FT DOMAIN 1 98 C2 DOMAIN.
FT DOMAIN 171 221 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 249 298 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 378 638 PROTEIN KINASE.
FT NP_BIND 384 392 ATP (BY SIMILARITY).
FT BINDING 407 407 ATP (BY SIMILARITY).
FT ACT_SITE 502 522 BY SIMILARITY.
SQ SEQUENCE 707 AA; 92122 MW; 3DC762C8A7A7BA64 CRC64;

Query Match 77.6%; Score 38; DB 1; Length 736;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
Db 570 MMAGQPPPE 578

RESULT 24
KPCF_RABIT
ID KPCF_RABIT STANDARD; PRT; 736 AA.
AC P28832.
DT 31-JUL-1989 (Rel. 11, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.1.1) (nPKC-epsilon).
GN PKCE
OS Cyrtolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Cricetidae.
OX NCBI_TaxID:9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:8823367; PubMed:3370472;
RA Chao S., Akita Y., Kondo Y., Iwajiro S., Suzuki K.
PT "A novel, phorbol ester receptor/protein kinase, related to
PT related to the protein kinase C family."
RL C.R. 53:331-741(1988).
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.

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CC or send an email to licenses@isb-sib.ch).
CC -----
DR EMBL; M20014; AAA31426.1; -
DR HSP; P28867; IPTQ
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG_PE_BIND.
DR InterPro; IPR000961; Pkinase_C.

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DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00130; DAG_PE_BIND; 2.
DR Pfam; PF00089; pkinase; 1.
DR Pfam; PF00433; pkinase; 1.
DR PRINTS; P000008; DAGPEDOMAIN.
DR ProDom; P000001; Prot_kinase; 1.
DR SMART; SMC0109; C1; 2.
DR SMART; SMC0239; C2; 1.
DR SMART; SMC0133; S-TK_X; 1.
DR SMART; SMC0220; S-TK; 1.
DR PROSITE; PS00004; C2 DOMAIN 2; 1.
DR PROSITE; PS00479; DAG PE BIND DOM 1; 1.
DR PROSITE; PS00081; DAG PE BIND DOM 2; 2.
DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00109; C1; 2.
DR PROSITE; PS00109; C2; 1.
KW Repeat; ATP-binding; Transferase; Phosphorylation;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT DOMAIN 1 99 C2 DOMAIN.
FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 407 667 PROTEIN KINASE.
FT NP_BIND 413 421 ATP (BY SIMILARITY).
FT BINDING 436 436 ATP (BY SIMILARITY).
FT ACT_SITE 531 531 BY SIMILARITY.
FT MOD_RES 702 702 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 709 709 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 736 AA; 83515 MW; 261C4FE5959BFEB CRC64;

Query Match 77.6%; Score 38; DB 1; Length 736;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
Db 599 MMAGQPPPE 607

RESULT 25
KPCF_HUMAN
ID KPCF_HUMAN STANDARD; PRT; 737 AA.
AC Q02156; Q9J081.
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.1.1) (nPKC-epsilon).
GN PKCE OR PKCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:9303318; PubMed:1382605;
RA Basta P., Strickland M.B., Holmes W., Loomis C.R., Ballas L.M.,
RA Burns D.J.;
RT "Sequence and expression of human protein kinase C-epsilon.";
RL Biochim. Biophys. Acta 1132:154-160(1992).
RN [2]
RP SEQUENCE OF 1-116 FROM N.A.
RA Waterston R.
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

```

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CC PKC SUBFAMILY.
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CC or send an email to licenses@isb-sib.ch).
CC -----
DR EMBL: X65293; CAA46388.1;
DR EMBL: U51244; AAC08955.1;
DR PIR: S28942; S28942.
DR HSSP: P28867; 1PTQ.
DR Genew: HGNC: 94C1; PKRCE.
DR MIM: 176975;
DR GO: GO:005524; C:membrane fraction; TAS.
DR GO: GO:004697; F:protein kinase C activity; TAS.
DR GO: GO:0034871; F:signal transducer activity; TAS.
DR GO: GO:006917; F:induction of apoptosis; TAS.
DR GO: GO:0066468; F:protein amino acid phosphorylation; TAS.
DR InterPro: IPR000008; C2.
DR InterPro: IPR002219; DAG_PE-bind.
DR InterPro: IPR000961; PKinase_C.
DR InterPro: IPR020719; Prot_kinase.
DR InterPro: IPR022290; Ser_thr_kinase.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00130; DAG_PE-bind; 2.
DR Pfam: PF00069; PKinase_C; 1.
DR Pfam: PF00433; PKinase_C; 1.
DR PR-NTS: PR00008; DAGPEDOMAIN.
DR PR-NTS: PR00001; Prot_kinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SM00239; C2; 1.
DR SMART: SM00133; S-TK_X; 1.
DR SMART: SM00220; S-TK; 1.
DR PROSITE: PS00004; C2_DOMAIN_2; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00113; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Repeat: ATP-binding; Transferase; Phosphorylation;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT DOMAIN 170 99 C2_DOMAIN
FT DOMAIN 170 220 PHORBOL-ESTER AND ZINC BINDING 1
FT DOMAIN 244 292 PHORBOL-ESTER AND ZINC BINDING 2
FT DOMAIN 404 669 PROTEIN_KINASE
FT NP_BIND 414 422 ATP (BY SIMILARITY)
FT BINDING 437 437 ATP (BY SIMILARITY)
FT ACT_SITE 532 532 BY SIMILARITY
FT MOD_RES 703 703 PHOSPHORYLATION (ACTS AS POTENTIAL)
FT MOTIF_RES 710 710 PHOSPHORYLATION (ACTS AS POTENTIAL)
SQ SEQUENCE 717 AA; 83673 MW; 8503250A091A:FTF CR64;
Query Match 77.6%; Score 35; CR 1; Length 737;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 3; Gaps 0;
QY 1 MLLGKPPPE 9
DB 600 MWAGQPPPE 608
RESULT 26
KCE XCUSE
ID KCE_MOUSE STANDARD; PROT 737 AA.
AC P16054.
DC 01-APR-1990 (Rel. 14, Created)
EC 01-APR-1993 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.11.1) (PKC-epsilon).
GN PKC-epsilon OR PKCEA

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=89137541; PubMed=2917656;
RA Schaap D., Parker P.J., Bristol A., Kriz R., Knopf J.;
RT "Unique substrate specificity and regulatory properties of
RT PKC-epsilon: a rationale for diversity.";
RL FEBS Lett. 243:351-357(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=98127436; PubMed=9467942;
RA Wang Q.J., Acs P., Goodnight J., Blumberg P.M., Mischak H.,
RA Mushinski J.P.;
RT "The catalytic domain of PKC-epsilon, in reciprocal PKC-delta and -
RT epsilon chimeras, is responsible for conferring tumorigenicity to
RT NIH3T3 cells, whereas both regulatory and catalytic domains of
RT PKC-epsilon contribute to in vitro transformation.";
RL Oncogene 16:53-60(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Tissue=Brain;
RA Wheeler D.L.;
RA Submitted (DEC-2000); to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC or send an email to licenses@isb-sib.ch).
CC -----
DR EMBL: AF228009; AAS94489.1;
DR EMBL: AF325507; AAG53892.1;
DR PIR: S02270; KINMSE.
DR HSSP: P28867; 1PTQ.
DR MGD: MGI:97559; Prkce.
DR GO: GO:004659; F:calcium independent protein kinase C activity; IDA.
DR InterPro: IPR000008; C2.
DR InterPro: IPR002219; DAG_PE-bind.
DR InterPro: IPR000961; PKinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00130; DAG_PE-bind; 2.
DR Pfam: PF00069; PKinase; 1.
DR Pfam: PF00433; PKinase_C; 1.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR PRODOM: PD000001; Prot_kinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SM00239; C2; 1.
DR SMART: SM00133; S-TK_X; 1.
DR SMART: SM00220; S-TK; 1.
DR PROSITE: PS00004; C2_DOMAIN_2; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE: PS00091; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00113; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

```


KW Repeat; ATP binding; Transferase; Phosphorylation;
 KW Serine/threonine-protein kinase; phorbol-ester binding; Zinc;
 FT DOMAIN 1 99 C2 DOMAIN
 FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1;
 FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2;
 FT DOMAIN 408 668 PROTEIN KINASE
 FT NP BIND 414 422 ATP (BY SIMILARITY)
 FT BINDING 437 437 ATP (BY SIMILARITY)
 FT ACT SITE 532 532 BY SIMILARITY
 FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-) (POTENTIAL)
 FT MOD_RES 710 710 PHOSPHORYLATION (AUTO-) (POTENTIAL)
 SQ SEQUENCE 737 AA: 83660 MW: 74893000 GPC44;
 Query Match 77.6%; Score 38; DB 1; Length 737;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGKPPPE 9
 DE 600 MMAGQPPPE 608
 RESULT 27
 KPC2 RAT
 ID KPC2 RAT STANDARD; PRT; 737 AA.
 AC PC9216;
 DT 01-MAR-1989 (Rel. 10, Created;
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DE Protein kinase C, epsilon type (EC 2.7.11.-) (PKC-epsilon).
 GN PKCE OR PKCE.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 PC TISSUE=Brain;
 RX MEDLINE=8829421; PubMed=2834397;
 RA Cho Y., Fujita T., Ogita K., Kikkawa U., Igarashi F., Nishizuka Y.,
 RA "The structure, expression, and properties of additional members of
 RI the protein kinase C family."
 RL J. Biol. Chem. 263:6927-6932(1988).
 RN [2]
 RP SEQUENCE OF 135-297 FROM N.A.
 RX MEDLINE=8829421; PubMed=3691511;
 RA Cho Y., Fujita T., Ogita K., Kikkawa U., Igarashi F., Nishizuka Y.,
 RI "Identification of three additional members of the protein kinase C
 RI family: delta-, epsilon-, and zeta-subfamilies."
 RL FEBS Lett. 226:125-128(1987).
 CC -1- FUNCTION: THIS IS CALCIUM INDEPENDENT, PHOSPHO-LIPID-DEPENDENT,
 CC SERINE- AND THREONINE-SPECIFIC ENZYME.
 CC -1- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
 CC -1- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC -1- SIMILARITY: Contains 1 C2 domain.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC
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 CC
 CC EMBL: M18331; AAA41872.1;
 CC PIR: B28163; KRTCE.
 CC PDB: 1GM1; 25-OCT-01.
 CC InterPro: IPR000008; C2.

DR InterPro: IPR002219; DAG PE-bind.
 DR InterPro: IPR000961; PKinase C.
 DR InterPro: IPR020719; Prot_kinase.
 DR InterPro: IPR022290; Ser_Thr_kinase.
 DR Pfam: PF00188; C2; 1.
 DR Pfam: PF00133; DAG PE-bind; 2.
 DR Pfam: PF0069; PKinase; 1.
 DR Pfam: PF0433; PKinase C; 1.
 DR PRINTS: PR00008; DAGPEDOMA; N.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00109; C1; 2.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00133; S_TK_X; 1.
 DR SMART: SM00220; S_TK; 1.
 DR PROSITE: PS00004; C2 DOMAIN 2; 1.
 DR PROSITE: PS00479; DAG PE BIND DOM 1; 2.
 DR PROSITE: PS00081; DAG PE BIND DOM 2; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW Repeat; ATP-binding; Transferase; Phosphorylation;
 KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
 KW 3D-structure.
 FT DOMAIN 1 99 C2 DOMAIN
 FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1;
 FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2;
 FT DOMAIN 408 668 PROTEIN KINASE
 FT NP BIND 414 422 ATP (BY SIMILARITY)
 FT BINDING 437 437 ATP (BY SIMILARITY)
 FT ACT SITE 532 532 BY SIMILARITY
 FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-) (POTENTIAL)
 FT MOD_RES 710 710 PHOSPHORYLATION (AUTO-) (POTENTIAL)
 SQ SEQUENCE 737 AA: 83478 MW: 64699995 PDD2659F CRC64;
 Query Match 77.6%; Score 38; DB 1; Length 737;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGKPPPE 9
 DE 600 MMAGQPPPE 608
 RESULT 28
 KPC2 APLCA
 ID KPC2 APLCA STANDARD; PRT; 743 AA.
 AC Q16975;
 DT 15-JUL-1999 (Rel. 38, Created;
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Calcium-independent protein kinase C (EC 2.7.11.-) (APL 1).
 GN PRKC2.
 OS Aplysia californica (California sea hare).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 CC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidaea;
 CC Aplysioidea; Aplysiidae; Aplysia.
 CC NCBI_TaxID=6500;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91332620; PubMed=1869917;
 RA Kruger K.E., Sossin W.S., Sacktor T.C., Bergold P.J., Beushausen S.,
 RA Schwartz J.H.,
 RT "Cloning and characterization of Ca(2+)-dependent and Ca(2+)-
 RT independent PKCs expressed in Aplysia sensory cells."
 RL J. Neurosci. 11:2303-2313(1991).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=91194877; PubMed=8449941;
 RA Sossin W.S., Diaz-Arreastia R., Schwartz J.H.,
 RT "Characterization of two isoforms of protein kinase C in the nervous
 RT system of Aplysia californica."
 RL J. Biol. Chem. 268:5763-5768(1993).
 RN [3]

RP DOMAIN C2.
RX MEDLINE=93349616; PubMed=8346555;
RA Sossin W.S., Schwartz J.H.;
RT "Ca(2+)-independent protein kinase Cs contain an amino terminal domain
RT similar to the C2 consensus sequence";
RL Trends Biochem. Sci. 18:207-208(1993);
[4].
RP CHARACTERIZATION.
RX MEDLINE=98334636; PubMed=9668089;
RA Pepio A.M., Fan X., Sossin W.S.;
RT "The role of C2 domains in Ca2+ activated and Ca2+- independent protein
RT kinase Cs in apoptosis";
RL J. Biol. Chem. 273:19340-19348(1998);
[5].
RP ERRATUM.
RA Pepio A.M., Fan X., Sossin W.S.;
RL J. Biol. Chem. 273:22856-22856(1998);
[6].
RP CHARACTERIZATION.
RX MEDLINE=98334636; PubMed=9477951;
RA Pepio A.M., Sossin W.S.;
RT "The C2 domain of the Ca(2+)-independent protein kinase C Apl. II
RT inhibits phorbol ester binding to the C1 domain in a phosphatidic
RT acid-sensitive manner";
RL Biochemistry 37:1256-1263(1998);
[7].
CC FUNCTION: THIS IS CALCIUM INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
CC SIMILARITY).
CC ENZYME REGULATION: REQUIRES HIGH LEVELS OF PHOSPHATIDYL-SERINE TO
CC BE ACTIVATED. THE PRESENCE OF THE C2 DOMAIN LOWERS THE AFFINITY OF
CC PROTEIN KINASE C ACTIVATORS FOR THE C1 DOMAINS AND THIS INHIBITION
CC CAN BE REMOVED BY PHOSPHATIDYL-SERINE. PHOSPHATIDIC ACID, HOWEVER,
CC IS MUCH MORE POTENT THAN PHOSPHATIDYL-SERINE IN REDUCING C2 DOMAIN-
CC MEDIATED INHIBITION, SUGGESTING THAT PHOSPHATIDIC ACID MAY BE A
CC REQUIRED COFACTOR FOR THE ACTIVATION OF APL II.
CC SUBCELLULAR LOCATION: Membrane associated.
CC TISSUE SPECIFICITY: EXPRESSED IN NERVOUS TISSUES, OVOTESTIS AND
CC GUT.
CC SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC SIMILARITY: Contains 1 C2 domain.
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch.)
CC
CC EMBL; Y94854; AAA27771.1; ..
CC HSSP; P28867; IPTQ.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002219; DAG_PE-bind.
CC InterPro; IPR0005961; Kinase_C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase
CC Pfam; PF00168; C2; 1.
CC Pfam; PF00130; DAG_PE-bind; 2.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF04333; pkinase; C1.
CC PRINTS; PR00008; DAGPEDOMAIN.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00109; C1; 2.
CC SMART; SM00239; C2; 1.
CC SMART; SM00133; S TK X; 1.
CC SMART; SM00220; S TKC; 1.
CC PROSITE; PS00499; C2_DOMAIN_1; FALSE_NEG.

DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE-ST; 1.
KW ATP-binding; Transferase; Serine/threonine-protein kinase;
KW Phorbol-ester binding; Zinc; Repeat.
FT DOMAIN 1 108
FT DOMAIN 177 226 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 248 297 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 403 663 PROTEIN KINASE.
FT NP_BIND 409 417 ATP (BY SIMILARITY).
FT BINDING 432 432 ATP (BY SIMILARITY).
FT ACT_SITE 527 527 BY SIMILARITY.
SQ SEQUENCE 743 AA; 84413 MW; 4C982C63CA2B659 CRC64;

Query Match 77.6%; Score 38; DB 1; Length 743;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MLLGKPPFE 9
Db 595 MMAGQPPFE 603

RESULT 29
KOKO_YEAST STANDARD; PRT; 1081 AA.
AC Q12236;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable serine/threonine-protein kinase YOL100W (EC 2.7.1.1-).
GN YOL100W OR HRC1081.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
ON NCBI_TaxID=4932;
RX SEQUENCE FROM N.A.
RP MEDLINE=96076631; PubMed=7502582;
RA Vandenbol M., Durand P., Portetelle D., Hilger F.;
RT "Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV
RT including the Ty1-H3 retrotransposon, the sufl(+) frameshift
RT suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-1a and a
RT delta element";
RL Yeast 11:1069-1075(1995).
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch.)
CC
CC EMBL; Z48149; CAA88162.1; ..
CC EMBL; Z74842; CAA99113.1; ..
CC PIR; S51899; S51899.
CC HSSP; O63450; 1A06.
CC SGD; S0005460; PKH2.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:000196; P:MAPKK cascade (cell wall biogenesis); IGI.
CC GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00239; S TKC; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

Dfam; PF00659; POLO_box; 2.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00078; POLO_BOX; 2.
KW ATP-binding; Serine/threonine-protein kinase; Transferase; Repeat;
KW Nuclear protein.
FT DOMAIN 35 286 PROTEIN_KINASE.
FT NP_BIND 4 49 ATP (BY SIMILARITY).
FT BINDING 64 64 ATP (BY SIMILARITY).
FT ACT_SITE 158 158 BY SIMILARITY.
FT DOMAIN 402 463 POLO_BOX 1.
FT DOMAIN 505 573 POLO_BOX 2.
FT DOMAIN 615 AA; 70436 MW; D510C727329C4B26 CRC64;
SQ SEQUENCE 615 AA; 70436 MW; D510C727329C4B26 CRC64;

Query Match 75.5%; Score 37; DB 1; Length 615;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps
QY 1 MLLGKPPFE 9
: | | | |
DB 225 LLFGSPPE 233

RESULT 31
KPCI_APLCA
ID KPCI_APLCA STANDARD; PRT; 649 AA.
AC Q16974;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calcium-dependent protein kinase C (EC 2.7.1.1-) (APL I).
DE PKC β .
GN Aplysia californica (California sea harel).
OS Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
OC Aplysioidae; Aplysiidae; Aplysia.
OX NCBI_TaxID:6500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91332620; PubMed-1869917;
RA Kruger K.E., Sossin W.S., Sacktor T.C., Bergold P.J., Reushausen S.,
RT Schwartz C.H.;
RT "Cloning and characterization of Ca(2+)-dependent and Ca(2+)-
independent PKCs expressed in Aplysia sensory cells.";
RL J. Neurosci. 11:2303-2313(1991).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE-93194877; PubMed-8449941;
RA Sossin W.S., Diaz-Arrias R., Schwartz J.H.;
RT "Characterization of two isoforms of protein kinase C in the nervous
system of Aplysia californica.";
RL J. Biol. Chem. 268:5763-5768(1993).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE-98334636; PubMed-9668085;
RA Picot A.M., Fan X., Sossin W.S.;
RT "The role of C2 domains in Ca2+-activated and Ca2+-independent protein
kinase Cs in aplysia.";
RL J. Biol. Chem. 273:19040-19048 (1998).
RN [4]
RP ERRATUM.
RA Picot A.M., Fan X., Sossin W.S.;
RL J. Biol. Chem. 273:22856-22856(1998).
CC -/- FUNCTION: THIS IS CALCIUM-DEPENDENT. PHOSPHOLIPID-DEPENDENT.
CC SERINE- AND THREONINE-SPECIFIC ENZYME. ACTIVATION OF PKC BY
CC SEROTONIN RESULTS IN PRESYNAPTIC FACILITATION OF DEPRESSED
CC SENSORY-TO-MOTOR NEURON SYNAPSES, WHICH IS THOUGHT TO UNDERLIE
CC BEHAVIORAL D:SHAB:TUATION.
CC -/- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS

CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
CC SIMILARITY).
CC -!- ENZYME REGULATION: ACTIVATED BY PHOSPHATIDYLISERINE.
CC -!- SUBCELLULAR LOCATION: CYTOSOL; PLASMA MEMBRANE; TRANSLOCATED TO NEURONAL
CC MEMBRANES.
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC
CC EMBL: M94883; AAA27770.2;
CC HSPF; P05697; ITBN.
CC InterPro: IPR000008; C2.
CC InterPro: IPR002219; DAG_PE-bind.
CC InterPro: IPR000961; Pkinase C.
CC InterPro: IPR000719; Prot_kinase
CC InterPro: IPR002290; Ser_thr_pkinase.
CC Pfam: PF00168; C2; 1.
CC Pfam: PF00130; DAG_PE-bind; 2.
CC Pfam: PF00069; pkinase; 1.
CC Pfam: PF00433; pkinase C; 1.
CC PRINTS: PR00160; C2DOMAIN.
CC PRINTS: PR00008; DAGPEDOMAIN.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00109; C1; 2.
CC SMART: SM00239; C2; 1.
CC SMART: SM00133; S_TK_X; 1.
CC SMART: SM00220; S_TKC; 1.
CC PROSITE: PS00499; C2_DOMAIN_1; 1.
CC PROSITE: PS50004; DAG_PE_BIND_DOM_1; 2.
CC PROSITE: PS00479; DAG_PE_BIND_DOM_2; 2.
CC PROSITE: PS50081; DAG_PE_BIND_DOM_2; 2.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC ATP-binding: Transferase; Serine/threonine-protein kinase;
CC Phorbol-ester binding; Zinc; Repeat.
CC DOMAIN 22 71 PHORBOL-ESTER AND DAG BINDING 1.
CC DOMAIN 86 135 PHORBOL-ESTER AND DAG BINDING 2.
CC DOMAIN 157 244 C2 DOMAIN
CC DOMAIN 320 578 PROTEIN KINASE
CC NP_BIND 326 334 ATP (BY SIMILARITY).
CC BINDING 349 349 ATP (BY SIMILARITY).
CC ACT_SITE 444 444 BY SIMILARITY.
CC SEQUENCE 649 AA; 74079 MW; A53253399284E332 CRC64;
Query Match 75.5%; Score 37; DB 1; Length 649;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY : MLCKPPEE 9
Db 512 MLAGPPFD 520
RESULT 32
KPC1_LYTP1 STANDARD; PRT; 658 AA.
AC Q25378;
DT 15-JUL-1999 (Rel. 38, Created;
DT 15-JUL-1999 (Rel. 38, Last sequence update);
DT 15-JUL-1999 (Rel. 38, Last annotation update);
DE Protein kinase C (EC 2.7.11.-).
GN PKC1.

OS Lytechinus pictus (Painted sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Temnopneustidae;
OC Lytechinus.
OX NCBI_TaxID=7653;
RN [..]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Rakow T.L., Shen S.S.;
RT "Molecular cloning and characterization of protein kinase C from the
RL sea urchin Lytechinus pictus."
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME (BY SIMILARITY).
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
CC SIMILARITY).
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC
CC EMBL: U02967; AAA03447.1;
CC HSPF; P05697; ITBN.
CC InterPro: IPR000008; C2.
CC InterPro: IPR002219; DAG_PE-bind.
CC InterPro: IPR000961; Pkinase C.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC InterPro: IPR001245; Tyr_pkinase.
CC Pfam: PF00168; C2; 1.
CC Pfam: PF00130; DAG_PE-bind; 2.
CC Pfam: PF00069; pkinase; 1.
CC Pfam: PF00433; pkinase C; 1.
CC PRINTS: PR00160; C2DOMAIN.
CC PRINTS: PR00008; DAGPEDOMAIN.
CC PRINTS: PR00108; TYRKINASE.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00109; C1; 2.
CC SMART: SM00239; C2; 1.
CC SMART: SM00133; S_TK_X; 1.
CC SMART: SM00220; S_TKC; 1.
CC PROSITE: PS00499; C2_DOMAIN_1; 1.
CC PROSITE: PS50004; DAG_PE_BIND_DOM_1; 2.
CC PROSITE: PS00479; DAG_PE_BIND_DOM_2; 2.
CC PROSITE: PS50081; DAG_PE_BIND_DOM_2; 2.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC ATP-binding: Transferase; Serine/threonine-protein kinase;
CC Phorbol-ester binding; Zinc; Repeat.
CC DOMAIN 28 77 PHORBOL-ESTER AND DAG BINDING 1.
CC DOMAIN 93 142 PHORBOL-ESTER AND DAG BINDING 2.
CC DOMAIN 164 251 C2 DOMAIN
CC DOMAIN 325 583 PROTEIN KINASE
CC NP_BIND 331 339 ATP (BY SIMILARITY).
CC BINDING 354 354 ATP (BY SIMILARITY).
CC ACT_SITE 449 449 BY SIMILARITY.
CC SEQUENCE 658 AA; 74871 MW; 74B5A27A49C835A2 CRC64;
Query Match 75.5%; Score 37; DB 1; Length 658;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGKPPPE 9
 DB 517 MLGQPPFD 525

RESULT 33
 KPCA_BOVIN STANDARD; PRT: 672 AA.
 AC P34309;
 DT 13-AUG-1987 (Rel. 05, Created);
 DT 13-AUG-1987 (Rel. 05, Last sequence update);
 DT 15-SEP-2003 (Rel. 42, Last annotation update);
 DE Protein kinase C, alpha type (EC 2.7.1.37); (PKC alpha) (PKC-A);
 GN PKCA;
 OS Bos taurus (Bovine);
 CC Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos;
 CC NCBI_TaxID=9913;
 RN [1];
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 FX MEDLINE=86289425; PubMed=3755547;
 RA Parker P.J., Coussens L., Lee L., Young S., Chen E.,
 RA Stabel S., Waterfield M.D., Ullrich A.;
 FT "The complete primary structure of protein kinase C - the major
 FT phorbol ester receptor.";
 PL Science 233:853-859 (1986).
 RN [2];
 RP REVIEW.
 RX MEDLINE=88318921; PubMed=3045562;
 SA Nishizuka Y.;
 RT "The molecular heterogeneity of protein kinase C and its implications
 RT for cellular regulation.";
 YL Nature 334:661-665 (1988).
 CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
 CC serine- and threonine-specific enzyme.
 CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn
 CC phosphorylates a range of cellular proteins. PKC also serves as
 CC the receptor for phorbol esters, a class of tumor promoters.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBUNIT: Interacts with PRKCHP (by similarity).
 CC -!- SIMILARITY: Contains 2 zinc-dependent phosphatase and DAG
 CC binding domains.
 CC -!- SIMILARITY: Contains 1 CD domain.
 CC -!- SIMILARITY: BELONGS TO THE SER-THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
 CC
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 CC
 CC EVAL: M33973; AAA3706.1;
 CC PAR: A0821; K1E0C.
 CC HSP: P05697; IRTN.
 CC InterPro: IPR000008; C2.
 CC InterPro: IPR002219; DAG_PE_bind.
 CC InterPro: IPR000961; Kinase C.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR002290; Ser_thr_kinase.
 CC Pfam: PF00168; C2; 1.
 CC Pfam: PF00130; DAG_PE_bind; 2.
 CC Pfam: PF00069; kinase; 1.
 CC Pfam: PF00433; kinase C; 1.
 CC PRINTS: PR00360; C2DOMAIN.
 CC PRINTS: PR00008; DAGPEDOMAIN.
 CC ProDom: PD002001; Prot_kinase; 1.
 CC SMART: SM00139; C1; 2.
 CC

DR SMART; SM00239; C2; 1.
 DR SMART; SM00139; S_TK_X; 1.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS00499; C2_DOMAIN_1; 1.
 DR PROSITE; PS00004; C2_DOMAIN_2; 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
 DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00009; PROTEIN_KINASE_ST; 1.
 KW Calcium-binding; Repeat; ATP-binding; Phorbol-ester binding; 2zinc;
 KW Serine/threonine-protein kinase; Phorbol-ester binding; 2zinc;
 KW Phosphorylation.
 FT DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 172 260 C2 DOMAIN
 FT DOMAIN 339 597 PROTEIN KINASE
 FT NP_BIND 345 353 ATP (BY SIMILARITY).
 FT BINDING 368 368 ATP (BY SIMILARITY).
 FT ACT_SITE 463 463 BY SIMILARITY.
 FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 SQ SEQUENCE 672 AA; 76837 MW; 97BF46DB80FCF21A CRC64;
 Query Match 75.5%; Score 37; DA 1; Length 672;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLGKPPPE 9
 DB 531 MLGQPPFD 539

RESULT 34
 KPCA_HUMAN STANDARD; PRT: 672 AA.
 AC P17252; O15137; Q96RE4;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
 GN PKCA OR PKCA OR PRKCA.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1];
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=90245676; PubMed=2336401;
 RA Finkenzeller G., Marne D., Hug H.;
 RT "Sequence of human protein kinase C alpha.";
 RL Nucleic Acids Res. 18:2183-2183 (1990).
 RN [2];
 RP SEQUENCE OF 15-445 FROM N.A.
 RX MEDLINE=9132033; PubMed=1714454;
 RA McSwine-Kennick R.L., McKeegan E.M., Johnson M.D., Morin M.J.;
 RT "Phorbol diester-induced alterations in the expression of protein
 RT kinase C isoforms and their mRNAs. Analysis in wild-type and phorbol
 RT diester-resistant HL-60 cell clones.";
 RL J. Biol. Chem. 266:15135-15143 (1991).
 RN [3];
 RP SEQUENCE OF 1-57 FROM N.A.
 RA Haridas V., Hackenbruck J., Glazer R.I.;
 RT "Homo sapiens protein kinase C alpha 5-flanking sequence.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
 CC serine- and threonine-specific enzyme.
 CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn
 CC phosphorylates a range of cellular proteins. PKC also serves as
 CC the receptor for phorbol esters, a class of tumor promoters.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBUNIT: Interacts with PRKCAP (By similarity).
 CC

CC -1- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC -1- SIMILARITY: Contains 1 C2 domain.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.

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CC EMBL: X52479; CAA36718.1; ...
 CC EMBL: M22199; AAK60098.1; ...
 CC EMBL: AF395929; AAK84184.1; ...
 CC PIR: S09496; KIHUCA.
 CC HSSP: F04410; 1A25.
 CC Genew: HGNC:9393; PRKCA.
 CC MIM: 176960; ...
 CC DR GO: G0005624; C-membrane fraction; TAS.
 CC DR GO: G0004697; F-protein kinase C activity; TAS.
 CC DR GO: G0008624; P-induction of apoptosis by extracellular sig ...; TAS.
 CC DR GO: G0000374; P-regulation of cell cycle; TAS.
 CC DR InterPro: IPR000008; C2.
 CC DR InterPro: IPR002219; DAG-PE-bind.
 CC DR InterPro: IPR000961; PKinase C.
 CC DR InterPro: IPR000719; Prot_kinase.
 CC DR InterPro: IPR002290; Ser_Thr_Pkinase.
 CC Pfam: PF00168; C2_1.
 CC Pfam: PF00130; DAG-PE-bind; 2.
 CC Pfam: PF00069; PKinase C; 1.
 CC Pfam: PF00433; PKinase C; 1.
 CC PRINTS: PR00360; C2DOMAIN.
 CC PROSITE: PR00008; DAGPEDOMAIN.
 CC PROSITE: PR00009; Prot_kinase; 1.
 CC SMART: SM00109; C1; 2.
 CC SMART: SM00239; C2; 1.
 CC SMART: SM00133; S_TK_X; 1.
 CC SMART: SM00220; S_TK_X; 1.
 CC PROSITE: PS00499; C2 DOMAIN 1; 1.
 CC PROSITE: PS00004; C2 DOMAIN 2; 1.
 CC PROSITE: PS00479; DAG-PE BIND DOM 1; 2.
 CC PROSITE: PS00051; DAG-PE BIND DOM 2; 2.
 CC PROSITE: PS00109; PROTEIN KINASE-ATP; 1.
 CC PROSITE: PS00001; PROTEIN KINASE-DOM 1; 1.
 CC PROSITE: PS00108; PROTEIN KINASE-SER; 1.
 CC Calcium-binding; Repeat; ATP-binding; Threonine;
 CC Serine/threonine-protein kinase; Phorbol ester; Kinase; Zinc;
 CC Phosphorylation.
 CC FT DOXA1N 37 86 PHORBOL-ESTER AND DAG BINDING 1.
 CC FT DOXA1N 102 151 PHORBOL-ESTER AND DAG BINDING 2.
 CC FT DOXA1N 172 260 C2 DOMAIN.
 CC FT DOXA1N 339 597 PROTEIN KINASE.
 CC FT NP_BIND 345 353 ATP (BY SIMILARITY).
 CC FT BINDING 368 368 ATP (BY SIMILARITY).
 CC FT ACT_SITE 463 463 BY SIMILARITY.
 CC FT MOD_RES 631 631 PHOSPHORYLATION (AUTOCATALYTIC) (POTENTIAL).
 CC FT MOD_RES 638 638 PHOSPHORYLATION (AUTOCATALYTIC) (POTENTIAL).
 CC FT CONFLICT 50 50 C<->S (IN REF. 2).
 CC CONFLICT 50 50
 CC SEQUENCE 672 AA; 76764 MW; 8780C0501B8C12DA CRC64;

Query Match 75.5%; Score 37; E: 1; Length 672;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 1; Indels 3; Gaps 0;
 QY 1 MLGKPFEE 9
 |||
 CC 531 MLGQPPED 539

RESULT 16

KPCA_MOUSE
 ID_KPCA_MOUSE STANDARD; PRT; 672 AA.
 AC P20444;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Protein kinase C, alpha type (EC 2.7.1.37) (PKC-alpha) (PKC-A).
 GN PRKCA OR PKCA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:89232737; PubMed:2469625;
 RA Rose-John S., Dietrich A., Marks F.;
 RT "Molecular cloning of mouse protein kinase C (PKC) cDNA from Swiss
 RT 3T3 fibroblasts.";
 RJ Gene 74:465-471(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE:90098082; PubMed:2601739;
 RA Megidish T., Mazurek N.;
 RT "A mutant protein kinase C that can transform fibroblasts.";
 RJ Nature 342:807-811(1989).
 RN [3]
 RP INTERACTION WITH PRKCABP.
 RX MEDLINE:95146534; PubMed:7844141;
 RA Staendiger J., Zhou J., Burgess R., Elledge S.J., Olson E.N.;
 RT "PICK1: A perinuclear binding protein and substrate for protein kinase
 RT C isolated by the yeast two-hybrid system.";
 RJ J. Cell Bio. 128:263-271(1995).
 CC -1- FUNCTION: This is a calcium-activated, phospholipid-dependent,
 CC serine- and threonine-specific enzyme.
 CC -1- FUNCTION: PKC is activated by diacylglycerol which in turn
 CC phosphorylates a range of cellular proteins. PKC also serves as
 CC the receptor for phorbol esters, a class of tumor promoters.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBUNIT: Interacts with PRKCABP.
 CC -1- DISEASE: Expression of the mutant form UV25 causes malignant
 CC transformation of cells.
 CC -1- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
 CC binding domains.
 CC -1- SIMILARITY: Contains 1 C2 domain.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC PKC SUBFAMILY.
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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).

EMBL: M25811; AAA39934.1; ALT_SEQ.
 EMBL: X52685; CAA36908.1; ...
 EMBL: X52684; CAA36907.1; ...
 PIR: S07104; KIMSCA.
 HSSP: P04410; 1A25.
 MGD: MG1197595; PRKCA.
 GO: G0004698; F:calcium dependent protein kinase C activity; IDA.
 InterPro: IPR000008; C2.
 InterPro: IPR002219; DAG-PE-bind.
 InterPro: IPR000961; PKinase C.
 InterPro: IPR000719; Prot_kinase.
 InterPro: IPR002290; Ser_Thr_Pkinase.
 Pfam: PF00168; C2; 1.
 Pfam: PF00130; DAG-PE-bind; 2.
 Pfam: PF00069; PKinase; 1.
 Pfam: PF00433; PKinase C; 1.
 PRINTS: PR00360; C2DOMAIN.

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DR PRINTS; PR00008; DAGPEDOXAIN.
DR ProDom; P0000001; Prot_Kinase; 1.
DR SMART; SM02009; C1; 2.
DR SMART; SM02039; C2; 1.
DR SMART; SM02039; S-TK_X; 1.
DR SMART; SM02039; S-TK; 1.
DR PROSITE; PS00439; C2_DOMAIN_1; 1.
DR PROSITE; PS00439; C2_DOMAIN_2; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase.
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
Phosphorylation.
KW Phorbol-ester and DAG binding 1.
FT DOMAIN 37 96 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT NP_BIND 339 597 PROTEIN KINASE.
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 636 636 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT VARIANT 106 106 I -> V (IN MUTANT FORM U255).
FT VARIANT 111 111 S -> G (IN MUTANT FORM U255).
FT VARIANT 240 240 L -> Q (IN MUTANT FORM U255).
FT VARIANT 339 339 F -> L (IN MUTANT FORM U255).
FT CONFLICT 147 147 C -> V (IN REF. 2).
FT CONFLICT 218 218 N -> T (IN REF. 2).
FT CONFLICT 277 278 AH -> AS (IN REF. 2).
FT CONFLICT 313 313 V -> A (IN REF. 2).
FT CONFLICT 467 467 N -> D (IN REF. 2).
FT CONFLICT 472 472 N -> D (IN REF. 2).
FT CONFLICT 576 576 Q -> S (IN REF. 2).
SQ SEQUENCE 672 AA; 76852 MW; 3948480952RRD50 Q5764;

Query Match 75.5%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 1 ML00KPPPE 9
DE 531 ML00KPPPE 539

RESULT 16
ID KPCA RABIT STANDARD; PFI 17. AA.
AC F11162;
DT 01-MAR-1989 (Rel. 10, Created)
DI 01-MAR-1989 (Rel. 10, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein Kinase C, alpha type (EC 2.7.11.37) (PKC-alpha) (PKC-A).
OS PRKCA.
OS Oryctolagus cuniculus (Rabbit).
CC Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87115883; PubMed=3808273;
RA Chnc S., Kawasaki H., Imajoh S., Sasaki K., Inagaki Y., Yokoyama H.,
RA Sakai T., Hidaka H.;
RT "Tissue-specific expression of three distinct types of rabbit protein
kinase C";
RL Nature 325:161-166(1987).
RN [2]
RP REVIEW.
RX MEDLINE=88318921; PubMed=3041561;
RA Nishizuka Y.,

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RT PRINTS; PR00008; DAGPEDOXAIN.
RT ProDom; P0000001; Prot_Kinase; 1.
RL Nature 334:661-665(1988).
CC -!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
CC serine- and threonine-specific enzyme.
CC -!- FUNCTION: PKC is activated by diacylglycerol which in turn
CC phosphorylates a range of cellular proteins. PKC also serves as
CC the receptor for phorbol esters, a class of tumor promoters.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts with PKCABP (by similarity).
CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X04796; CAA28483.1; .
CC PIR; C26037; KIRSC.
CC HSP; P04410; IAZ5.
CC InterPro; IPR000008; C2.
CC InterPro; IPR002219; DAG_PE-bind.
CC InterPro; IPR000961; Kinase_C.
CC InterPro; IPR003719; Prot_Kinase.
CC InterPro; IPR002290; Ser_Thr_kinase.
CC Pfam; PF00168; C2; 1.
CC Pfam; PF00168; DAG_PE-bind; 2.
CC Pfam; PF00433; pkinaase; 1.
CC Pfam; PF00433; pkinaase; C; 1.
CC PRINTS; PR00360; C2DOMAIN.
CC PRINTS; PR00008; DAGPEDOXAIN.
CC ProDom; P000001; Prot_Kinase; 1.
CC SMART; SM00139; C1; 2.
CC SMART; SM00239; C2; 1.
CC SMART; SM00139; S-TK_X; 1.
CC SMART; SM00220; S-TK; 1.
CC PROSITE; PS00499; C2_DOMAIN_1; 1.
CC PROSITE; PS00499; C2_DOMAIN_2; 1.
CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
CC PROSITE; PS00479; DAG_PE_BIND_DOM_2; 2.
CC PROSITE; PS00081; DAG_PE_BIND_DOM_1; 2.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ST; 1.
KW Calcium-binding; Repeat; ATP-binding; Transferase;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
Phosphorylation.
KW Phorbol-ester and DAG binding 1.
FT DOMAIN 37 96 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 172 260 C2 DOMAIN.
FT NP_BIND 339 597 PROTEIN KINASE.
FT BINDING 368 368 ATP (BY SIMILARITY).
FT ACT_SITE 463 463 BY SIMILARITY.
FT MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 636 636 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 672 AA; 76782 MW; 3031136703577A77 CRC64;

Query Match 75.5%; Score 37; DB 1; Length 672;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 1 ML00KPPPE 9
DE 531 ML00KPPPE 539

```

DR	SMART; SMO0109; C1; 2.
DR	SMART; SMO0239; C2; 1.
DR	SMART; SMO0133; S TK X; 1.
DR	SMART; SMO0220; S TKC; 1.
DR	PROSITE; PS00499; C2 DOMAIN 1; 1.
DR	PROSITE; PS00499; C2 DOMAIN 2; 1.
DR	PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR	PROSITE; PS00081; DAG_PE_BIND_DOM_2; 2.
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR	PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR	PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW	Calcium-binding; Repeat; ATP-binding; Transferase;
KW	Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW	Phosphorylation; 3D-structure
FT	DOMAIN 37 86 PHORBOL-ESTER AND DAG BINDING 1.
FT	DOMAIN 102 151 PHORBOL-ESTER AND DAG BINDING 2.
FT	DOMAIN 172 260 C2 DOMAIN.
FT	DOMAIN 339 597 PROTEIN KINASE.
FT	NP_BIND 345 353 ATP (BY SIMILARITY).
FT	BINDING 368 368 ATP (BY SIMILARITY).
FT	ACT_SITE 463 463 BY SIMILARITY.
FT	MOD_RES 631 631 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT	MOD_RES 638 638 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SEQ	SEQUENCE 672 AA; 76792 MW; 94889E7339C17719 CRC64;
Query Match 75.5%; Score 37; DB 1; Length 672;	
Best Local Similarity 66.7%; Pred No. 19;	
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	
OY	1 MLGKPPFE 9
DB	
	531 MLAGQPFED 539
RESULT 38	
ID	KPCG_BOVIN STANDARD; PRT; 682 AA.
AC	P05128;
DT	13-AUG-1987 (Rel. 05, Created)
DD	13-AUG-1987 (Rel. 05, Last sequence update)
DE	15-JUL-1989 (Rel. 38, Last annotation update)
DE	Protein Kinase C, gamma type (EC 2.7.1.37) (PKC-gamma) (Fragment).
GN	PRCKG.
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Bovidae; Bovinae; Bos.
OX	NCB1_TaxID=9913;
RN	[1]
RP	SEQUENCE FROM N.A.
RR	MEDLINE=86289426; PubMed=3755548;
RA	Coussens L., Parker P.J., Rhee L.;
RA	"The molecular heterogeneity of protein kinase C and its implications
RA	for cellular regulation";
RT	Nature 334:661-665(1988);
RL	[2]
CC	-!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
CC	SERINE- AND THREONINE-SPECIFIC ENZYME.
CC	-!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC	PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC	THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC	-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC	-!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC	binding domains.
CC	-!- SIMILARITY: Contains 1 C2 domain.
CC	-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC PKC SUBFAMILY.

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CC -----

DR EMBL: M13976; AAA30704.1;

DR PIR: C24664; KIBOCC.

DR HSSP: P05697; ITBN.

DR InterPro: IPR000308; C2.

DR InterPro: IPR002219; DAG PE-bind.

DR InterPro: IPR000961; PKinase C.

DR InterPro: IPR000019; Prot_Kinase.

DR InterPro: IPR002290; Ser_Tyr_kinase.

DR InterPro: IPR01245; Tyr_kinase.

DR Pfam: PF0168; C2.1.

DR Pfam: PF00130; DAG PE-bind; 2.

DR Pfam: PF00069; PKinase; 1.

DR Pfam: PF0433; PKinase C; 1.

DR PRINTS: PR00369; C2DOMAIN.

DR PRINTS: PR00038; DAGPEDOMAIN.

DR PRINTS: PR00109; TYRKINASE.

DR PROSITE: PS00001; Prot_Kinase; 1.

DR SMART: SM00109; C1; 2.

DR SMART: SM0239; C2; 1.

DR SMART: SM0133; S TK X; 1.

DR SMART: SM0220; S TK; 1.

DR PROSITE: PS00499; C2 DOMAIN; 1.

DR PROSITE: PS00004; C2 DOMAIN; 2.

DR PROSITE: PS00479; DAG PE BIND DOM; 2.

DR PROSITE: PS00081; DAG PE BIND DOM; 2.

DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.

DR PROSITE: PS00108; PROTEIN KINASE ST; 1.

CC Calcium binding; Repeat, ATP-binding; Transferase.

CC Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;

CC Phosphorylation.

FT NON_TER 1 1

FT DOMAIN 21 70 PHORBOL-ESTER AND DAG BINDING 1.

FT DOMAIN 86 135 PHORBOL-ESTER AND DAG BINDING 2.

FT DOMAIN 155 245 C2 DOMAIN.

FT DOMAIN 335 539 PROTEIN KINASE.

FT BINDING 142 352 ATP-PP1 INTERACTION.

FT BINDING 165 365 ATP-PP1 INTERACTION.

FT ACT_SITE 465 465 BY SIMILARITY.

FT ACT_SITE 603 633 PHOSPHORYLATION AND (POTENTIAL).

FT MCD_RES 640 640 PHOSPHORYLATION /AUN 1 (POTENTIAL).

CC SEQUENCE 682 AA; 77156 MW; 23392011.86C310 C4764;

Query March 75.5%; Score 47.25; Length 692;

Best Local Similarity 66.7%; Pred. No 19;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAGKPPPE 9

Qb 533 MLAGQPPFD 541

RESULT 39

KPCG HUMAN

ID KPCG HUMAN STANDARD; PRT; 697 AA.

AC P55129;

DT 13-AUG-1987 (Rel. 05, Created;

DT 01-FEB-1994 (Rel. 28, Last sequence update);

DT 15-SEP-2003 (Rel. 42, Last annotation update);

DE Protein Kinase C, gamma type (BC 2.7.1.37) (PKC-gamma);

GN PKCG OR PKCG.

OS Homo sapiens (human).

CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Cui W.C., Yu L., Chu Y.Y., Wang J., Zheng L.H., Zhou G.J., Zhao S.Y.;

RC Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 1-318 FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=86289426; PubMed=3755548;

RA Coussens L., Parker P.J., Rhee E., Yang-Feng T.L., Chen E.,

RA Waterfield M.D., Francke U., Ulrich A.;

RT "Multiple, distinct forms of bovine and human protein kinase C

RT suggest diversity in cellular signaling pathways.";

RL Science 233:859-866(1986).

RN [3]

RP SEQUENCE OF 162-697 FROM N.A.

RC TISSUE=Hippocampus;

RX MEDLINE=93387312; PubMed=8375396;

RA Kochs G., Meyer D., Hug H., Marne D., Sarre T.F.;

RT "Activation and substrate specificity of the human protein kinase C

RT alpha and zeta isoenzymes.";

RL Eur. J. Biochem. 216:597-606(1993).

RN [4]

RP VARIANTS CYS-141; GLN-415; ASP-523 AND SER-659.

RX MEDLINE=98213587; PubMed=9543393;

RA Al-Maghthien M., Vithana E.N., Inglehearn C.F., Moore T., Bird A.C.,

RA Bhattacharya S.S.;

RT "Segregation of a PKCG mutation in two RP11 families.";

RL Am. J. Hum. Genet. 62:1248-1252(1998).

RN [5]

RP SHOWS THAT THE VARIANTS ARE NOT A CAUSE OF RP11.

RX MEDLINE=99375047; PubMed=10441600;

RA Dryja T.P., McEvoy J., McGeer T.L., Berson E.L.;

RT "No mutations in the coding region of the PKCG gene in three families

RT with retinitis pigmentosa linked to the RP11 locus on chromosome

RT 19q.";

RL Am. J. Hum. Genet. 65:926-928(1999).

CC -!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,

CC SERINE- AND THREONINE-SPECIFIC ENZYME.

CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN

CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS

CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.

CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

CC -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG

CC binding domains.

CC -!- SIMILARITY: Contains 1 C2 domain.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC PKC SUBFAMILY.

CC -!- DATABASE: NAME=Mutations of the PKCG gene;

CC NOTE=Retina International's Scientific Newsletter;

CC WWW="http://www.retina-international.com/sci-news/prkcgmut.htm".

CC -----

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CC -----

DR EMBL: AF345987; AAK13533.1;

DR EMBL: M13977; AAA60102.1; ALT_TERM.

DR EMBL: Z15114; CAA78820.1;

DR PIR: D24664; D24664.

DR HSSP: P05697; ITBN.

DR Genew: HGNC:9402; PKCG.

DR WIM: 176980;

DR GO: GO:0004697; F:protein kinase C activity; TAS.

DR GO: GO:0006469; P:protein amino acid phosphorylation; TAS.

DR InterPro: IPR000008; C2.

DR InterPro: IPR002219; DAG PE-bind.

DR InterPro: IPR000961; PKinase_C.

```
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00133; DAG_PE_bind; 2.
DR Pfam: PF00069; Kinase; 1.
DR Pfam: PF0433; Kinase_C; 1.
DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR00008; DAGPEBIND_2.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD00600; Prot_kinase; 1.
DR SMART: SM00109; C2; 2.
DR SMART: SM00239; C2; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00499; C2_DOMAIN_1; 1.
DR PROSITE: PS00004; C2_DOMAIN_2; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE: PS00481; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00109; Repeat; ATP-binding; Transferrase;
KW Calcium-binding; Repeat; ATP-binding; Phorbol-ester binding; Zinc;
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc;
KW Phosphorylation; Polymorphism.
FT DOMAIN 36 185 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 170 260 C2 DOMAIN.
FT DOMAIN 351 614 PROTEIN KINASE.
FT NP_BIND 357 365 ATP (BY SIMILARITY).
FT BINDING 380 380 ATP (BY SIMILARITY).
FT ACT_SITE 480 480 BY SIMILARITY.
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT VARIANT 141 141 R>S.
FT VARIANT 415 415 H>C.
FT VARIANT 523 523 A>D.
FT VARIANT 659 659 R>S.
SQ SEQUENCE 637 AA: 78447 MW: 16911856 REF13241 CR756;
Query Match 75.54; Score 19.18; E-Value 6.94;
Best Local Similarity 66.79; Fragment 197;
Matches 6; Conservative 23; Miscellaneous 11; Labels 0; Gaps 0;
QY 1 MLAGPPPE 9
DE 548 MLAGPPPE 556

RESULT 40
KPCG MOUSE
ID KPCG_MOUSE STANDARD; PRT: 647 AA.
AC P05657;
DT 01-NOV-1998 (Rel. 39, Created)
DT 01-NOV-1998 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein kinase C, gamma type (EC 2.7.1.37) (PAC gamma).
GN PRKCG OR PKCG OR PKCC OR PKCC.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090, 10116;
RN 1;
RP SEQUENCE FROM N.A.
RC SPECIES=Brain; TISSUE=Brain;
RX MEDLINE=88262515; PubMed=3387228;
RA Oda Y., Fujii T., Igarashi K., Kikkawa U., Ogita K., Nishizuka Y.;
RT "Nucleotide sequences of cDNAs for alpha and gamma subtypes of rat
brain protein kinase C.";
Nucleic Acids Res. 16:5199-5200(1988).
[2]
SEQUENCE FROM N.A.
SPECIES=Brain;
MEDLINE=86272097; PubMed=3755379;
Knopf J.S., Lee M.-H., Suftman L.A., Kriz R.W., Loomis C.R.,
Hewick R.M., Bell R.M.;
"Cloning and expression of multiple protein kinase C cDNAs.";
Cell 46:491-502(1986).
[3]
SEQUENCE OF 1-56 FROM N.A.
SPECIES=Brain;
MEDLINE=91060619; PubMed=2246272;
Chen K.H., Widen S.G., Wilson S.H., Huang K.P.;
"Characterization of the 5'-flanking region of the rat protein kinase
C gamma gene.";
J. Biol. Chem. 265:19961-19965(1990).
[4]
SEQUENCE FROM N.A.
SPECIES=Mouse; TISSUE=Brain;
MEDLINE=93154595; PubMed=8428669;
Bowers B.J., Parham C.L., Sikela J.M., Wehner J.M.;
"Isolation and sequence of a mouse brain cDNA coding for protein
kinase C-gamma isozyme.";
Gene 123:263-265(1993).
[5]
SEQUENCE FROM N.A.
SPECIES=Mouse; STRAIN=BA1B/c; TISSUE=Brain;
Tseng C.P., Verma A.;
Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
[6]
STRUCTURE BY NMR OF 91-172.
SPECIES=Brain;
MEDLINE=97419134; PubMed=9211501;
Xu R.X., Pawelczyk T., Xia T.-H., Brown S.C.;
"NMR structure of a protein kinase C-gamma phorbol-binding domain and
study of protein-lipid micelle interactions.";
Biochemistry 36:10709-10717(1997).
-!- FUNCTION: THIS IS A CALCIUM-ACTIVATED, PHOSPHOLIPID-DEPENDENT,
SERINE- AND THREONINE-SPECIFIC ENZYME.
-!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
binding domains.
-!- SIMILARITY: Contains 1 C2 domain.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
PKC SUBFAMILY.
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EMBL: X07287; CAA30267.1;
EMBL: M13707; AAA41874.1;
EMBL: M55417; AAA41873.1;
EMBL: X67129; CAA47608.1;
EMBL: L28035; AAA39939.1;
PIR: A05105; KIRTGC.
PIR: JN0548; JN0548.
PDB: 1TBN; 29-APR-98.
PDB: 1TBC; 29-APR-98.
MGD: MGI:97597; Prkcc.
InterPro: IPR000308; C2.
InterPro: IPR002219; DAG_PE_bind.
InterPro: IPR000361; Kinase_C.
InterPro: IPR000719; Prot_kinase.
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DR InterPro: IPR002290; Ser_thr_kinase
DR InterPro: IPR001245; Tyr_kinase
DR Pfam: PF00168; C2_1
DR Pfam: PF00130; DAG_PE_bind; 2
DR Pfam: PF00069; pkinase_1
DR Pfam: PF0433; pkinase_C1
DR PRINTS: PR00360; C2DOMAIN
DR PRINTS: PR00008; DAGPECDOMAIN
DR PRINTS: PR00109; TYRKINASE
DR ProDom: PD000001; Prot_kinase; 1
DR SMART: SM00109; C1_2
DR SMART: SM00235; C2_1
DR SMART: SM00131; STHX; 1
DR SMART: SM0220; STHX; 1
DR PROSITE: PS00459; C2_DOMAIN_1; 1
DR PROSITE: PS00004; C2_DOMAIN_2; 1
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2
DR PROSITE: PS00061; DAG_PE_BIND_DOM_2; 2
DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1
DR PROSITE: PS00111; PROTEIN_KINASE_DOM_1
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1
KW Calcium-binding; Repeat; ATP-binding; Transferase
KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc
KW Phosphorylation; 3D-structure
FT DOMAIN 36 85 PHORBOL-ESTER AND DAG BINDING 1
FT DOMAIN 101 150 PHORBOL-ESTER AND DAG BINDING 2
FT DOMAIN 170 260 C2 DOMAIN
FT DOMAIN 351 614 PROTEIN KINASE
FT N-TERM 357 365 ATP (BY SIMILARITY)
FT BINDING 390 390 ATP (BY SIMILARITY)
FT ACT_SITE 480 480 BY SIMILARITY
FT MCD_RES 648 648 PHOSPHORYLATION (AUT-1) (POTENTIAL)
FT MCD_RES 655 655 PHOSPHORYLATION (AUT-1) (POTENTIAL)
FT STRAND 103 105
FT STRAND 113 113
FT STRAND 120 120
FT TURN 123 124
FT STRAND 129 131
FT TURN 132 134
FT STRAND 137 138
FT TURN 140 145
SQ SEQUENCE 697 AA; 78357 MW; E5D97A1B91642FF 05C64
Query Match 75.5% Score 47.05 E-11 Length 197
Pos. Local Similarity 66.7% PId No. 191
Matches 61 Conservative 21 Mismatches 11 Gaps 0
QY 1 NLGGPPPP 9
DB 548 MLAGPPPD 556

```

Search completed: November 14, 2003, 13:11:49
 Job time: 6.68571 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 11:18:40 ; Search time 27 Seconds
(without alignments)
86,018 Million cell updates/sec

Title: US-09-736-076-17

Perfect score: 49

Sequence: 1 MLGKPPFE 9

Scoring table: SLOSCV62

Gapop 10.0, Gapext 0.5

Searched: 630525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 330525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0

Maximum Match 100

Listing first 45 summaries

Database :

- 1: sp_archea:
- 2: sp_bacteria:
- 3: sp_fungi:
- 4: sp_human:
- 5: sp_invertebrate:
- 6: sp_mammal:
- 7: sp_mhc:
- 8: sp_organellar:
- 9: sp_phage:
- 10: sp_plant:
- 11: sp_rodent:
- 12: sp_virus:
- 13: sp_vertebrate:
- 14: sp_unclassified:
- 15: sp_rviro:
- 16: sp_bacterioph:
- 17: sp_archeap:

Pred. No. is the number of results identified by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	93.9	316	Q9BDK4	Q9BDK4 sus scrofa
2	46	93.9	372	Q8N7M6	Q8N7M6 homo sapien
3	46	93.9	666	Q9XYS4	Q9XYS4 xenopus lae
4	46	93.9	682	Q8X226	Q8X226 mus musculu
5	45	91.8	456	Q8MYF1	Q8MYF1 dictyostell
6	43	87.8	526	Q9BDP9	Q9BDP9 sus scrofa
7	43	87.8	582	Q9GB7	Q9GB7 hemicefrot
8	43	87.8	598	P70012	P70012 xenopus lae
9	43	87.8	623	Q8LUC5	Q8LUC5 asterina pe
10	42	83.7	80	Q91891	Q91891 xenopus lae
11	41	83.7	305	Q61427	Q61427 caenorhabdi
12	40	81.6	673	Q62567	Q62567 superifres d
13	40	81.6	677	Q96997	Q96997 geodia cydo
14	40	81.6	766	Q03407	Q03407 saccharomyc
15	40	81.6	769	Q97143	Q97143 drosophila
16	40	81.6	2893	Q8PEX7	Q8PEX7 xanthomonas

17	39	79.6	270	5	Q95ZT2	Q95ZT2 caenorhabdi
18	39	79.6	325	5	Q8MQ39	Q8MQ39 caenorhabdi
19	39	79.6	371	5	Q20541	Q20541 caenorhabdi
20	39	79.6	454	10	Q9M3V7	Q9M3V7 asparagus o
21	39	79.6	465	10	Q8LFC1	Q8LFC1 arabidopsis
22	39	79.6	480	10	Q43380	Q43380 avena sativ
23	39	79.6	582	3	Q12701	Q12701 schizosacch
24	39	79.6	1759	16	Q8F6Y5	Q8F6Y5 leptospira
25	39	79.6	2483	16	Q8XQB2	Q8XQB2 raistonia s
26	39	79.6	2497	16	Q8XYB9	Q8XYB9 raistonia s
27	38	77.6	240	11	Q63432	Q63432 rattus norv
28	38	77.6	324	11	Q9CVR6	Q9CVR6 mus musculu
29	38	77.6	332	16	Q9AJZ9	Q9AJZ9 streptomyce
30	38	77.6	534	5	Q9ST78	Q9ST78 drosophila
31	38	77.6	568	5	Q8MXG6	Q8MXG6 caenorhabdi
32	38	77.6	646	16	Q8NJ98	Q8NJ98 corynebacte
33	38	77.6	661	5	Q8L669	Q8L669 hydra atten
34	38	77.6	707	5	Q20953	Q20953 caenorhabdi
35	38	77.6	749	5	Q8MXG7	Q8MXG7 caenorhabdi
36	38	77.6	754	5	Q8MXB6	Q8MXB6 limulus pol
37	38	77.6	780	5	Q76360	Q76360 caenorhabdi
38	38	77.6	925	11	Q8K215	Q8K215 mus musculu
39	38	77.6	925	11	Q64702	Q64702 mus musculu
40	38	77.6	970	4	Q96Q95	Q96Q95 homo sapien
41	38	77.6	970	4	Q00444	Q00444 homo sapien
42	38	77.6	970	4	Q81YF0	Q81YF0 homo sapien
43	38	77.6	1036	4	Q75119	Q75119 homo sapien
44	38	77.6	1036	4	Q81YF8	Q81YF8 homo sapien
45	38	77.6	1037	11	Q9WTP4	Q9WTP4 mus musculu

ALIGNMENTS

RESULT 1

Q9BDK4 ID Q9BDK4 PRELIMINARY; PRT; 316 AA.

AC Q9BDK4; DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serum-inducible kinase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RA Anger M., Kues W.A., Klira J., Motlik J., Carnwath J.W., Niemann H.;
RT "Porcine serum-inducible kinase."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF348424; AAK27154.1; ..
DR InterPro: IPR000959; POLO_box.
DR InterPro: IPR000729; Prot_Kinase.
DR Pfam: PF00069; pkinase; ..
DR Pfam: PF00659; POLO_Box; 1.
DR ProDom: PD003001; Prot_Kinase; 1.
DR PROSITE: PS03378; POLO_BOX; 1.
KW ATP-binding; Kinase; Transferase.
FT NON_TER 1 316
FT NON_TER 316 316
SQ SEQUENCE 316 AA; 35330 MW; F63BBE4A2691D62F CRC64;

Query Match 93.9%; Score 46; DB 6; Length 316;

Best Local Similarity 88.9%; Pred. No. 0.49; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPFE 9

DB 25 MLGKPPFE 33

```
RESULT 2
Q9XK54
ID Q9XK54 PRELIMINARY; PRT; 372 AA.
DR Q8N7V6;
DR InterPro: IPR000719; PROTOX;
DR InterPro: IPR000719; PROTOX;
DR Pfam: PF00069; PKINASE; 1.
DR Pfam: PF00069; PKINASE; 1.
DR ProDom: PD000001; PROTOX; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00078; PROTOX; 2.
DR PROSITE: PS00107; PROTOX; 1.
DR PROSITE: PS00107; PROTOX; 1.
DR PROSITE: PS00108; PROTOX; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 372 AA; 42632 MW; 75303F6502A009 CRC64;

Query Match 93.9%; Score 46; DB 13; Length 662;
Best Local Similarity 88.9%; Pred. No. 1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGKPPPE 9
Db 254 MLLGKPPPE 262
|||||
|

RESULT 4
Q8K226 PRELIMINARY; PRT; 682 AA.
ID Q8K226
DR Q8K226;
DR 01-OCT-2002 (TremBurel_22, Created)
DT 01-OCT-2002 (TremBurel_22, Last sequence update)
DT 01-MAR-2003 (TremBurel_23, Last annotation update)
DE Serum-inducible kinase.
GN SNK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N. A.
RA Strausberg R.;
DR EMBL: BC034513; AAH34513.1; -.
DR MGD: MGI:1095790; Snk.
DR InterPro: IPR000719; PROTOX;
DR InterPro: IPR000719; PROTOX;
DR InterPro: IPR000719; PROTOX;
DR Pfam: PF00069; PKINASE; 1.
DR Pfam: PF00069; PKINASE; 1.
DR ProDom: PD000001; PROTOX; 1.
DR SMART: SM00220; S_TK; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00078; PROTOX; 2.
DR PROSITE: PS00107; PROTOX; 1.
DR PROSITE: PS00107; PROTOX; 1.
DR PROSITE: PS00108; PROTOX; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 682 AA; 77777 MW; 98BA65C8DFAFFD95 CRC64;

Query Match 93.9%; Score 46; DB 11; Length 682;
Best Local Similarity 88.9%; Pred. No. 1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGKPPPE 9
Db 270 MLLGKPPPE 278
|||||
|

RESULT 5
Q8MYF1 PRELIMINARY; PRT; 456 AA.
ID Q8MYF1
AC Q8MYF1;
DR 01-OCT-2002 (TremBurel_22, Created)
DT 01-OCT-2002 (TremBurel_22, Last sequence update)
DT 01-MAR-2003 (TremBurel_23, Last annotation update)
DE Hypothetical protein; ATP-binding; Transferase.
SQ SEQUENCE 456 AA; 50000 MW; 75303F6502A009 CRC64;

Query Match 93.9%; Score 46; DB 13; Length 662;
Best Local Similarity 88.9%; Pred. No. 1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLGKPPPE 9
Db 254 MLLGKPPPE 262
|||||
|

RESULT 3
Q9XK54 PRELIMINARY; PRT; 666 AA.
ID Q9XK54
DR Q9XK54;
DR 01-DEC-2001 (TremBurel_19, Created)
DT 01-DEC-2001 (TremBurel_19, Last sequence update)
DT 01-MAR-2003 (TremBurel_23, Last annotation update)
DE Polio-like kinase 2.
GN PLX2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]_TaxID=8355;
RP SEQUENCE FROM N. A.
RA Duncan P.I.; Pollet N.; Niehrs C.; Nigg E.A.;
RT "Cloning and Characterization of p1x2 and p1x3, Two Additional Polio-
like Kinases from Xenopus laevis."
RC Exp. Cell Res. 270:78-87(2001).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
```

DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE RAC family serine/threonine kinase homology.
 OS Dictyostelium discoideum (Slime mold)
 OC Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
 CX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gloeckner G., Eichinger L., Szatranski K., Pachebat C., Dear P.,
 RA Lehman R., Baumgart C., Parra S., April C.F., Guiso R., Kumpf K.,
 RA Tungal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.,
 RT "Sequence and Analysis of Chromosome 2 of Dictyostelium";
 RJ Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC11708.1; AAA43765.1;
 DR InterPro; IPR000961; Pkinase.C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00669; Pkinase; 1.
 DR Pfam; PF00433; Pkinase.C; 1.
 DR PRINTS; PR00139; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00133; S_TKc; 1.
 DR SMART; SM00219; TYRKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 456 AA; 51154 MW; EB8749EC64C89309 CRC64;

 Query Match 91.8%; Score 45; DB 5; Length 456;
 Best Local Similarity 77.8%; Pred. No. 1.3;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MLLGKPPPE 9
 DB 319 MLLGKPPPE 327

 RESULT 5
 Q9GRB8 PRELIMINARY; PRT; 526 AA.
 AC Q9GRB8
 DT 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Polo-like protein kinase (fragment)
 OS Sus scrofa (Pig)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 CX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ander M., Kues W.A., Klima J., Melenz M., Motlik J., Carnwath J.W.,
 RA Nigam H.
 RT "Expression of Polo-like Kinase in Cell Cycle Synchronized Porcine
 RT Fetal Fibroblasts";
 RJ Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AF33901.1; AAK28550.1;
 DR HSP; C63450.1; IAC6.
 DR InterPro; IPR000959; POLO_BOX.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_pkinase.
 DR Pfam; PF00669; Pkinase; 1.
 DR Pfam; PF02659; POLO_BOX; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00078; POLO_BOX; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON_TER 1
 FT NON_TER 526
 SQ SEQUENCE 526 AA; 60399 MW; 1AFA1E5E09B2CB3 CRC64;

 Query Match 87.8%; Score 43; DB 6; Length 526;
 Best Local Similarity 77.8%; Pred. No. 3.7;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MLLGKPPPE 9
 DB 199 LLVGKPPPE 207

 RESULT 7
 Q9GRB7 PRELIMINARY; PRT; 582 AA.
 AC Q9GRB7
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Polo-like kinase.
 GN UPLK.
 OS Hemiechinotus pulcherrimus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinozoa; Echinacea; Echinozoa; Strongylocentrotidae;
 OC Hemiechinotus.
 CX NCBI_TaxID=7650;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yonemura I., Fujimoto H., Mabuchi I.;
 RT "Cloning of sea urchin plk.";
 RJ Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AB043897; BAB18588.1;
 DR InterPro; IPR001395; Aldo/ket_red.
 DR InterPro; IPR000959; POLO_BOX.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_pkinase.
 DR Pfam; PF00669; Pkinase; 1.
 DR Pfam; PF00659; POLO_BOX; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00063; ALDO-KETO_REDUCTASE_3; 1.
 DR PROSITE; PS00078; POLO_BOX; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 582 AA; 66429 MW; A3774A0CAACFDESD CRC64;

 Query Match 87.8%; Score 43; DB 5; Length 582;
 Best Local Similarity 77.8%; Pred. No. 3.7;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MLLGKPPPE 9
 DB 218 LLVGKPPPE 226

 RESULT 8
 P70032 PRELIMINARY; PRT; 598 AA.
 ID P70032
 DT 01-FEB-1997 (TEMBLrel. 02, Created)
 DT 01-FEB-1997 (TEMBLrel. 02, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)

```

DE Plxl.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
CC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=96355660; PubMed=8703070;
RA Kumagai A, Dunphy W.G.;
RT "Purification and molecular cloning of Plxl, a Cdc25-regulatory kinase
RT from Xenopus egg extracts."
RJ Science 273:1377-1382(1996).
CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U58205; AAC60317.1;
DR HSP: G63450; IAD6.
DR InterPro: IPR003959; POLO_BOX.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00659; PKINASE; 1.
DR Pfam: PF00659; POLO_BOX; 2.
DR ProDom: PD000001; Prot_Kinase; 1.
DR SMART: SMC0220; S_TK_1.
DR PROSITE: PS00078; POLO_BOX; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 598 AA; 68211 MW; 2467195911F225E6 CRC64;

Query Match 87.8%; Score 43; DB 13; Length 598;
Best Local Similarity 77.8%; Pred. No. 3.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPFE 9
DB 235 LLVGKPPFE 243

RESULT 9
Q81D35 PRELIMINARY; PRT: 623 AA.
ID Q81U35;
CT 01-MAR-2003 (TRENBLrel. 23, Created);
CT 01-MAR-2003 (TRENBLrel. 23, Last sequence update);
CT 01-MAR-2003 (TRENBLrel. 23, Last annotation update);
DE CONTAINS SIMILARITY TO PFAM domain PF00069 (PKINASE).
DE E-VALUE=2.8E-85; N=1 (AIR-2) (PKINASE).
GN Polio-like kinase.
CS Asterina pectinifera (Starfish).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
CC Asterozoa; Valvatacea; Valvatida; Asterozoa; Asterozoa;
OX NCBI_TaxID=7594;
RN [1];
RP SEQUENCE FROM N.A.
RA Uchida T, Tachibana K, Kishimoto T;
RT "Starfish Plk."
RC Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RW EMBL: ABC84465; BAC22692.1;
KW Kinase.
SQ SEQUENCE 623 AA; 70929 MW; CFC0190C82D724A CRC64;

Query Match 87.8%; Score 43; DB 5; Length 623;
Best Local Similarity 77.8%; Pred. No. 3.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPFE 9
DB 220 LLVGKPPFE 228

RESULT 10
Q91891 PRELIMINARY; PRT: 80 AA.
ID Q91891

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Q91891;
DT 01-NOV-1996 (TRENBLrel. 01, Created);
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update);
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update);
DE Hypothetical 9.4 kDa protein (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
CC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1];
RP SEQUENCE FROM N.A.
RA Bouvet P, Orillio F, ARLOT-BONNEVAIN Y, Legagneux V, Roghi C,
RA Bassez T, OSCORNE H.;
RT "Deadenylation conferred by the 3' untranslated region of a
RT developmentally controlled mRNA in xenopus embryos is switched to
RT polyadenylation by deletion of a short sequences element."
RJ Mol. Cell. Biol. 14:1893-1900(1995).
DR EMBL: Z24453; CAAC826.1;
DR InterPro: IPR000719; Prot_Kinase.
DR Pfam: PF00069; PKINASE; 1.
DR ProDom: PD000001; Prot_Kinase; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; ATP-binding; Transferase.
ST NON-TER 1;
SQ SEQUENCE 80 AA; 9388 MW; 8DFCDBA14BE14FB CRC64;

Query Match 83.7%; Score 41; DB 13; Length 80;
Best Local Similarity 87.5%; Pred. No. 1.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LLGKPPFE 9
DB 3 LVGKPPFE 10

RESULT 11
Q01427 PRELIMINARY; PRT: 305 AA.
ID Q01427;
DT 01-JUL-1997 (TRENBLrel. 04, Created);
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update);
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update);
DE C. ELEGANS AUPORA/1PL1-related protein KINASE 2 (AIR-2) (GB:AF071207).
DE CONTAINS SIMILARITY TO PFAM domain PF00069 (PKINASE).
DE E-VALUE=2.8E-85; N=1 (AIR-2) (PKINASE).
GN Air-2.
CS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
CC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Henkhaus J, Wohldmann P;
RT "The sequence of C. elegans cosmid B0207."
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [3];
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [4];
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;

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RA Waterston R.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN 5;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN 6;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN 17;
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2 BRISTOL;
 RA Schumacher J.M., Golden A., Donovan P.J.;
 RT "AIR-2: An aurora/jpl-related protein kinase associated with
 RT chromosomes and midbody microtubules is required for polar body
 RT extrusion and cytokinesis in *C. elegans* embryos.";
 RL J. Cell Biol. 0:0-0(1998).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: J97796; AAB52459.2;
 DR EMBL: AF071207; AAC70945.1;
 DR HSSP: P24941; IACI
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM0220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 345 AA; 34749 MW; 163563602E14011 CRC64;

Query Match 83.7%; Score 41; DB 5; Length 355;
 Best Local Similarity 87.5%; Pred. No. 48;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MLCKPPE 9
 DB 220 LVGRPPE 227

RESULT 2
 ID C62567 PRELIMINARY; PRT; 677 AA.
 AC C62567;
 DT 01-AUG-1999 (TrEMBLrel. 07, Created)
 DT 01-AUG-1999 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Serine/threonine protein kinase.
 CS Subunit domainula (Sponge).
 CC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
 CC Hadromerida; Suberitidae; Suberites.
 CX NCBI_TaxID=55567;
 RN 11;
 RP SEQUENCE FROM N.A.
 RA Mueller W.E.G.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN 12;
 RP SEQUENCE FROM N.A.
 EX MEDLINE=96394688; PubMed=8798342;
 RA Kruse M., Gamulin V., Cetkovic H., Parker Z., Mueller I.M.,
 RA Mueller W.E.G.;
 RT "Molecular evolution of the Metazoan protein kinase C multigene
 RT family";
 RJ J. Mol. Evol. 41:374-383(1996).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 DR EMBL: Y23099; CAA73553.1;
 DR HSSP: P28867; IPTC.
 DR InterPro: IPR000008; C2.

DR InterPro: IPR001064; Crystallin.
 DR InterPro: IPR002219; DAG_PE-bind.
 DR InterPro: IPR000961; Pkinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00130; DAG_PE-bind; 2.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00433; Pkinase_C; 1.
 DR PRINTS: PRO3360; C2DOMAIN.
 DR PRINTS: PRO3308; DAGPEDOMAIN.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00109; C1; 2.
 DR SMART: SM00219; C2; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00133; S_TK_X; 1.
 DR PROSITE: PS00499; C2_DOMAIN_1; 1.
 DR PROSITE: PS00009; C2_DOMAIN_2; 1.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 1.
 DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
 DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 673 AA; 77344 MW; 86D24E55497C293 CRC64;

Query Match 81.6%; Score 40; DB 5; Length 673;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCKPPE 9
 DB 535 MLVGRPPE 543

RESULT 13
 ID O96997 PRELIMINARY; PRT; 677 AA.
 AC O96997;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Protein kinase C.
 GN PKC2.
 OS Geodia cydonium (Sponge).
 CC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
 CC Astrophorida; Geodiidae; Geodia.
 CX NCBI_TaxID=5047;
 RN 11;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99147839; PubMed=10023072;
 RA Seack J., Kruse M., Mueller I.M., Mueller W.E.G.;
 RT "Promoter and exon-intron structure of the protein kinase C gene from
 RT the marine sponge Geodia cydonium: Evolutionary considerations and
 RT promoter activity";
 RL Biochim. Biophys. Acta 1444:241-253(1999).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 DR EMBL: Y17882; CAA76911.1;
 DR HSSP: P28867; IPTC.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR001064; Crystallin.
 DR InterPro: IPR002219; DAG_PE-bind.
 DR InterPro: IPR000961; Pkinase_C.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00130; DAG_PE-bind; 2.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00433; Pkinase_C; 1.
 DR PRINTS: PF00168; C2DOMAIN.
 DR PRINTS: PRO3308; DAGPEDOMAIN.


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Qy      1 MLUGKPPFE 9
      1
      1
Db      330 MLAGKPEPK 338

RESULT 15
C57143 PRELIMINARY; PRT; 769 AA.
AC C57143;
DT 01-MAY-1999 (T=EMBLrel. 10, Created)
DT 01-MAY-1999 (T=EMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (T=EMBLrel. 23, Last annotation update)
DE SAK protein.
GN SAK OR C57186.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachyceta; Muscomorpha;
OC Ephyraoidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananikian P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan C.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Saxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchan M.R., Brock J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell C.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mantei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Par S., Pollard J.J., Puri V., Reese M.G.,
RA Reinart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shier B.C., Sider-Kimani I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye C., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng C.,
RA Zheng X.H., Zheng F., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Hudson J.W., Dennis J.W.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; AEO03594; AAF51737.1;
DR EMBL; AF106952; RAD19607.1;
DR HSP; P00518; 1PHK.
DR FlyBase; FBGN0026371; SAK.
DR InterPro; IPR0003959; POLO box.
DR InterPro; IPR000719; Prot Kinase.
DR InterPro; IPR002290; Ser Thr kinase.

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DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PRODOM: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00078; POLO_BOX; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 769 AA; 85856 MW; F0508F60A5094AA4 CR764;

Query Match 81.6%; Score 40; DB 5; Length 769.
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGKPPPE 9
Db 206 LLVGRPPPE 214

RESULT 16
Q95ZT2 PRELIMINARY; PRT; 2883 AA.
AC Q95ZT2;
DT 01-DEC-2001 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Shikimate kinase.
GN XAC4213.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92823;
RN 1;
RP SEQUENCE FROM N.A.
RA STRAIN=356 / ATCC 13902 / XV 107;
RX MESJ:NE22022145; PubMed:12024217;
RA da Silva A.C.R., Ferro J.A., Reinach P.C., Parah C.S., Furlan L.R.,
RA Guaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves J.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A., P.,
RA Camarotte G., Cannan F., Cardoso C., Chamergo F., Chapina L.P.,
RA Cicarelli R.M.B., Coutinho L.S., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira P.C.C., Ferro M.T.T.,
RA Fomighieri E.F., Franco M.C., Gueglio C.C., Gruber A.,
RA Katsuyama A.M., Kishi D.T., Leite R.F., Lemos E.G.M., Lemos M.V.F.,
RA Locati E.C., Machado M.A., Madalita A.M.B.N., Martins-Ferreira V.R.,
RA Martins E.C., Naldanis C., Mack R.M., Miyake C.Y., Moon J.H.,
RA Moreira L.V., Novo M.T.M., Okura V.B., Oliveira M.L., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tavares E.B., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.N., White P.F.,
RA Setubal J.C., Kitajima J.P.;
PT "Comparison of the genomes of two Xanthomonas pathogens with differing
PT host specificities";
RL Nature 417:459-463(2002).
DR EXBL: AE012073; AAC39048.1;
DR InterPro: IPR003439; ABC transporter;
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW Kinase; Complete proteome.
SQ SEQUENCE 2883 AA; 313973 MW; 6AE03D657E4577D3 CRC64;

Query Match 81.6%; Score 40; DB 16; Length 2883;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGKPPPE 9
Db 1966 LLGKPPPD 1974

RESULT 17
Q95ZT2 PRELIMINARY; PRT; 270 AA.
AC Q95ZT2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein F47F2.1a.
GN F47F2.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN 1;
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN 2;
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Bentley D.;
RA "The sequence of C. elegans cosmid F47F2.";
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN 3;
RP SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U40943; AAK39236.1;
DR WormPep: F47F2.1a; CE27.66.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR Pfam: PF00433; Pkinase_C; 1.
DR PRINTS: PR00109; TYRKINASE.
DR PRODOM: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00133; S_TKc_X; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 270 AA; 31346 MW; CEFFB41BC995B6A5 CRC64;

Query Match 79.6%; Score 39; DB 5; Length 270;
Best Local Similarity 75.3%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLGKPPPE 8
Db 150 MMVGKPPPE 157

RESULT 18
Q8MQ39 PRELIMINARY; PRT; 325 AA.
AC Q8MQ39;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein F47F2.1c.
GN F47F2.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN 1;
RP SEQUENCE FROM N.A.
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RC STRAIN=Bristol N2;
 RX MEJLINE=99069613; PubMed=9851916;
 RA Waterston R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RL investigating biology. The C. elegans Sequencing Consortium.";
 RN Science 282:2012-2018(1998).
 RP SEQUENCE FROM N.A.
 PC STRAIN=Bristol N2;
 PA Bentley D.;
 RT "The sequence of C. elegans cosmid F47F2.";
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 PC STRAIN=Bristol N2;
 PA Waterston R.;
 RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; U40943; AA669117.1; --
 DR WormPep; F47F2.1b; CE04603.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR02290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase_1.
 DR Pfam; PF00433; pkinase_C_1.
 DR PRINTS; PR00139; TYRKINASE.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00133; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 RX Hypothetical protein; ATP-binding; Transferase.
 SQ SEQUENCE 325 AA; 37528 MW; 2.00DF8A13FC18D7 CRC64;

Query Match 79.6%; Score 39; DB 5; Length 325;
 Best Local Similarity 75.0%; Pred. No. 13;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 : : : : :
 DB 205 MWVGKPPF 212

RESULT 19
 Q20541 ID Q20541 PRELIMINARY; PRT: 212 AA.
 AC Q20541
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cyclic AMP-dependent protein kinase, catalytic subunit (EC 2.7.1.37)
 DE Hypothetical protein F47F2.1b;
 GN F47F2.1.
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 CX NCBI_TaxID=6239;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2;
 RX MEDLINE=99187058; PubMed=10055246;
 RA "Abish M., Clegg R.A., Rees H.H., Fisher M.J.;
 RT "Organization and alternative splicing of the Caenorhabditis elegans
 RT cyclic AMP-dependent protein kinase (PKA) catalytic subunit gene
 RT (kin-1).";
 RC Blochem. J. 339:209-216(1999).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;

RT STRAIN=Bristol N2;
 RL Science 282:2012-2018(1998).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Bentley D.;
 RT "The sequence of C. elegans cosmid F47F2.";
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN (4)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AJ012357; CAB41352.1; --
 DR EMBL; U40943; AAK72061.1; --
 DR HSSP; P05132; IATP.
 DR WormPep; F47F2.1b; CE04603.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR02290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase_1.
 DR Pfam; PF00433; pkinase_C_1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00133; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 371 AA; 42486 MW; 0C4873B5F3A45661 CRC64;

Query Match 79.6%; Score 39; DB 5; Length 371;
 Best Local Similarity 75.0%; Pred. No. 15;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGKPPF 8
 : : : : :
 DB 251 MWVGKPPF 258

RESULT 20
 Q9M3V7 ID Q9M3V7 PRELIMINARY; PRT: 454 AA.
 AC Q9M3V7
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE S6 ribosomal protein kinase.
 GN PK1.
 OS Asparagus officinalis (Garden asparagus).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asparagaceae;
 CC Asparagus.
 CX NCBI_TaxID=4686;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Concoers Colossal;
 RA Deacon K., Warner S.A.J., Draper J.;
 RT "Characterisation of an Asparagus S6 ribosomal protein cDNA and an S6
 RT ribosomal protein kinase homologue.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AJ277534; CAB89082.1; --
 DR HSSP; G63450; IA06.
 DR InterPro; IPR000961; Pkinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR02290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase_1.

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DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00110; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Ribosomal protein;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 454 AA; 50467 MW; 0E45C5A5C9997C5 CRC64;

Query Match 79.6%; Score 39; DB 10; Length 465;
Best Local Similarity 87.5%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 315 MLTGKPPF 322

RESULT 21
Q8JFCL PRELIMINARY; PRT; 465 AA.
AC Q8JFCL;
DT 01-OCT-2002 (TrEMBLrel. 22, Created);
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Putative ribosomal protein S6 kinase ATPK6.
CS Arabidopsis thaliana (Mouse-ear cress);
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC eucosids I; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID:3702;
RN [1];
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White G., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 6:0-3(2002).
RN [2];
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Li Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CS EMBL; AY084935; AAY61496.1;
DR InterPro; IPR000361; Kinase_C;
DR InterPro; IPR000379; Prot_Kinase;
DR InterPro; IPR002290; Ser_Thr_Kinase;
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR SMART; SM00219; Tyr_K; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 465 AA; 52587 MW; 5B1E58F1159B923 CRC64;

Query Match 79.6%; Score 39; DB 10; Length 465;
Best Local Similarity 87.5%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 324 MLTGKPPF 331

RESULT 22

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Q43380 PRELIMINARY; PRT; 480 AA.
AC Q43380;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Putative pp70 ribosomal protein S6 kinase.
GN ASPK11.
OS Avena sativa (Oat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Avenae; Avena.
OX NCBI_TaxID=4498;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Rhiannon; TISSUE=Aleurone;
RX MEDLINE=95284341; PubMed=7766874;
RA Huttly A.K., Phillips A.L.;
RT "gibberellin regulated expression in oat aleurone cells of two kinases
RT that show homology to nap kinase and a ribosomal protein kinase.";
RL Plant Mol. Biol. 27:1043-1052(1995);
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; X79992; CAA56313.1;
DR HSP; P05132; ICTP.
DR InterPro; IPR000961; Pkinase_C;
DR InterPro; IPR000719; Prot_Kinase;
DR InterPro; IPR002290; Ser_Thr_Kinase;
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Ribosomal protein;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 480 AA; 53532 MW; 33596A101DBB077D CRC64;

Query Match 79.6%; Score 39; DB 10; Length 480;
Best Local Similarity 87.5%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPF 8
DB 341 MLTGKPPF 348

RESULT 23
Q12701 PRELIMINARY; PRT; 592 AA.
AC Q12701;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DT 01-NOV-1996 (TrEMBLrel. 08, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Protein kinase (EC 2.7.1.37).
GN KSI OR SPCC576.15C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=H90;
RA Niederberger C.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=972H;
RA Wood V., Raebdram M.A., Barrell B.G., Murphy L., Harris D.;
RA Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RL -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

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DR EMBL: X59280; CAA67672.1; ...
DR EMBL: AL031798; CAA21194.1; ...
DR GeneDB_Sporob: SPCC576.15c; ...
DR InterPro: IPR001849; PH.
DR InterPro: IPR007119; Prot_kinase.
DR InterPro: IPR022290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD00001; Prot_kinase; 1.
DR SMART: SMC2233; PH; 1.
DR SMART: SMC2220; S_TK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00117; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00138; PROTEIN_KINASE_ST; 1.
KW: ATP-binding; Kinase; Serine/threonine-protein kinase; Transferrase.
SC SEQUENCE 592 AA; 65661 MW; B9A857D1989F2C61 CRC64;

Query Match 79.6%; Score 39; ID 3; Length 592;
Best Local Similarity 87.5%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLJGKPPF 8
DB 305 MLAGKPPF 312

RESULT 24
Q8F6Y5 PRELIMINARY; PRT; 1759 AA.
AC Q8F6Y5;
DT 01-MAR-2002 (TrEMBLrel. 23, Created);
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Probable serine/threonine-protein kinase.
GN Jall184.
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
CX NCBI_TaxID:173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Setovar ia;
RA Ref. S.;
RJ Submitted (MAR-2002) to the EMBL/GenBank/DBS databases.
RE EMBL: AF011299; AAN48163.1; 1.
RW Kinase; Complete proteome.
SC SEQUENCE 1759 AA; 203645 MW; 80B441C41E8DB94C CRC64;

Query Match 79.6%; Score 39; ID 16; Length 1859;
Best Local Similarity 87.5%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LAGKPPF 9
DB 205 LAGKPPF 212

RESULT 25
Q8XQB2 PRELIMINARY; PRT; 2481 AA.
AC Q8XQB2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created);
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update);
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update);
DE SWP protein 2.
GN RSP1374 CR RS02084.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC P.asmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
CX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM:1000;
RJ MEDLINE=21681879; PubMed=11821852;

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RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunhac S., Denange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002);
DR EMBL: AL646084; CAD18525.1; 1.
KW Plasmid; Complete proteome.
SQ SEQUENCE 2493 AA; 272286 MW; 21E5F0A4EBA83614 CRC64;

Query Match 79.6%; Score 39; ID 16; Length 2483;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLJGKPPF 9
DB 1521 VLLGKPPYD 1529

RESULT 26
Q8XYB9 PRELIMINARY; PRT; 2497 AA.
AC Q8XYB9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created);
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update);
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update);
DE SWP protein 4.
GN RSC1839 OR RS04276.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Ralstoniaceae; Ralstonia.
CX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM:1000;
RJ MEDLINE=21681879; PubMed=11821852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunhac S., Denange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002);
DR EMBL: AL646087; CAD15541.1; 1.
KW Complete proteome.
SQ SEQUENCE 2497 AA; 270604 MW; 128F29A75D3C5F99 CRC64;

Query Match 79.6%; Score 39; ID 16; Length 2497;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLJGKPPF 9
DB 1545 VLLGKPPYD 1553

RESULT 27
Q63432 PRELIMINARY; PRT; 240 AA.
AC Q63432;
DT 01-NOV-1996 (TrEMBLrel. 01, Created);
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Rat protein kinase C-family related (fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

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EX MEDLINE=87147193; PubMed=3459647;
RA Housley G.V., O'Brian C.A., Johnson M.D., Kirschreier P.,
RA Weinstein I.B.,
RT "Isolation of cDNA clones encoding protein kinase C: Evidence for a
RT protein kinase C-related gene family.";
PJ Proc. Natl. Acad. Sci. U.S.A. 94:1065-1069(1997).
QC "SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES."
LR EMBL: M15523; AAA41877.1;
DR HSP: C63450; IAJ6.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR022290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PDC00001; Prot_kinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
LR EMBL: M15523; AAA41877.1;
DR HSP: C63450; IAJ6.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR022290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PDC00001; Prot_kinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1 1
FT TER 240 240
SQ SEQUENCE 240 AA; 26848 MW; 289334FE257E4682 CRC64;
Query Match 77.6%; Score 38; DB 11; Length 240;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLGKPPFE 9
DB 204 XMAGPPFE 212
RESULT 28
Q9CVR6 Q9CVR6 PRELIMINARY; PRT; 324 AA.
AC Q9CVR6
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serine/threonine kinase 18 (Fragment).
GN STK18
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21086660; PubMed=1121785;
RA Kawai C., Shingawa A., Shibata K., Yoshida K., Itoh M., Ishii Y.,
RA Akawa T., Hata A., Fukunishi Y., Komada H., Auchi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kento S., Yanagita I.,
RA Saito T., Okazaki Y., Goyobori T., Hata H., Kasakawa T., Saito K.,
RA Kadota K., Matsuda H.A., Aschburner V., Barilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pasolo G., Clackson J.,
RA Schirra L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Acno H., Baldarelli R., Barsh G.,
RA Blake C., Boffelli D., Bozung N., Cantini P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher K., Fujita M., Gariboldi M.,
RA Gustavich S., Hill D., Hofmann M., Hone D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli L., Nombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez L., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki K., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawayi H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full length mouse cDNA collection.";
RJ Nature 409:685-690(2001).
DR EMBL: AK006927; BAB24759.1; -;
DR HSP: Q00534; 1B18.
DR YGC: MG1101783; STK18.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR022290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.

DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PRO0139; TYRKINASE.
DR ProDom: PDC00001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Transferase.
FT NON_TER 324 324
FT TER 324 324
SQ SEQUENCE 324 AA; 36568 MW; C4247065DFB198CC CRC64;
Query Match 77.6%; Score 38; DB 11; Length 324;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGKPPFE 9
DB 204 XMAGPPFE 212
RESULT 29
Q9AJZ9 Q9AJZ9 PRELIMINARY; PRT; 332 AA.
AC Q9AJZ9
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SCO7729.
GN SCO7729 OR SC8011.20.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OC NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Saunders D.C., Harris D.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=2196410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wierzbicki A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RJ Nature 417:141-147(2002).
DR EMBL: AL939132; CAC22737.1; -;
DR InterPro: IPR03829; DJF209.
DR Pfam: PFC2678; DJF209; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 332 AA; 36974 MW; 7E05869A9386B0ED CRC64;

Query Match: 77.6%; Score 18; DB 16; Length 132;
 Best Local Similarity 77.8%; Pred. No. 21;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
 :||| |||
 DB 262 ILLGPPPE 270

RESULT 30

G93T78 PRELIMINARY; PRT: 554 AA;
 AC Q95778; DT 01-DEC-2001 (TREMBLrel. 19, Created);
 DT 31-DEC-2001 (TREMBLrel. 19, Last sequence update);
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update);
 DE GH13631P;
 GN PKC98E OR CG1954;
 OS Drosophila melanogaster (Fruit fly);
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila;
 CX NCBI_TaxID=7227;
 RN [1] -
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Charpe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guan H., Li P., Rao G., Miranda A., Mungali C.J.,
 RA Nuno J., Pacleb A., Paragas V., Park S., Phoumenavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.W., Colnaker S.;
 EC Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/HR FAMILY OF PROTEIN KINASES.
 DR EMBL: AY062291; AAC25332.1; -;
 DR Flybase: F53N003093; PKC98E;
 DR InterPro: IPR002219; DAG-PE-bind;
 DR InterPro: IPR000961; PKinase C;
 DR InterPro: IPR000719; Prot_kinase;
 DR InterPro: IPR002290; Ser_Thr_kinase;
 DR Pfam: PF00130; DAG-PE-bind; 1;
 DR Pfam: PF00069; pkinase; 1;
 DR Pfam: PF00433; pkinase C; 1;
 DR PRINTS: PR00008; DAGPEDOMAN;
 DR ProDom: PD000091; Prot_kinase; 1;
 DR SMART: SM01224; S_TK_X; 1;
 DR SMART: SM01224; S_TK_X; 1;
 DR PROSITE: PS00479; DAG-PE BINDING; 1;
 DR PROSITE: PS00081; DAG-PE BINDING; 1;
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1;
 DR PROSITE: PS00111; PROTEIN KINASE; 1;
 DR PROSITE: PS00108; PROTEIN KINASE; 1;
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 554 AA; 61598 MW; 106FA905939316F4 3064;

Query Match: 77.6%; Score 18; DB 5; Length 554;
 Best Local Similarity 66.7%; Pred. No. 35;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 3;

QY 1 MLLGKPPPE 9
 :||| |||
 DB 415 NXAGGPPPE 423

RESULT 31

Q8XG6 PRELIMINARY; PRT: 446 AA;
 AC Q8XG6;
 DT 01-OCT-2002 (TREMBLrel. 22, Created);
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update);
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update);
 DE Rel. 4 Protein (corresponding sequence P55A8 24);

GN P55A8.2 OR EGL-4;
 OS Caenorhabditis elegans;
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis;
 OX NCBI_TaxID=6239;
 RN [1] -
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Waterston R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium";
 RL Science 282:2312-2318 (1998);
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Langston Y., Wohldmann P., Ducke's G.;
 RT "The sequence of C. elegans cosmid F55A8";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF067612; AAM98011.1; -;
 DR WormPep: P55A8.cd; CE31542;
 DR InterPro: IPR002373; GMP_kin.
 DR InterPro: IPR002374; GMP_kin.
 DR InterPro: IPR000595; GMP-binding;
 DR InterPro: IPR000961; PKinase C;
 DR InterPro: IPR000719; Prot_kinase;
 DR InterPro: IPR002290; Ser_Thr_kinase;
 DR InterPro: IPR001245; Tyr_kinase;
 DR Pfam: PF00027; GMP-binding; 2;
 DR Pfam: PF00069; pkinase; 1;
 DR Pfam: PF00433; pkinase C; 1;
 DR PRINTS: PR00133; GMPKINASE;
 DR PRINTS: PR00104; GMPKINASE;
 DR ProDom: PD000001; Prot_kinase; 1;
 DR SMART: SM01200; GMP; 1;
 DR SMART: SM01224; S_TK; 1;
 DR SMART: SM01224; S_TK_X; 1;
 DR SMART: SM00219; TyKc; 1;
 DR PROSITE: PS00888; GMP BINDING; 1;
 DR PROSITE: PS00889; GMP BINDING; 1;
 DR PROSITE: PS00442; GMP BINDING; 2;
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1;
 DR PROSITE: PS00111; PROTEIN KINASE; 1;
 DR PROSITE: PS00108; PROTEIN KINASE; 1;
 KW ATP-binding; Transferase;
 SQ SEQUENCE 568 AA; 65094 MW; 423AB3BD6E52ACF4 CRC64;

Query Match: 77.6%; Score 18; DB 5; Length 568;
 Best Local Similarity 55.6%; Pred. No. 36;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPPE 9
 :||| |||
 DB 446 LMLGPPPEQ 456

RESULT 32

Q8NU98 PRELIMINARY; PRT: 646 AA;
 ID Q8NU98;
 AC Q8NU98;
 DT 01-OCT-2002 (TREMBLrel. 22, Created);
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update);
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update);
 DE Serine/threonine protein kinases (EC 2.7.1.-);
 GN G5L004;
 OS Corynebacterium glutamicum (Brevibacterium flavum);
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Corynebacteriaceae; Corynebacterium;

Query Match 77.6%; Score 38; DB 5; Length 707;
 Best Local Similarity 66.7%; Pred. No. 45;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 :|:|:
 DB 570 MWAGQPPE 578

RESULT 35

Q8MXG7 PRELIMINARY: PRT; 749 AA.
 AC Q8MXG7: 22, Created;
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update);
 DT 01-OCT-2002 (TRENBLrel. 23, Last annotation update);
 DE EGL-4 protein (corresponding sequence F55A8.2c);
 DE F55A8.2 OR EGL-4;
 GN F55A8.2;
 OS Caenorhabditis elegans;
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis
 OX NCBI_TaxID:6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 SC STRAIN=Bristol N2;
 RX MEDLINE:99569613; PubMed:995916;
 RA Waterston R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium";
 RL Science 282:2012-2016(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 SC STRAIN=Bristol N2;
 RX Submitted (JUG-2002) to the EMBL/GenBank/DBJ databases.
 RA Langston Y., Weidmann P., Duckers G.;
 RT "The sequence of C. elegans cosmid F55A8";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]

QY SEQUENCE FROM N.A.
 :|:|:
 DB 570 MWAGQPPE 578
 :|:|:
 ID Q8MXG7 PRELIMINARY: PRT; 749 AA.
 AC Q8MXG7: 22, Created;
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update);
 DT 01-OCT-2002 (TRENBLrel. 23, Last annotation update);
 DE EGL-4 protein (corresponding sequence F55A8.2c);
 DE F55A8.2 OR EGL-4;
 GN F55A8.2;
 OS Caenorhabditis elegans;
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis
 OX NCBI_TaxID:6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 SC STRAIN=Bristol N2;
 RX MEDLINE:99569613; PubMed:995916;
 RA Waterston R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium";
 RL Science 282:2012-2016(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 SC STRAIN=Bristol N2;
 RX Submitted (JUG-2002) to the EMBL/GenBank/DBJ databases.
 RA Langston Y., Weidmann P., Duckers G.;
 RT "The sequence of C. elegans cosmid F55A8";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]

Query Match 77.6%; Score 38; DB 5; Length 749;
 Best Local Similarity 55.6%; Pred. No. 48;
 Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 :|:|:
 DB 629 LMLGPPFPQ 637

RESULT 36

Q8MXB6 PRELIMINARY: PRT; 754 AA.
 AC Q8MXB6: 22, Created;
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update);
 DT 01-OCT-2002 (TRENBLrel. 23, Last annotation update);
 DE Hypothetical protein;
 OS Limulus polyphemus (Atlantic horseshoe crab);
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Limulus;
 OX NCBI_TaxID:6850;
 RN [1]
 RP SEQUENCE FROM N.A.
 SC MEDLINE:20356442; PubMed:10901270;
 RX Wang Y., Cao Z., Reid E.A., Newkirk R.F., Ivy M.T., Townes J.G.;
 RT "The use of competitive PCR mimic to evaluate a Limulus lambda phage
 RT genomic DNA library";
 RL Cell Mol Neurobiol 20:509-520(2000).
 CC -1: SIMILARITY: CONTAINS 1 C2 DOMAIN.
 DR EMBL: AF289084; AAM90321.1; -;
 DR InterPro: IPR000008; C2;
 DR InterPro: IPR002219; DAG_PE-bind;
 DR InterPro: IPR000961; PKinase_C;
 DR InterPro: IPR000719; Prot_kinase;
 DR InterPro: IPR002290; Ser_thr_kinase;
 DR InterPro: IPR001245; Tyr_kinase;
 DR Pfam: PF00168; C2; 1;
 DR Pfam: PF00130; DAG_PE-bind; 2;
 DR Pfam: PF00069; PKinase; 1;
 DR Pfam: PF00433; PKinase_C; 1;
 DR PRINTS: PRC0008; DAGPEDOMAIN;
 DR ProDom: PD000001; Prot_kinase; 1;
 DR SMART: SM00139; C1; 2;
 DR SMART: SM00239; C2; 1;
 DR SMART: SM00220; S_TKc; 1;
 DR SMART: SM00133; S_TK_X; 1;
 DR SMART: SM00219; TYR_KC; 1;
 DR PROSITE: PS00004; C2_DOMAIN_2; 1;
 DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2;
 DR PROSITE: PS00381; DAG_PE_BIND_DOM_2; 2;
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1;
 DR PROSITE: PS00109; PROTEIN_KINASE_ST; 1;
 KW Hypothetical protein; ATP-binding; Transferase.
 SQ SEQUENCE 754 AA; 85488 MW; BF16A40497E2BB40 CRC64;

Query Match 77.6%; Score 38; DB 5; Length 754;
 Best Local Similarity 66.7%; Pred. No. 48;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGKPPFE 9
 :|:|:
 DB 607 MWAGQPPE 615

RESULT 37

Q76360 PRELIMINARY: PRT; 780 AA.
 AC Q76360: 08, Created;
 DT 01-NOV-1998 (TRENBLrel. 12, Last sequence update);
 DT 01-NOV-1998 (TRENBLrel. 23, Last annotation update);
 DE Hypothetical 86.7 kDa protein F55A8.2 in chromosome IV.
 GN F55A8.2;
 OS Caenorhabditis elegans;
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis

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OM protein - protein search, using sw mode

Run on: November 14, 2003, 12:54:54 / Search time 34.7143 Seconds
(without alignment)
41,151 Million Cells updates/sec

Title: US-09-736-076-18

Perfect score: 49

Sequence: 1 LRRPFFERS 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1:07863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1:07863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0
Maximum Match 100
Listing first 45 summaries

Database: A Geneseq 19Jun03:

1	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1380.DAT
2	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1391.DAT
3	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1392.DAT
4	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1393.DAT
5	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1394.DAT
6	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1395.DAT
7	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1396.DAT
8	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1397.DAT
9	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1398.DAT
10	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1399.DAT
11	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1400.DAT
12	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1401.DAT
13	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1402.DAT
14	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1403.DAT
15	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1404.DAT
16	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1405.DAT
17	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1406.DAT
18	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1407.DAT
19	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1408.DAT
20	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1409.DAT
21	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1410.DAT
22	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1411.DAT
23	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1412.DAT
24	/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1413.DAT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	9	20	AAW74162
2	49	100.0	9	23	AAU98318
3	49	100.0	11	20	AAW74163
4	49	100.0	11	23	AAU98319
5	46	93.9	469	22	AAU98318
6	46	93.9	469	22	AAU98319
7	46	93.9	626	21	AAU98318
8	46	93.9	685	20	AAU98319
9	46	93.9	685	20	AAU98318

10	46	93.9	685	23	AB261474
11	46	93.9	753	23	AB261492
12	43	87.8	20	20	AAW74173
13	43	87.8	20	23	AAU98306
14	43	87.8	329	21	AAU98306
15	43	87.8	531	23	AAU74656
16	43	87.8	603	16	AAU74620
17	43	87.8	603	23	AAU79306
18	43	87.8	603	23	AAU79308
19	43	87.8	603	23	AAU79309
20	43	87.8	603	23	AAU79310
21	43	87.8	603	23	AAU79311
22	43	87.8	603	23	AAU79312
23	43	87.8	603	23	AAU79313
24	43	87.8	603	23	AAU79314
25	43	87.8	603	23	AAU79315
26	43	87.8	603	23	AAU79316
27	43	87.8	603	23	AAU79317
28	43	87.8	603	23	AAU79318
29	43	87.8	603	23	AAU79319
30	43	87.8	603	23	AAU79320
31	43	87.8	603	24	ABR49196
32	42	85.7	769	22	ABR49196
33	42	81.6	9	20	AAW74159
34	42	81.6	9	23	AAU98315
35	42	81.6	10	20	AAW74213
36	40	81.6	10	23	AAU98357
37	40	81.6	416	17	AAU92176
38	40	81.6	464	17	AAU92214
39	40	81.6	925	17	AAU92177
40	40	81.6	925	23	ABR52773
41	40	81.6	970	22	AAU78833
42	40	81.6	970	22	AAU39244
43	40	81.6	980	22	AAU79817
44	40	81.6	980	22	AAU41030
45	39	79.6	183	20	AAU36843

ALIGNMENTS

RESULT 1
AAW74162
ID AAW74162 standard; peptide; 9 AA.
XX
AC AAW74162;
XX

DT 05-MAY-1999 (first entry)
DE HJ loop peptide 7-45.

XX HJ loop peptide 7-45.

XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
XX haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
XX inflammatory disorder; central nervous system disease; septic shock;
XX Parkinson's disease; hypertension.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 7 /note= "acetylated"

FT Modified-site 9 /note= "acetylated"

XX WO9853050-A2.

XX 26-NOV-1998.

XX 20-MAY-1998. 98WO-US10319

XX 21-MAY-1997. 98US-0861338

XX CHILDREN'S MEDICAL CENT.

PA (YISS) YISSUM RES & DEV CO.
 XX Ben-Sasson SA;
 XX --
 XX WP: 1999-070142/06.
 XX
 XX New peptides for modulating serine/threonine kinase activity
 PT comprise a sequence corresponding to the H3 loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders
 XX
 XX Claim 14; Fig 4; 70pp; English.
 XX
 CC This sequence represents a peptide of the invention, and is a derivative
 CC of the H3 loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the H3 loop of the STK
 CC from which the peptide was derived.
 XX
 SQ Sequence 9 AA;
 Query March 100.0%; Score 49; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LGRPPFFETS 9
 | | | | |
 DB 1 LGRPPFFETS 9
 | | | | |
 RESULT 2
 AAU98318
 ID AAU98318 standard; Peptide; 9 AA.
 AC AAU98318;
 XX 13-AUG-2003 (first entry)
 DE Polo kinase serine-threonine kinase H3 loop peptide J-45.
 XX H3 loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cysticotic; antidiabetic; anorectic; neurological;
 KW anti-inflammatory; immunosuppressive; cardiac; haemostatic;
 KW modulating STK activity; polo kinase, J-45.
 XX
 CS Unidentified.
 CS Synthetic.
 FH Key Location/Qualifiers
 FT Modified-site 7 /note= "N-terminal acetyl"
 FT Misc-difference /note= "Benzyl ester of Glutamic acid"
 FT Modified-site 9 /note= "C-terminal amide"
 XX
 PN US2002049301-A1.
 XX 25-APR-2002.
 PD
 XX

PF 13-DEC-2000; 2000US-0736076.
 XX 21-MAY-1997; 97US-0861338.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX Ben-Sasson SA;
 XX WP: 2002-462787/49
 XX New peptide from the H3 loop of serine-threonine kinase, useful for
 XX treating e.g. cancer and for producing diagnostic antibodies -
 XX Disclosure: Fig 4; 41pp; English.
 XX The present invention relates to new peptides derived from the H3 loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the H3 loop.
 CC The present amino acid sequence represents the polo kinase
 CC serine-threonine kinase H3 loop peptide J-45. This sequence is one of
 CC the short peptides of the invention that selectively modulate the
 CC activity of STK.
 XX
 SQ Sequence 9 AA;
 Query March 100.0%; Score 49; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LGRPPFFETS 9
 | | | | |
 DB 1 LGRPPFFETS 9
 | | | | |
 RESULT 3
 AAU74163
 ID AAU74163 standard; peptide; 11 AA.
 AC AAU74163;
 XX 05-MAY-1999 (first entry)
 DE H3 loop peptide J-46.
 XX H3 loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 XX Parkinson's disease; hypertension.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "acetylated"
 FT Modified-site 11 /note= "amidated"
 FT
 XX WO9853050-A2.
 XX 26-NOV-1998.
 PD
 XX 20-MAY-1998; 98WC-US10319.
 XX 21-MAY-1997; 97US-0861338.
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 PA (YISS) YISSUM RES & DEV CO.

```

XX  Ben-Sasson SA;
XX  WPI; 1999-070-42/36.
XX
XX  New peptides for modulating serine/threonine kinase activity
XX  comprise a sequence corresponding to the H3 loop of a
XX  serine/threonine kinase, used for treating, e.g. cancers,
XX  inflammatory disorders or autoimmune disorders
XX
XX  Claim 14; Fig 4; 70pp; English.
XX
XX  This sequence represents a peptide of the invention, and is a derivative
XX  of the H3 loop of a serine/threonine kinase (STK). The peptides can be
XX  used for the treatment of disorders caused by overactivity or
XX  underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
XX  shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
XX  arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
XX  hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
XX  psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
XX  of organ transplant rejection, multiple sclerosis, inflammatory bowel
XX  disease and AIDS), central nervous system diseases (e.g. Alzheimer's
XX  disease, stroke and trauma), septic shock, Parkinson's disease or
XX  hypertension. The peptides can also be used to produce antibodies which
XX  can be used to identify cells expressing the STK and to study the
XX  intracellular distribution of the STK. In addition, the peptides can be
XX  used to identify and quantitate ligands which bind the H3 loop of the STK
XX  from which the peptide was derived.
XX
XX  Sequence 11 AA:
XX
XX  Query Match 100.0%; Score 49; DB 20; Length 11;
XX  Best Local Similarity 100.0%; Pred. No. 0.017;
XX  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 1 LGRPPPEETS 9
XX      |||||
XX  Db 3 LGRPPPEETS 11
XX
XX
XX  RESULT 4
XX  AAU98119
XX  ID AAU98119 standard; Peptide; 11 AA.
XX  AC AAU98119;
XX  DT 13-AUG-2002 (first entry)
XX  DE Polo kinase serine-threonine kinase H3 loop peptide J-46.
XX  KW H3 loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
XX  central nervous system disorder; inflammatory disorder;
XX  autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
XX  lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
XX  anti-inflammatory; immunosuppressive; cardiac; haemostatic;
XX  modulating STK activity; polo kinase; J-46.
XX  OS Unidentified.
XX  SS Synthetic.
XX
XX  Key Location/Qualifiers
XX  Modified-site 1
XX  FT Modified-site 1 /note= "N-terminal acety."
XX  FT Misc-difference 9 /note= "Benzy ester of Glutamic acid"
XX  FT Modified-site 11 /note= "C-terminal amide"
XX  FT
XX  FT
XX  US2002049301-A1.
XX  PN
XX  XX
XX  25-APR-2002.
XX  PD
XX  13 DEC-2000; 2000US-0736076.
XX  PT

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```

XX  21-MAY-1997; 97US-0861338.
XX  (CHILD-) CHILDRENS MEDICAL CENT.
XX
XX  Ben-Sasson SA;
XX  WPI; 2002-462787/49.
XX
XX  New peptide from the H3 loop of serine-threonine kinase, useful for
XX  treating e.g. cancer and for producing diagnostic antibodies -
XX
XX  Disclosure; Fig 4; 41pp; English.
XX
XX  The present invention relates to new peptides derived from the H3 loop
XX  of a serine/threonine kinase (STK). The peptides of the invention are
XX  used to modulate STK activity, especially for treating cancer, diabetes,
XX  obesity or a wide variety of central nervous system, inflammatory,
XX  autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
XX  regulating lipid metabolism. The peptides are also used to generate
XX  antibodies that bind specifically to the parent STK, used e.g. for
XX  identifying STK-expressing cells and to study intracellular distribution
XX  of STK, and to identify or quantify ligands that bind to the H3 loop.
XX  The present amino acid sequence represents the polo kinase
XX  serine-threonine kinase H3 loop peptide J-46. This sequence is one of
XX  the short peptides of the invention that selectively modulate the
XX  activity of STK.
XX
XX  Sequence 11 AA:
XX
XX  Query Match 100.0%; Score 49; DB 23; Length 11;
XX  Best Local Similarity 100.0%; Pred. No. 0.017;
XX  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY 1 LGRPPPEETS 9
XX      |||||
XX  Db 3 LGRPPPEETS 11
XX
XX
XX  RESULT 5
XX  AAB94717
XX  ID AAB94717 standard; Protein; 469 AA.
XX  AC AAB94717;
XX  DT 26-JUN-2001 (first entry)
XX  DE Human protein sequence SEQ ID NO:15726.
XX  KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX  OS Homo sapiens.
XX  XX
XX  EP1074617-A2.
XX  XX
XX  07-FEB-2001.
XX  XX
XX  28-JUL-2000; 2000EP-0116126.
XX  XX
XX  29-JUL-1999; 99JP-0248036.
XX  27-AUG-1999; 99JP-0300253.
XX  11-JAN-2000; 2000JP-0118776.
XX  02-MAY-2000; 2000JP-0183767.
XX  09-JUN-2000; 2000JP-0241899.
XX  XX
XX  (HELI-) HELIX RES INST.
XX  XX
XX  Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX  Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX  WPI; 2001-318749/34.
XX
XX  Primer sets for synthesizing polynucleotides, particularly the 5602
XX  PT

```

PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full length cDNAs -
 XX Claim 8; SEQ ID 15726; 2537pp - CD ROM; English.
 XX The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5' end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAC83166 to AAC83628 and
 CC AAC83633 to AAC89742 represent human cDNA sequences; AAC92446 to
 CC AAC95893 represent human amino acid sequences, and AAC83629 to AAC83632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 XX
 SQ Sequence 459 AA;

Query Match 93.9%; Score 46; DB 22; Length 469;
 Best Local Similarity 88.9%; Pred. No. 2.5;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LGRRPFETS 9
 |||||
 Db 59 LGRRPFETT 67

RESULT 6
 AAG67426
 ID AAG67426 standard; Protein; 469 AA.
 AC AAG67426;
 XX
 XX 26-NOV-2001 (first entry)
 XX
 XX Human acid sequence of a human protein kinase/tyrosine phosphatase.
 XX Human; Protein Kinase; protein phosphatase; signal transduction;
 KW intracellular signalling pathway.
 XX
 XX Homo sapiens.
 XX
 XX WO200109345-A1.
 XX
 XX 08 FEB-2001.
 XX
 XX 28-JUL-2000; 2000WO-JP05060.
 XX
 XX 29-JUL-1999; 99JP-0248036.
 PR 18-OCT-1999; 99US-0159590.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 17-FEB-2000; 2000US-0183322.
 PR 02-MAY-2000; 2000JP-0183767.
 XX
 XX (HEU:1) HELIX RES INST.

XX Ota T., Isogai T., Nishikawa T., Hayashi K., Saito K., Yamamoto J.;
 XX Ishii S., Sugiyama T., Wakamatsu A., Nagai K., Otsuki T., Furukashi S.;
 PI Senoo C., Nezu C.

DR WPI; 2001-564736/63.
 DR N-PSDB; AAH78069.
 XX
 PT New genes encoding protein kinase and protein phosphatase, useful for
 PT identifying modulators which can be used to treat human or animal
 PT disorders associated with the expression or function of these enzymes -
 XX
 XX Claim 2; Page 136-139; 336pp; Japanese.
 XX The present sequence represents a human protein kinase/protein
 CC phosphatase. The polypeptides are expected to participate in signal
 CC transduction in cells. The kinase phosphatases are connected with
 CC intracellular signalling pathways. Antisense oligonucleotides and
 CC compounds identified by screening agonists or antagonists, can be
 CC used to treat human or animal disorders associated with the expression
 CC or function of the protein. In addition, the polypeptides may be used
 CC as target molecules for drug development.

SQ Sequence 469 AA;

Query Match 93.9%; Score 46; DB 22; Length 469;
 Best Local Similarity 88.9%; Pred. No. 2.5;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LGRRPFETS 9
 |||||
 Db 59 LGRRPFETT 67

RESULT 7
 AAB35805
 ID AAB35805 standard; Protein; 626 AA.
 AC AAB35805;
 XX

DT 23-FEB-2001 (first entry)
 XX
 XX Protein involved in cell cycle regulation SEQ ID 46.

XX Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
 KW cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
 KW cotton; rice; barley; millet.

OS Zea mays.
 XX
 XX WO2000065040-A2.
 XX
 XX 02-NOV-2000.
 XX
 XX 13-APR-2000; 2000WO-US09975.
 XX
 XX 22-APR-1999; 99US-0130849.
 XX
 XX (PION-) PIONEER HI-BRED INT INC.

XX Helentjaris TG, Habben JE, Sun Y;
 XX
 XX WPI; 2000-687333/67.
 DR N-PSDB; AAC83112.
 XX
 XX Nucleic acids useful for producing transgenic plants, preferably maize,
 PT with increased cell cycle gene activity, preferably activity of cyclin
 PT and/or cyclin-dependent kinase -
 XX
 XX Claim 16; Page 117-118; 122pp; English.

XX Polynucleotide sequences AAC83101 - AAC83113 encode proteins AAB35794 -
 CC AAB35806 which are involved in regulating the cell cycle. The protein and
 CC DNA sequences have been isolated from Zea mays (corn), and the invention
 CC also includes oligonucleotides AAC83114 - AAC83139 which are related to
 CC the cell cycle polynucleotides. The cell cycle polynucleotide sequences
 CC are useful for producing transgenic plants such as maize, soybean,
 CC sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and

CC millet with increased levels of cell cycle gene activity, such as
 CC activity of cyclin and cyclin-dependent kinases. The DNA sequences are
 CC also useful as probes for detecting deficiencies in the level of mRNA in
 CC screening for desired transgenic plants, for detecting mutations in the
 CC gene, for monitoring upregulation of expression or changes in enzyme
 CC activity in screening assays of compounds, for detecting any number of
 CC allelic variants, orthologs or paralogues of the gene, and site directed
 CC mutagenesis in eukaryotic cells. The DNA sequences are also useful for
 CC recombinant expression of the encoded polypeptides and as immunogens for
 CC preparing and screening antibodies. A transgenic plant comprising an
 CC expression cassette including a cell cycle regulatory gene is useful for
 CC assaying enzyme agonists and antagonists, and as immunogens or antigens
 CC to obtain antibodies. The antibodies are useful in assaying expression
 CC levels of cell cycle regulatory proteins, for identifying and isolating
 CC nucleic acids from expression libraries, for identifying homologues of
 CC polypeptides from other species, and for purification of the proteins.

XX
 XX
 SQ Sequence 626 AA;

Query Match 93.9%; Score 46; DB 21; Length 626;
 Best Local Similarity 89.9%; Pred. No. 14;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LGRPPFFTS 9
 : : : : :
 Db 230 VGRPPFFTS 239

RESULT 2
 AAY00915
 ID AAY00915 standard; Protein: 685 AA.
 AC AAY00915;
 DE 26-MAY-1999 (first entry)
 DE Human serum inducible kinase.
 XX Serum inducible kinase; SNK protein; human; proliferative disease;
 KW leukemia; solid tumor cancer; metastasis; chronic inflammatory;
 KW psoriasis; rheumatoid arthritis; proliferative cardiovascular disease;
 KW restenosis; ocular disorder; diabetic retinopathy; haemangioma;
 KW benign hyperproliferative disease; diagnosis;
 XX
 CS Homo sapiens.
 XX
 PN WO9909146 A1.
 XX
 PD 25-FEB-1999.
 XX
 PF 20-AUG-1998; 98WO-US17249.
 XX
 PR 20-AUG-1997; 97US-0056112.
 XX
 PA (SMK : SMITHKLINE BEECHAM CORP.
 XX
 P: Anderson XX, Bouzyk M, Hensbury M, Jackson JR,
 P: Nerurkar SS, Roshak AK;
 XX
 XX WPI: 1999-181027/15.
 DR N-PSUB: AAX27227.
 XX
 XX New serum inducible kinase (SNK) polypeptides and polynucleotides -
 PF useful for treating proliferative diseases

XX
 PS Claim 1: Page 39-40; 41pp; English.
 XX
 XX This sequence is a human serum inducible kinase (SNK) of the
 CC invention. The invention relates to diagnostic assays or kits for
 CC detecting diseases associated with inappropriate SNK activity or levels.
 CC Disease states that can be diagnosed include proliferative diseases such
 CC as leukemia, solid tumor cancers and metastases, chronic inflammatory
 CC proliferative diseases such as psoriasis and rheumatoid arthritis.

CC proliferative cardiovascular diseases such as restenosis, proliferative
 CC ocular disorders such as diabetic retinopathy and benign
 CC hyperproliferative diseases such as haemangiomas. The polynucleotides can
 CC be used as hybridisation probes for cDNA and genomic DNA or as primers
 CC for a nucleic acid amplification (PCR) reaction, to isolate full-length
 CC cDNAs and genomic clones encoding polypeptides of this invention and to
 CC isolate cDNA and genomic clones of other genes which have a high sequence
 CC similarity to the SNK coding sequence. The differences between cDNA and
 CC genomic sequences can be observed and therefore mutations detected. Any
 CC mutations may then be attributed to likely causative agents of disease.
 CC The nucleotide sequences are also useful for chromosome identification.

XX
 SQ Sequence 685 AA;

Query Match 93.9%; Score 46; DB 20; Length 685;
 Best Local Similarity 89.9%; Pred. No. 3.7;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFTS 9
 : : : : :
 Db 275 LGRPPFFTS 283

RESULT 9
 AAW88432
 ID AAW88432 standard; Protein: 685 AA.
 AC AAW88432;
 XX
 XX 26-APR-1999 (first entry)
 XX
 DE Disease associated protein kinase DAPK-1.

XX DAPK-1; disease associated protein kinase; human; diagnosis;
 KW therapy; adult respiratory distress syndrome; allergy; asthma;
 KW arteriosclerosis; bronchitis; emphysema; hyperosinophilia;
 KW myocardial inflammation; pericardial inflammation; anaemia;
 KW rheumatoid arthritis; Addison's disease; AIDS; atherosclerosis;
 KW atopic dermatitis; dermatomyositis; diabetes mellitus;
 KW glomerulonephritis; gout; Grave's disease; lupus erythematosus;
 KW multiple sclerosis; myasthenia gravis; osteoarthritis;
 KW osteoporosis; pancreatitis; polycystic kidney disease;
 KW polymyositis; scleroderma; Sjogren's syndrome;
 KW autoimmune thyroiditis; cancer; infection; trauma;
 KW cell proliferation.
 XX
 XX Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Binding-site 91..96
 FT /note= "potential ATP binding site"
 FT Peptide 506..513
 FT /note= "presumed regulatory sequence common to
 FT polo family protein kinases"

XX WO9858052-A2.
 XX
 XX 23-DEC-1998.
 XX
 XX 19-JUN-1998; 98WO-US12813.
 XX
 XX 19-JUN-1997; 97US-0878989.
 XX
 XX (INCY-) INCYTE PHARM INC.
 XX
 XX Bandman O, Corley NC, Goli SK, Guegler KJ, Hillman JL;
 PI Lal P, Shan P;

XX WPI: 1999-080952/37.
 DR N-PSUB: AAX06831.
 XX
 XX New disease associated protein kinases - used to stimulate cell
 PF proliferation and to treat the immune response and cancer

XX Claim 1: Page 54-56; 93pp; English.

XX This is the amino acid sequence of human disease associated protein

XX kinase DAPK-1, as deduced from a consensus sequence (see AAX0681).

XX of overlapping cDNA clones from libraries which are immortalised

XX or cancerous and show inflammatory or immune responses. DAPK-1

XX shows 53% homology to human proliferation-related protein kinase

XX PRK (GI 1498563). The invention provides DAPK-1 to DAPK-7

XX polypeptides (see AAX06812-38) and cDNA clones encoding them (see

XX AAX0681 35 and AAX0682), as well as expression vectors, host cells,

XX agonists, antagonists and antibodies. The invention further

XX provides uses of such products in the diagnosis, prevention and

XX treatment of diseases associated with cell proliferation,

XX especially cancer or an immune response (claimed). Conditions

XX that may be treated include adult respiratory distress syndrome,

XX allergies, asthma, arteriosclerosis, bronchitis, emphysema,

XX hyperesotriophilia, myocardial or pericardial inflammation,

XX rheumatoid arthritis, Addison's disease, AIDS, anaemia,

XX atherosclerosis, various diseases of the digestive system, atopic

XX dermatitis, dermatomyositis, diabetes mellitus, glomerulonephritis,

XX gout, Grave's disease, lupus erythematosus, multiple sclerosis,

XX myasthenia gravis, osteoarthritis, osteoporosis, pancreatitis,

XX polycystic kidney disease, polyposis, scleroderma, Sjogren's

XX syndrome, autoimmune thyroiditis, complications of cancer,

XX extracorporeal circulation, viral, bacterial, fungal, parasitic,

XX protozoal, and helminthic infections, and trauma (disclosed).

XX

SQ Sequence 695 AA;

Query Match 93.9%; Score 46; DB 20; Length 655;

Best Local Similarity 88.9%; Pred. No. 3.7;

Matches 8; Conservative 1; Mismatches 0; Gaps 3;

Qy 1 LGRPFFETS 9

Db 275 LGRPFFETT 283

RESULT 1:

ABP41992

ID ABP41992 standard: Protein; 753 AA.

XX AC ABP41992;

XX 22-AUG-2002 (first entry)

XX Human ovarian antigen HACM08, SEQ ID NO:3124.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;

XX ovarian cancer; breast cancer; tumour; reproductive system disorder;

XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;

XX PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;

XX inflammatory condition; immune disorder; blood disorder;

XX cardiovascular disorder; respiratory disorder; neurological disorder;

XX gastrointestinal disorder; urinary system disorder; drug screening;

XX gene therapy; chromosome mapping; forensic analysis;

XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;

XX anti-inflammatory; gynaecological; reproductive; chromosome 5.

XX

OS Homo sapiens.

XX WC200200677-A1.

XX 23-JAN-2002.

XX 07-JUN-2001; 2001WO-US18569.

XX 07-JUN-2000; 2000US-239467P.

XX (HUYA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI; 2002-147878/19.

XX N-PSDB; ABQ55069.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,

XX useful in the prevention, treatment and diagnosis of cancer (e.g.

XX ovarian cancer), immune disorders, cardiovascular disorders and

XX neurological diseases.

XX Claim 11; SEQ ID NO 3124; 2922pp; English.

PT NF-approximatelykB activating gene and expressed protein, applicable in

PT diagnosis and screening inhibitors or promoters to control excessive

PT activation or inhibition for treating e.g. inflammations, autoimmune

PT diseases and cancer.

PS Claim 1: Page 448-453; 841pp; Japanese.

XX The invention relates to a purified protein (I), comprising one of 93

XX fully defined sequences (ABP61424-ABP61513) or a protein based on any of

XX the sequences but with some amino acids deleted, substituted or added and

XX with a NF-kB (nuclear factor kappa B) activating effect. The protein and

XX encoding gene (ABQ91912-ABQ9203) are useful in diagnosis and screening

XX inhibitors or promoters to control excessive activation or inhibition

XX and for treating e.g. inflammations, autoimmune diseases, cancers,

XX infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic

XX disorders.

SQ Sequence 685 AA;

Query Match 93.9%; Score 46; DB 23; Length 685;

Best Local Similarity 88.9%; Pred. No. 3.7;

Matches 8; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 LGRPFFETS 9

Db 275 LGRPFFETT 283

RESULT 1:

ABP41992

ID ABP41992 standard: Protein; 753 AA.

XX AC ABP41992;

XX 22-AUG-2002 (first entry)

XX Human ovarian antigen HACM08, SEQ ID NO:3124.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;

XX ovarian cancer; breast cancer; tumour; reproductive system disorder;

XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;

XX PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;

XX inflammatory condition; immune disorder; blood disorder;

XX cardiovascular disorder; respiratory disorder; neurological disorder;

XX gastrointestinal disorder; urinary system disorder; drug screening;

XX gene therapy; chromosome mapping; forensic analysis;

XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;

XX anti-inflammatory; gynaecological; reproductive; chromosome 5.

XX

OS Homo sapiens.

XX WC200200677-A1.

XX 23-JAN-2002.

XX 07-JUN-2001; 2001WO-US18569.

XX 07-JUN-2000; 2000US-239467P.

XX (HUYA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI; 2002-147878/19.

XX N-PSDB; ABQ55069.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,

XX useful in the prevention, treatment and diagnosis of cancer (e.g.

XX ovarian cancer), immune disorders, cardiovascular disorders and

XX neurological diseases.

XX Claim 11; SEQ ID NO 3124; 2922pp; English.

CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP41228) and to cDNAs encoding them (ASQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prophesying or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory system disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 753 AA;

Query Match 93.9%; Score 46; DB 23; Length 753;
 Best Local Similarity 88.9%; Pred. No. 4;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
 DB 343 LGRPPFETT 351
 |||||

RESULT 12
 AAU74173
 ID AAU74173 standard; peptide; 20 AA.

XX AAU74173;
 XX
 DT 05-MAY-1999 (first entry)
 DE HJ loop peptide POLO.
 XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.

XX Synthetic.

XX WC9853050-A2.

XX 26-NOV-1998.

XX 20-MAY-1998; 98WO-US-0319.

XX 21-MAY-1997; 97US-0861338.

XX (CHILD-) CHILDRENS MEDICAL CENT.

XX (VISS) VISSUM RES & DEV CO.

XX Ben-Sasson SA;

XX WPI; 1999-070142/56.

XX

PT New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders
 XX Claim 41; Fig 3b; 70pp; English.

XX This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.

SQ Sequence 20 AA;

Query Match 87.9%; Score 43; DB 20; Length 20;
 Best Local Similarity 77.8%; Pred. No. 0.4;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
 DB 5 VGKPPFETS 13
 |||||

RESULT 13

AAU98306

ID AAU98306 standard; Peptide; 20 AA.

XX AAU98306;

XX 13-AUG-2002 (first entry)

DE Peptide sequence of HJ loop of serine-threonine kinase polo kinase.

XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 KW anti-inflammatory; immunosuppressive; cardiant; haemostatic;
 KW modulating STK activity; polo kinase.

XX Unidentified.

XX US2002049301-A1.

XX 25-APR-2002.

XX 13-DEC-2000; 2000US-0736076.

XX 21-MAY-1997; 97US 0861338.

XX (CHILD-) CHILDRENS MEDICAL CENT.

XX Ben-Sasson SA;

XX WPI; 2002-462787/49.

PT New peptide from the HJ loop of serine-threonine kinase, useful for
 PT treating e.g. cancer and for producing diagnostic antibodies -

XX Claim 33; Fig 3; 41pp; English.

CC The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the peptide sequence of the HJ
 CC loop of serine-threonine kinase polo kinase. This sequence is one of the
 CC short peptides of the invention that selectively modulate the activity
 CC of STK.

XX SQ Sequence 20 AA;

Query Match 87.8%; Score 43; DB 23; Length 20;

Best Local Similarity 77.8%; Pred. No. 0.4;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9

DB 5 VGKPPFFETS 13

RESULT 14

AA05669C

ID AAB56690 standard; Protein; 329 AA.

XX AC AAB56690;

XX DC 13-MAR-2001 (first entry)

XX DE Human prostate cancer antigen protein sequence SEQ ID NO:1269.

XX KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 XX KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
 XX KW vulnary; gastrointestinal; nephrotoxic; antiinfective; gynaecological;
 XX KW antibacterial; gene therapy; neural; immune; reproductive; renal;
 XX KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 XX KW wound; infectious disease.

XX OS Homo sapiens.

XX FN WO200055174-A1.

XX PD 21 SEP-2000.

XX PF 08 MAR-2000; 2000WO-US05988.

XX PE 12 MAR 1999; 99US-0124270.

XX FA (HUMA-) HUMAN GENOME SCI INC.

XX PA (ROSE/) ROSEN C A.

XX PI Rosen CA, Ruben SM;

XX DR WP: 2000-587513/55.

XX DR N-PSDB; AAF15893.

XX PT Prostate cancer associated gene sequences, referred to as prostate

XX cancer antigens, useful for treatment, prevention, and diagnosis of

XX disorders such as prostate cancer.

XX PS Claim 11; Page 1691-1692; 2338pp; English.

XX CC AAF:5566 to AAF16505 encode the human prostate cancer associated
 CC proteins, called prostate cancer antigens, given in AAF556633 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytostatic,
 CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,
 CC nephrotoxic, antiinfective, gynaecological and antibacterial activities,
 CC and can be used in gene therapy. The prostate cancer antigen
 CC polynucleotides may be used for detection of prostate cancer, chromosome

CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The prostate cancer antigens may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC AAB57103 represent sequences used in the exemplification of the present
 CC invention.

XX SQ Sequence 329 AA;

Query Match

Best Local Similarity 87.8%; Score 43; DB 21; Length 329;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9

DB 262 VGKPPFFETS 270

RESULT 15

AAU74656

ID AAU74656 standard; Protein; 53; AA.

XX AC AAU74656;

XX DT 09-APR-2002 (first entry);

XX DE Mammalian polo-like kinase (Plx).

XX KW Polo-like kinase; Plx; polo-box; cytostatic; neoplasm;
 XX KW hyperproliferative disorder; cytokinesis; solid tumour;
 XX KW carcinoma; sarcoma; cancer; small cell carcinoma; adenocarcinoma;
 XX KW Mullerian tumour; squamous cell carcinoma; protein.

XX OS Mammalia.

XX FH Key Location/Qualifiers

XX FT Misc-difference 130 /label= Unknown

XX FT Misc-difference 131 /label= Unknown

XX FT Misc-difference 132 /label= Unknown

XX FT Misc-difference 133 /label= Unknown

XX FT Misc-difference 134 /label= Unknown

XX FT Misc-difference 135 /label= Unknown

XX FT Misc-difference 136 /label= Unknown

XX FT Misc-difference 137 /label= Unknown

XX FT Misc-difference 138 /label= Unknown

XX FT Misc-difference 139 /label= Unknown

XX FT Misc-difference 140 /label= Unknown

XX FT Misc-difference 141 /label= Unknown

XX FT Misc-difference 142 /label= Unknown

XX FT Misc-difference 143 /label= Unknown

XX FT Misc-difference 144 /label= Unknown

XX FT Misc-difference 145 /label= Unknown

XX FT Misc-difference 146 /label= Unknown

XX FT Misc-difference 147 /label= Unknown

XX FT Misc-difference 148 /label= Unknown

XX FT Misc-difference 149 /label= Unknown

XX FT Misc-difference 150 /label= Unknown

XX FT Misc-difference 151 /label= Unknown

XX FT Misc-difference 152 /label= Unknown

XX FT Misc-difference 153 /label= Unknown

XX FT Misc-difference 154 /label= Unknown

XX FT Misc-difference 155 /label= Unknown

XX FT Misc-difference 156 /label= Unknown

XX FT Misc-difference 157 /label= Unknown

XX FT Misc-difference 158 /label= Unknown

XX FT Misc-difference 159 /label= Unknown

XX FT Misc-difference 160 /label= Unknown

XX FT Misc-difference 161 /label= Unknown

XX FT Misc-difference 162 /label= Unknown

XX FT Misc-difference 163 /label= Unknown

XX FT Misc-difference 164 /label= Unknown

XX FT Misc-difference 165 /label= Unknown

FT Misc-difference 353 /label= Unknown
 FT Misc-difference 354 /label= Unknown
 FT Misc-difference 355 /label= Unknown
 FT Misc-difference 356 /label= Unknown
 FT Misc-difference 357 /label= Unknown
 FT Misc-difference 358 /label= Unknown
 FT Misc-difference 359 /label= Unknown
 FT Misc-difference 360 /label= Unknown
 FT Misc-difference 361 /label= Unknown
 FT Misc-difference 362 /label= Unknown
 FT Misc-difference 363 /label= Unknown
 FT Misc-difference 364 /label= Unknown
 FT Misc-difference 365 /label= Unknown
 FT Region 4:0..439
 FT /label= Polo-box
 FT /note= "Core polo-box consensus sequence"
 XX WC2001904C1-A2.
 PN 29-NOV-2001.
 XX 23-MAY-2002; 2001WO-US16903.
 XX 23-MAY-2000; 2000US-206588P.
 PA (HARC) HARVARD COLLEGE.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (USSH) US NAT INST OF HEALTH.
 PI Lee KS, Song S, Erikson R;
 PI WPI: 2002 106210/14.
 DR Identifying polo-like kinase modulators by contacting eukaryotic cells
 DR expressing polo-box peptides with test compounds and evaluating changes
 DR in dominant negative cytokinesis-defective growth patterns -
 XX Example 2; Fig 5; 57pp; English.
 PS The invention describes a novel method of detecting compounds with
 PS polo-like kinase (PLK) modulating activity. This comprises contacting
 PS eukaryotic cells expressing polo-box or polo-box related peptides,
 PS binding peptides comprising 25 contiguous residues from a polo-like
 PS kinase C-terminal region, with a test compound. Ectopic expression of a
 PS polo box in a eukaryotic cell causes a severe cytotoxic defect in the
 PS cell. These eukaryotic cells can also be tested with the test compound
 PS used in the method of the invention. The polo-box related peptides and
 PS polo like kinase activity modulatory compounds can be used to inhibit or
 PS enhance cellular proliferation and subsequently for treating
 PS hyper-proliferative disorders including neoplasm, solid tumours,
 PS carcinomas, sarcomas and cancers e.g. small cell carcinoma,
 PS adenocarcinoma, Mullerian tumours and squamous cell carcinomas. This
 PS is the amino acid sequence of a mammalian polo-like kinase (Plk),
 PS uncontrolled expression of the Plk family is implicated in the
 PS development of human cancers, discussed in the method of the invention.
 XX SQ Sequence 531 AA;
 Query Match 87.8%; Score 43; DB 23; Length 531;
 Best Local Similarity 77.8%; Pred. No. 10;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LGRPPFETS 9
 Db 206 VGKPPFETS 214
 RESULT 16
 AAR74620
 ID AAR74620 standard; Protein; 603 AA.
 XX
 AC AAR74620;
 XX
 DT 25-MAR-2003 (updated);
 DT 26-OCT-1995 (first entry)
 XX
 DE Human lung tumour Polo-like kinase.
 XX
 KW Polo-like kinase; PLK; serine threonine kinase; human; lung tumour;
 KW autoimmune disease; lymphocyte activity.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Binding-site 60..86
 FT /label= ATP-binding_motif
 FT Region 174..177
 FT /note= "motif that is highly conserved in protein
 FT kinases"
 FT Region 194..196
 FT /note= "motif that is highly conserved in protein
 FT kinases"
 FT
 FT
 FT
 FT
 PN DE4329177-A1.
 XX
 PD 02-MAR-1995.
 XX
 PF 30-AUG-1993; 93DE-4329177.
 XX
 PR 30-AUG-1993; 93DE-4329177.
 XX
 PA (CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.
 XX
 XX Holtrich U, Rubsamens-Waigmann H, Strebhardt K;
 PI Ruebsamen-Waigmann H;
 XX
 DR WPI: 1995-099454/14.
 DR N-PSDB; AA088-55.
 XX
 PT A polo-like serine threonine kinase-protein - isolated from
 PT proliferating human tissue, useful in the determin of lymphocyte
 PT activity, eg in autoimmune diseases
 XX
 PS Claim 1; Page 8-10; lpp; German.
 XX
 CC A human lung tumour-derived cDNA (AA088155) was found to have high
 CC homology with sequences from members of the serine/threonine kinase
 CC family. Due to the strong homology with the Drosophila polo gene,
 CC the protein encoded by the new cDNA (AAR74620) was designated a polo-
 CC like kinase (PLK). PLK mRNA is expressed in proliferating cells such
 CC as placenta, colon and tumours of the lung, oesophagus, gut and
 CC intestine. Resting lymphocytes do not express the PLK gene but after
 CC stimulation with phytohaemagglutinin, PLK is expressed and can be
 CC used as an indicator of lymphocyte stimulation.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 603 AA;
 Query Match 87.8%; Score 43; DB 16; Length 603;
 Best Local Similarity 77.8%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LGRPPFETS 9

Db 246 VGKPPFETS 254

RESULT 17

AAU79306 standard; Peptide: 603 AA.

XX AC AAU79306;

XX 02-JUL-2002 (first entry)

XX Mouse polo-like kinase (Plk);

XX Polo box; PB1; cytostatic; fungicide; protozoicide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo like kinase; Plk.

XX OS Mus musculus.

XX PN US6358738-B1.

XX PD 19-MAR-2002.

XX PF 13-MAY-1999; 99US-0311311.

XX PR 13-MAY-1999; 98US-085296P.

XX PA (HARD : HARVARD COLLEGE.

XX PI Erikson RL, Lee KS;

XX DR WPI; 2002-314756/35.

XX Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections .
 PS Example 1; Column 59-64; 47pp; English.

CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of the polo-like kinase (Plk), a
 CC protein from which mitotic protein polo kinase inhibitory peptides are
 CC derived.

XX Sequence 603 AA;

Query Match 87.8%; Score 43; DB 21; Length 603;
 Best Local Similarity 77.8%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9

Db 246 VGKPPFETS 254

RESULT 18

AAU79308 standard; Peptide: 603 AA.

XX AC AAU79308;

XX 02-JUL-2002 (first entry)

XX Mouse polo-like kinase (Plk) T210D mutant .

XX Polo box; PB1; cytostatic; fungicide; protozoicide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutcin.

XX OS Mus musculus.

XX Synthetic.

XX Key Location/Qualifiers

XX FT Misc-difference 210 /note= "Wild type Thr substituted by Asp"

XX PN US6358738-B1.

XX PD 19-MAR-2002.

XX PF 13-MAY-1999; 99US-0311311.

XX PR 13-MAY-1998; 98US-085296P.

XX PA (HARD) HARVARD COLLEGE.

XX PI Erikson RL, Lee KS;

XX DR WPI; 2002-314756/35.

XX Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections .
 PS Example 1; Page : 47pp; English.

CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information
 CC given in the invention.

XX Sequence 603 AA;

Query Match 87.8%; Score 43; DB 23; Length 603;
 Best Local Similarity 77.8%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9

Db 246 VGKPPFETS 254

RESULT 19

AAU79309 standard; Peptide: 603 AA.

XX AC AAU79309;

XX 02-JUL-2002 (first entry)

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XX DE Mouse polo-like kinase (Pik) T210E mutant.
XX
XX Polo box; PBI; cytostatic; fungicide; protozoacide; antihelminthic;
XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX cancer of the uterus; ovarian cancer; cervical cancer;
XX epithelial cancer; brain cancer; retina cancer; prostate cancer;
XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;
XX Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX arthropod infection; mouse; polo-like kinase; Pik; mutant; mutain.
XX
XX Mus musculus.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc difference 210 /note= "Wild type Thr substituted by Glu"
XX
XX US6359738-B1.
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections
XX
XX Example 1; Page : 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Pik)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79310 using information
XX given in the invention.
XX
XX Query Match 87.8%; Score 43; DB 23; Length 603;
XX Best Local Similarity 77.8%; Pred. No. 12;
XX Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LGRPPFETS 9
XX :|||:
XX 246 VGRPPFETS 254
XX
XX RESULT 20
XX AAU79310
XX ID AAU79310 standard; Peptide; 603 AA.
XX
XX AC AAU79310;
XX
XX 02-JUL 2002 (first entry)
XX
XX Mouse polo-like kinase (Pik); T210V mutant.
XX

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XX Polo box; PBI; cytostatic; fungicide; protozoacide; antihelminthic;
XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX cancer of the uterus; ovarian cancer; cervical cancer;
XX epithelial cancer; brain cancer; retina cancer; prostate cancer;
XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;
XX Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX arthropod infection; mouse; polo-like kinase; Pik; mutant; mutain.
XX
XX Mus musculus.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc difference 210 /note= "Wild type Thr substituted by Val"
XX
XX US6358739-B1.
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections
XX
XX Example 1; Page : 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Pik)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
XX Query Match 87.8%; Score 43; DB 23; Length 603;
XX Best Local Similarity 77.8%; Pred. No. 12;
XX Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LGRPPFETS 9
XX :|||:
XX 246 VGRPPFETS 254
XX
XX RESULT 21
XX AAU79311
XX ID AAU79311 standard; Peptide; 603 AA.
XX
XX AC AAU79311;
XX
XX 02-JUL-2002 (first entry)
XX
XX Mouse polo-like kinase (Pik) E206V mutant.
XX
XX Polo box; PBI; cytostatic; fungicide; protozoacide; antihelminthic;

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KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
 OS Mus musculus.
 OS Synthetic.
 PH Key Location/Qualifiers
 FT Misc-difference 206 /note= "Wild type Glu substituted by Val"
 XX US6358738-B1.
 XX 19-MAR-2002.
 XX 13 MAY-1999; 99US-03113.1.
 XX 13-MAY-1999; 99US-085296P.
 XX (HARD) HARVARD COLLEGE.
 XX Erikson RL, Lee KS;
 XX WPI, 2002-314756/35.
 XX Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections
 XX Example 1; Page : 47pp; English.
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79312 using information
 CC given in the invention.
 XX Sequence 603 AA;
 SQ Query Match 87.8%; Score 43; DB 1; Length 603;
 Best Local Similarity 77.8%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LGKPPFFETS 9
 :|||:
 DB 246 VSKPPFFETS 254
 RESULT 22
 AAU79312
 ID AAU79312 standard; Peptide; 603 AA.
 XX AAU79312;
 AC AAU79312;
 XX 02-JUL-2002 (first entry)
 XX Mouse polo like kinase (Plk) E206N mutant
 XX Polo box; PBI; cytostatic; fungicide; protozoicide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;

KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
 OS Mus musculus.
 OS Synthetic.
 PH Key Location/Qualifiers
 FT Misc-difference 206 /note= "Wild type Glu substituted by Asn"
 XX US6358738-B1.
 XX 19-MAR-2002.
 XX 13-MAY-1999; 99US-03113.1.
 XX 13-MAY-1999; 98US-085296P.
 XX (HARD) HARVARD COLLEGE.
 XX Erikson RL, Lee KS;
 XX WPI, 2002-314756/35.
 XX Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections
 XX Example 1; Page : 47pp; English.
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information
 CC given in the invention.
 XX Sequence 603 AA;
 SQ Query Match 87.8%; Score 43; DB 23; Length 603;
 Best Local Similarity 77.8%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LGKPPFFETS 9
 :|||:
 DB 246 VSKPPFFETS 254
 RESULT 23
 AAU79313
 ID AAU79313 standard; Peptide; 603 AA.
 XX AAU79313;
 AC AAU79313;
 XX 02-JUL-2002 (first entry)
 XX Mouse polo-like kinase (Plk) E206V/T210V mutant.
 XX Polo box; PBI; cytostatic; fungicide; protozoicide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;

KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 206 /note= "Wild type Glu substituted by Val"
 FT Misc-difference 213 /note= "Wild type Thr substituted by Val"
 FT
 XX
 XX
 XX US6358738-B1.
 XX
 XX 19-MAR-2002.
 XX
 XX 13-MAY-1999; 99US-0311311.
 XX
 XX 13-MAY-1998; 98US-085296P.
 XX
 XX (HARD) HARVARD COLLEGE.
 XX
 XX Erikson RL, Lee KS;
 XX
 XX WPI; 2002-314756/35.
 XX
 XX Administering polo kinase inhibitors for the treatment of cancers and
 FT fungal infections
 PT
 PS
 XX
 XX Example 1; Page : 47pp; English.
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information
 CC given in the invention.
 XX
 XX Sequence 603 AA;
 SQ
 Query Match 97.8%; Score 43; DB 23; Length 603;
 Best Local Similarity 77.8%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LGRPPFETS 9
 Db 246 VGRPPFETS 254
 RESULT 24
 AAU79314
 ID AAU79314 standard; Peptide; 603 AA.
 XX
 AC AAU79314;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Mouse polo-like kinase (Plk) D-94N mutant.
 XX
 XX Polo box; Pbl; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;

KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 194 /note= "Wild type Asp substituted by Asn"
 FT
 XX
 XX US6358738-B1.
 XX
 XX 19-MAR-2002.
 XX
 XX 13-MAY-1999; 99US-0311311.
 XX
 XX 13-MAY-1998; 98US-085296P.
 XX
 XX (HARD) HARVARD COLLEGE.
 XX
 XX Erikson RL, Lee KS;
 XX
 XX WPI; 2002-314756/35.
 XX
 XX Administering polo kinase inhibitors for the treatment of cancers and
 FT fungal infections
 PT
 PS
 XX
 XX Example 1; Page : 47pp; English.
 CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information
 CC given in the invention.
 XX
 XX Sequence 603 AA;
 SQ
 Query Match 87.8%; Score 43; DB 23; Length 603;
 Best Local Similarity 77.8%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LGRPPFETS 9
 Db 246 VGRPPFETS 254
 RESULT 25
 AAU79315
 ID AAU79315 standard; Peptide; 603 AA.
 XX
 AC AAU79315;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Mouse polo-like kinase (Plk) D194R mutant.
 XX
 XX Polo box; Pbl; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;


```

KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
OS Mus musculus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 194 /note= "Wild type Asp substituted by Arg"
XX
XX US6358738-B1.
XX
XX 19 MAR-2002.
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARC ) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections
XX
XX Example 1; Page -; 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
XX Query Match 603 AA;
XX Best Local Similarity 87.8%; Score 43; DB 23; Length 603;
XX Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LGKPPFFETS 9
XX :|||:|
XX 246 VSKPPFFETS 254
XX
XX Db
XX
XX RESULT 26
XX AAU79316
XX ID AAU79316 standard; Peptide; 603 AA.
XX
XX AC AAU79316;
XX
XX 02-JUL-2002 (first entry)
XX
XX Mouse polo-like kinase (Plk) K28X mutant.
XX
XX Polo box; PBL; cytosolic; fungicide; protozoicide; antihelminthic;
XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX cancer of the uterus; ovarian cancer; cervical cancer;
XX epithelial cancer; brain cancer; retina cancer; prostate cancer;
XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;
XX Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX

```

```

OS Mus musculus.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 28 /note= "Wild type Lys substituted by Met"
XX
XX US6358738-B1.
XX
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARC ) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections
XX
XX Example 2; Page -; 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
XX Query Match 603 AA;
XX Best Local Similarity 87.8%; Score 43; DB 23; Length 603;
XX Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LGKPPFFETS 9
XX :|||:|
XX 246 VSKPPFFETS 254
XX
XX Db
XX
XX RESULT 27
XX AAU79317
XX ID AAU79317 standard; Peptide; 603 AA.
XX
XX AC AAU79317;
XX
XX 02-JUL-2002 (first entry)
XX
XX Mouse polo-like kinase (Plk) V415A mutant.
XX
XX Polo box; PBL; cytosolic; fungicide; protozoicide; antihelminthic;
XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX cancer of the uterus; ovarian cancer; cervical cancer;
XX epithelial cancer; brain cancer; retina cancer; prostate cancer;
XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;
XX Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX arthropod infection; mouse; polo-like kinase; Plk; mutant; mutein.
XX
XX Mus musculus.
XX Synthetic.
XX

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XX Key Location/Qualifiers
FH Misc-difference 415
FT /note= "Wild type Val substituted by Ala"
XX
XX US6358738-B1.
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections
XX
XX Example 7; Page -: 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU793106 using information
XX given in the invention.
XX
XX Sequence 603 AA;
XX
XX Query Match 87.8%; Score 43; DB 23; Length 603;
XX Best Local Similarity 77.8%; Pred. No. 12;
XX Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LGRPPPEETS 9
XX :|||:|
XX 246 VGRPPPEETS 254
XX
XX Db
XX
XX RESULT 28
XX AAU793106
XX ID AAU793106 standard; Peptide; 603 AA.
XX
XX AC AAU793106;
XX
XX DT 02-JUL-2002 (first entry);
XX
XX DE Mouse polo-like kinase (Plk) L427A mutant.
XX
XX KW Polo box; Pbl; cytosolic; fungicide; protozoacide; antihelminthic;
XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX cancer of the uterus; ovarian cancer; cervical cancer;
XX epithelial cancer; brain cancer; retina cancer; prostate cancer;
XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;
XX Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
XX
XX CS Mus musculus.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers

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FT Misc-difference 427
FT /note= "Wild type Lys substituted by Ala"
XX
XX US6358738-B1.
XX
XX 19-MAR-2002.
XX
XX 13-MAY-1999; 99US-0311311.
XX
XX 13-MAY-1998; 98US-085296P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Erikson RL, Lee KS;
XX
XX WPI; 2002-314756/35.
XX
XX Administering polo kinase inhibitors for the treatment of cancers and
XX fungal infections
XX
XX Example 7; Page -: 47pp; English.
XX
XX The invention describes a method of inhibiting growth of an isolated
XX population of cells by inhibiting a cell polo kinase by administering a
XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX carboxy terminal domain of the polo kinase which excludes the polo
XX kinase catalytic domain. The method is used for the treatment of cancer
XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX cervix, the epithelium, the brain, the retina, the prostate, and the
XX throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
XX mutant, used to determine the residues required for kinase activity.
XX Note: This sequence does not appear in the specification but has been
XX created from the wild type sequence shown in AAU79306 using information
XX given in the invention.
XX
XX Sequence 603 AA;
XX
XX Query Match 87.8%; Score 43; DB 23; Length 603;
XX Best Local Similarity 77.8%; Pred. No. 12;
XX Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LGRPPPEETS 9
XX :|||:|
XX 246 VGRPPPEETS 254
XX
XX Db
XX
XX RESULT 29
XX AAU79319
XX ID AAU79319 standard; Peptide; 603 AA.
XX
XX AC AAU79319;
XX
XX DT 02-JUL-2002 (first entry);
XX
XX DE Mouse polo-like kinase (Plk) N437; mutant.
XX
XX KW Polo box; Pbl; cytosolic; fungicide; protozoacide; antihelminthic;
XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX cancer of the uterus; ovarian cancer; cervical cancer;
XX epithelial cancer; brain cancer; retina cancer; prostate cancer;
XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;
XX Epidermophyton; Microsporium; protozoan infection; helminthes infection;
XX arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
XX
XX CS Mus musculus.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
FT Misc-difference 437
FT /note= "Wild type Asn substituted by Ile"

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XX PN US6358738-B1.
XX PD 19-MAR-2002.
XX PF 13-MAY-1999; 99US-0311311.
XX PR 13-MAY-1998; 98US-085296P.
XX PA (HARD ) HARVARD COLLEGE.
XX PI Erikson R., Lee KS.
XX DR WPI; 2002-314756/35.
XX PT Administering polo kinase inhibitors for the treatment of cancers and
XX PT fungal infections .
XX PS Example 7; Page -: 47pp; English.
XX CC The invention describes a method of inhibiting growth of an isolated
XX CC population of cells by inhibiting a cell polo kinase by administering a
XX CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX CC carboxy terminal domain of the polo kinase which excludes the polo
XX CC kinase catalytic domain. The method is used for the treatment of cancer
XX CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX CC cervix, the epithelium, the brain, the retina, the prostate, and the
XX CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX CC Epidermophyton, and Microsporum), protozoans, helminthes, and arthropods.
XX CC This is the amino acid sequence of a mouse polo-like kinase (pik)
XX CC mutant, used to determine the residues required for kinase activity.
XX CC Note: This sequence does not appear in the specification but has been
XX CC created from the wild type sequence shown in AAU79320 using information
XX CC given in the invention.
XX SQ Sequence 603 AA;

Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 1 LGKPPFFETS 9
DB 246 VGKPPFFETS 254
      |||||
      |||||

RESULT 30
AAU79320
ID AAU79320 standard; Peptide; 603 AA.
XX AC AAU79320;
XX DT 03-JUN-2002 (first entry)
XX DE Mouse polo-like kinase (pik) W414F/D114E mutant.
XX KW Polo box; PS; cytostatic; fungicide; proteolysis; antihelminthic;
XX KW arthropodicide; mitotic protein polo kinase polo kinase inhibitor;
XX KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
XX KW cancer of the uterus; ovarian cancer; cervical cancer;
XX KW epithelial cancer; brain cancer; retinal cancer; prostate cancer;
XX KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
XX KW Epidermophyton; Microsporum; Microsporium infection; helminthes infection;
XX KW arthropod infection; mouse; polo-like kinase; pik; mutant; muretin.
XX XA
XX OS Mus musculus.
XX OS Synthetic.
XX PH
XX FT Key Location/Qualifiers
XX FT Misc-difference 414 /note= "Wild type T1 substituted by P1e"
XX FT Misc-difference 210 /note= "Wild type T1 substituted by Asp"
XX FT

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XX PN US6358738-B1.
XX PD 19-MAR-2002.
XX PF 13-MAY-1999; 99US-0311311.
XX PR 13-MAY-1998; 98US-085296P.
XX PA (HARD ) HARVARD COLLEGE.
XX PI Erikson R., Lee KS.
XX DR WPI; 2002-314756/35.
XX PT Administering polo kinase inhibitors for the treatment of cancers and
XX PT fungal infections .
XX PS Example 10; Page -: 47pp; English.
XX CC The invention describes a method of inhibiting growth of an isolated
XX CC population of cells by inhibiting a cell polo kinase by administering a
XX CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
XX CC carboxy terminal domain of the polo kinase which excludes the polo
XX CC kinase catalytic domain. The method is used for the treatment of cancer
XX CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
XX CC cervix, the epithelium, the brain, the retina, the prostate, and the
XX CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
XX CC Epidermophyton, and Microsporum), protozoans, helminthes, and arthropods.
XX CC This is the amino acid sequence of a mouse polo-like kinase (pik)
XX CC mutant, used to determine the residues required for kinase activity.
XX CC Note: This sequence does not appear in the specification but has been
XX CC created from the wild type sequence shown in AAU79306 using information
XX CC given in the invention.
XX SQ Sequence 603 AA;

Query Match 87.8%; Score 43; DB 23; Length 603;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 1 LGKPPFFETS 9
DB 246 VGKPPFFETS 254
      |||||
      |||||

RESULT 31
ABR48196
ID ABR48196 standard; Protein; 603 AA.
XX AC ABR48196;
XX DT 12-JUN-2003 (first entry)
XX DE Human bladder cancer associated protein sequence SEQ ID NO:110.
XX KW Human; bladder cancer; cytostatic; gene therapy; vaccine.
XX OS Homo sapiens.
XX PN WO2003003906-A2.
XX PD 16-JAN-2003.
XX PF 03-JUL-2002; 2002WO-US21338.
XX PR 03-JUL-2001; 2001US-302814P.
XX PR 03-AUG-2001; 2001US-310099P.
XX PR 08-NOV-2001; 2001US-343705P.
XX PR 13-NOV-2002; 2001US-350666P.
XX PR 12-APR-2002; 2002US-372246P.
XX XA
XX OS (ECRB-) EOS BIOTECHNOLOGY INC.

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XX MacK DH, Aziz N;
 XX WP1: 2003-201532/19.
 DR N-PSDB; ACC51059.
 XX
 XX Detecting a bladder cancer-associated transcript in a cell from a
 PT patient, comprises contacting a biological sample from the patient with
 PT a bladder cancer-associated polynucleotide or antibody .
 XX
 XX Claim 10: Page 269; 307pp; English.
 XX
 XX The present invention describes a method for detecting a bladder cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with a polynucleotide
 CC that selectively hybridises to a sequence that is not identical to a
 CC table of sequences (see ACC50951 to ACC51059; ACC50951 to ACC51059
 CC encode the human bladder cancer-associated proteins given in ABR48146 to
 CC ABR48242). Bladder cancer-associated sequences from the present invention
 CC have cytostatic activities, and can be used in an antisense gene therapy and
 CC in vaccine production. The method can be used for detecting a bladder
 CC cancer-associated transcript in a cell from a patient. The method is
 CC useful in diagnosing or treating bladder cancer and in screening for
 CC compounds that modulate bladder cancer, such as hormones or antibodies.
 CC The nucleic acid molecules from the present invention may be used in
 CC various screening and diagnostic methods, and for gene therapy, vaccine
 CC and/or antisense/inhibition applications.
 XX
 XX Sequence 603 AA:
 XX
 XX Query Match 87.8%; Score 41; DB 24; Length 603;
 XX Best Local Similarity 77.8%; Pred. No. 12;
 XX Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 LGRRPPFET 9
 XX :|||||
 XX Db 246 VGRPPFET 254
 XX
 XX RESULT 32
 XX ABB63067
 XX ID ABB63067 standard; Protein; 769 AA.
 XX AC ABB63067;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide AB010 N91599.
 XX KW Drosophila developmental biology; cell signalling; insecticides;
 XX pharmacokinetics;
 XX OS Drosophila melanogaster.
 XX PN WC200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US09231.
 XX PP 23-MAR-2002; 2000US-191637P.
 XX PR 11-JUL-2000; 2000US-0614150.
 XX PX (PEKE) PE CORP NY.
 XX
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX WP1: 2001 556860/75.
 DR N-PSDB; ABL07170.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

XX Disclosure; SEQ ID NO 15993; 21pp + Sequence Listing; English.
 XX
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72372).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 769 AA;
 XX
 XX Query Match 95.7%; Score 42; DB 22; Length 769;
 XX Best Local Similarity 87.5%; Pred. No. 23;
 XX Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 LGRRPPFET 8
 XX :|||||
 XX Db 208 VGRPPFET 215
 XX
 XX RESULT 33
 XX AAW74159
 XX ID AAW74159 standard; peptide; 9 AA.
 XX AC AAW74159;
 XX DT 05-MAY-1999 (first entry)
 XX DE HJ loop peptide J-42.
 XX KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.
 XX OS Synthetic.
 XX PH Key Location/Qualifiers
 XX Modified-site ;
 XX Modified-site 9 /note= "acetylated"
 XX Modified-site 9 /note= "amidated"
 XX Modified-site 9 /note= "benzyl ester of Glu"
 XX
 XX PN WO9653050-A2.
 XX PD 26-NOV-1998.
 XX PF 20-MAY-1998; 98WO-US10319.
 XX PR 21-MAY-1997; 97US-0861338.
 XX
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX (YISS) YISSUM RES & DEV CO.
 XX
 XX Ben-Sasson SA;
 XX WP1: 1999-070142/06.
 XX
 XX New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders
 XX
 XX Claim 14; Fig 4; 76pp; English.
 XX

CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity of
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.

XX Sequence 9 AA;

Query Match 81.6%; Score 40; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFE 7
 |||||
 Db 3 LGRPPFE 9

RESULT 34

AAU98315
 ID AAU98315 standard; Peptide; 9 AA;

XX AC AAU98315;

DT 13-AUG-2002 (first entry)

XX Polio kinase serine-threonine kinase HJ loop peptide J-42.

XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 KW anti-inflammatory; immunosuppressive; cardiac; haemostatic;
 KW modulating STK activity; polo kinase; J 42.

XX Unidentified.
 CS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 4 /note= "N-terminal entry"

FT Modified-site 4 /note= "Benzyl ester at Glutamate 4"

FT Modified-site 4 /note= "C-terminal amide"

XX US2002049301-A1.

XX 25-APR-2002.

XX 13-DEC-2000; 2000US-0736076.

XX 21-MAY-1997; 97US-0861338.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Ben Sasson SA;

XX WPI; 2002-462787/49.

XX New peptide from the HJ loop of serine threonine kinase, useful for
 PT treating e.g. cancer and for producing diagnostic antibodies.

PS Disclosure; Fig 4; 41pp; English.

XX The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase
 CC serine-threonine kinase HJ loop peptide J-42. This sequence is one of
 CC the short peptides of the invention that selectively modulate the
 CC activity of STK.

XX Sequence 9 AA;

Query Match 81.6%; Score 40; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFE 7
 |||||
 Db 3 LGRPPFE 9

RESULT 35

AAW74213
 ID AAW74213 standard; peptide; 10 AA;

XX AC AAW74213;

DT 05-MAY-1999 (first entry);

XX HJ loop peptide K038H101.

XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "myristylated"

FT Modified-site 10 /note= "amidated"

XX WC9853050-A2.

XX 26-NOV-1998.

XX 20-MAY-1998; 98WO-US10319.

XX 21-MAY-1997; 97US-0861338.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX (YISS) YISSUM RES & DEV CO.

XX Ben Sasson SA;

XX WPI; 1999-070142/06.

XX New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders

XX Disclosure; Fig 6; 70pp; English.

XX This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be

CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.

XX
 XX
 SQ Sequence 10 AA;
 Query Match 81.6%; Score 40; DB 20; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.73; Indels 0; Gaps 0;
 Matches 7; Conservative C; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFE 7
 |||||
 DB 4 LGRPPFE 10

RESULT 36
 AAJ99357
 ID AAC98357 standard; Peptide; 10 AA.
 AC AAU98357;
 XX
 XX 13-AUG-2002 (first entry)
 DE Polio kinase SNX serine-threonine kinase HJ loop peptide K038H101.
 XX
 KW HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW Central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 KW antiinflammatory; immunosuppressive; cardiac; haerostatic;
 KW modulating STK activity; polo kinase; SNX; K038H101.
 XX
 OS Unidentified.
 OS Synthetic.

XX
 XX
 FH Key Location/Qualifiers
 FT Modified site 1 /note: "N-terminal 'pyrolysis'"
 FT Modified site 10 /note: "Benzyl Ester of Glutamic Acid, C-terminal amide"
 FT
 XX US200204931-A1.
 XX
 XX 25-APR-2002.
 XX
 IF 13 DEC-2000; 2000US-0736076.
 XX
 XX 21-MAY-1997; 97US-0861338.
 XX
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 P1 Ben: Sasson SA;
 XX
 XX WPI; 2002-462787/49.
 XX
 XX New peptide from the HJ loop of serine threonine kinase, useful for
 PT treating e.g. cancer and for producing diagnostic antibodies
 PT
 XX Disclosure; Fig 6; 41pp; English.
 PS
 XX The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are

CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase SNK
 CC serine-threonine kinase HJ loop peptide K038H101. This sequence is one
 CC of the short peptides of the invention that selectively modulate the
 XX activity of STK.

XX
 SQ Sequence 10 AA;
 Query Match 81.6%; Score 40; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.73;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFE 7
 |||||
 DB 4 LGRPPFE 10

RESULT 37
 AAR92176
 ID AAR92176 standard; Protein; 416 AA.
 XX
 AC AAR92176;
 XX
 XX 25-MAY-1996 (first entry)
 XX Sak serine-threonine kinase N-terminus.
 DE
 XX Sak; serine-threonine kinase; STK; agonist; antagonist;
 KW proliferative disease; cancer; tumour; antisense; transgenic animal;
 KW therapy.
 XX
 OS Mus musculus.
 XX
 XX CA2150789-A.
 XX
 PD 03-DEC-1995.
 XX
 PF 01-JUN-1995; 95CA-2150789.
 XX
 PR 02-JUN-1994; 94US-0252995.
 XX
 PA (MOUN) MOUNT SINAI HOSPITAL CORP.
 XX
 PI Dennis JW, Fode C, Heffernan M;
 XX
 XX WPI; 1996-123817/14.
 DR N-PSDB; AAT08710.
 XX
 XX Nucleic acid encoding Sak serine-threonine kinase - useful for
 PT identifying modulators potentially useful in treatment or prevention
 PT of proliferative disease.
 XX
 PS Claim 3; Page 46-48; 73pp; English.
 XX
 XX 2 Isoforms, sak-a and sak-b, of a novel serine/threonine kinase
 CC have an identical N-terminal sequence (AAR92176) that contains the
 CC kinase domain and that shows significant homology to the polo
 CC subfamily. The C-terminal sequences (each contg. 3 PEST regions)
 CC of the 2 isoforms differ (see AAR92177 and AAR92214). Sak-a and Sak-b
 CC are associated with mitotic and meiotic cell division, and may be
 CC involved in cell proliferation. They can be obtd. in recombinant
 CC form by expression of encoding sequences (see AAR08710-12) and used
 CC to test for inhibitory or stimulatory cpds. that may be useful
 CC in the treatment/diagnosis of proliferative disorders, such as
 CC cancer and viral (esp. HIV) infection.

XX
 SQ Sequence 416 AA;

```

Db          206 IGRPFDT 213

RESULT 39
AAR92177
ID AAR92177 standard; Protein; 925 AA.
XX AC AAR92177;
XX DT 25-MAY-1996 (first entry)
XX XX
XX DE SAK-a serine-threonine kinase.
XX XX
XX KW SAK-a; serine-threonine kinase; STK; agonist; antagonist;
XX KW proliferative disease; cancer; tumour; antisense; transgenic animal;
XX KW therapy.
XX OS Mus musculus.
XX XX
XX FH Location/Qualifiers
XX Domain 1..416
FT /label= N-terminal domain
FT /note= "contains the kinase domain"
FT 417..925
FT Domain
FT /label= C-terminal domain
FT /note= "contains 3 PEST regions"
XX XX
XX CA2150783-A.
XX XX
XX O3-DEC-1995.
XX XX
XX O1-JUN-1995; 95CA-2150789.
XX XX
XX O2-JUN-1994; 94US-0252995.
XX XX
XX (MOUN ) MOUNT SINAI HOSPITAL CORP.
XX XX
XX Dennis JW, Fode C, Heffernan M;
XX WP1; 1996-129817/:4.
XX DR N-PSDB; AAT08711.
XX XX
XX Nucleic acid encoding Sak serine-threonine kinase - useful for
XX PT identifying modulators potentially useful in treatment or prevention
XX PT of proliferative disease.
XX XX
XX Claim 5; Page 50-55; 73pp; English.
XX XX
XX 2 Isoforms, SAK-a (AAR92177; and SAK-b (AAR92214), of a novel
XX serine/threonine kinase are associated with mitotic and meiotic cell
XX division and are characterized by having a kinase domain at the
XX N-terminus and 3 PEST sequences (rich in Pro, Ser, Thr, Asp, Glu) at
XX the C-terminus. The N-terminal regions of the 2 isoforms are
XX identical (see AAR92176). SAK-a and SAK-b can be obd. in recombinant
XX form by expression of encoding sequences (see AAT08711-12), and used
XX to test for inhibitory or stimulatory cpds. useful in the
XX treatment/diagnosis of proliferative disorders such as cancer and
XX and viral (esp. HIV) infection, or used to raise antibodies.
XX XX
XX Sequence 925 AA;

Query Match 81.6%; Score 40; DB 17; Length 925;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps

QY 1 LGRPPFDT 8
Db          206 IGRPFDT 213

RESULT 40
ABB57273

```

ID AB857273 standard; Protein: 925 AA.
 XX
 AC AB857273;
 XX
 DT 07 MAR-2002 (first entry);
 XX
 DE Mouse ischaemic condition related Protein sequence SEQ ID NO:766.
 XX
 KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
 XX
 GS Mus musculus.
 XX
 EC K020C188186-A2.
 XX
 PD 22 NOV-2001.
 XX
 PF 18 MAY-2001; 2001WG-JP04192.
 XX
 PR 18 MAY-2000; 2000JP-0145977.
 XX
 PA (UNYI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 XX
 PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX
 DR WP1; 2002-034733/04.
 DR N-PSDS; AB199713.
 XX
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or
 PT by determining the expression profile of a gene group comprising these
 PT genes -
 XX
 PS Claim 2; Page 1893-1897; 2490pp; English.
 XX
 CC The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (1) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (1). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (AB199713 to AB199717, encoding
 CC the protein sequences in AB57020 to AP457394) or by determining the
 CC expression profile of a gene group comprising these genes. The
 CC expression levels or expression profiles produced by these genes are
 CC used as an indicator when screening for ischaemic condition improving
 CC drugs or therapeutics for ischaemic diseases. AB199713 and AB199714
 CC represent PCR primers for a mouse ischaemic condition related sequence,
 CC which are used in the exemplification of the present invention.
 XX
 SQ Sequence 325 AA;
 Query Match 81.6%; Score 4.18; E-Val 1.0e-04;
 Best Local Similarity 75.0%; Ident 13/14;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 LGPPPET 8
 : : : : :
 Eb 206 LGPPPET 213

Search completed: November 14, 2003, 13:45:01
 Job time : 34.7143 secs

GenCore version 5.1.6
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OX protein - protein search, using sw model

Run on: November 14, 2003, 13:23:00, Search time 11.8286 Seconds
(without alignments)
32.193 Million cell updates/sec

Title: US-09-736-076-18

Perfect score: 49

Sequence: 1 LGRPPFETS 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 329717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 329717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:

- 1: /cgn2_6/ptodata/1/aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/aa/ECTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/aa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	3	US-08-861-338-18
2	49	100.0	11	3	US-08-861-338-18
3	46	93.9	272	1	US-09-252-995D-12
4	46	93.9	272	2	US-08-834-108-6
5	46	93.9	685	2	US-08-834-108-6
6	46	93.9	685	3	US-09-252-995D-12
7	46	93.9	685	3	US-09-252-995D-12
8	46	93.9	685	3	US-09-252-995D-12
9	43	87.8	20	3	US-08-861-338-6
10	43	87.8	272	1	US-08-252-995D-14
11	43	87.8	272	2	US-08-834-108-14
12	43	87.8	603	3	US-09-198-122-2
13	43	87.8	603	4	US-09-311-110-16
14	40	81.6	9	3	US-08-861-338-15
15	40	81.6	273	2	US-08-252-995D-10
16	40	81.6	416	1	US-08-252-995D-10
17	40	81.6	416	2	US-08-834-108-2
18	40	81.6	464	1	US-08-252-995D-6
19	40	81.6	464	2	US-08-834-108-6
20	40	81.6	925	2	US-08-252-995D-4
21	40	81.6	925	2	US-08-834-108-4
22	40	81.6	271	1	US-08-252-995D-11
23	38	77.6	271	2	US-08-834-108-11
24	38	77.6	271	2	US-08-861-338-17
25	37	75.5	9	3	US-08-861-338-17
26	36	73.5	220	1	US-08-252-995D-2
27	36	73.5	220	1	US-08-463-472-2

28	36	73.5	607	2	US-08-878-989-15	Sequence 15, Appl
29	36	73.5	607	3	US-09-272-796-15	Sequence 15, Appl
30	35	71.4	182	4	US-09-134-001C-3742	Sequence 3742, Ap
31	35	71.4	403	2	US-08-755-728-4	Sequence 4, Appl1
32	35	71.4	403	2	US-08-974-655-4	Sequence 4, Appl1
33	35	71.4	403	3	US-09-283-011-4	Sequence 4, Appl1
34	34	69.4	226	4	US-09-134-001C-5260	Sequence 5260, Ap
35	34	69.4	254	4	US-09-252-991A-24255	Sequence 24255, A
36	34	69.4	344	2	US-08-755-728-3	Sequence 3, Appl1
37	34	69.4	344	2	US-08-974-655-3	Sequence 3, Appl1
38	34	69.4	344	3	US-09-283-011-3	Sequence 1, Appl1
39	34	69.4	347	2	US-09-016-000-1	Sequence 1, Appl1
40	34	69.4	1019	4	US-09-252-991A-24417	Sequence 244.7, A
41	34	69.4	1312	4	US-09-345-882-29	Sequence 29, Appl
42	33	67.3	243	4	US-09-107-532A-4655	Sequence 4655, Ap
43	33	67.3	354	1	US-09-569-806-6	Sequence 6, Appl1
44	33	67.3	327	1	US-08-420-235B-35	Sequence 35, Appl
45	33	67.3	327	3	US-08-793-624-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1

US-08-861-338-18
Sequence 18 Application US/08861338
Patent No. 6:74993
GENERAL INFORMATION:
APPLICANT: Ben-Sasson, Shmuel A.
TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/861,338
FILING DATE: 21-MAY-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brock, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CMCC-590
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "N-Acetyl Leucine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: /note= "Glutamic Acid Benzyl Ester"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9

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; OTHER INFORMATION: /note= "Serine-NH2"
US-08-861-338-18
Query Match: 100.0%; Score 49; DB 3; Length 9;
Best Local Similarity: 100.0%; Pred. No. 2.5e+05;
Matches: 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
DB 1 LGRPPFETS 9

RESULT 2
US-08-861-338-18
; Sequence 19, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861-338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CWC 590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURES:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Glutamic Acid Benzyl Ester"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Serine-NH2"
US-08-861-338-19
Query Match: 100.0%; Score 49; DB 3; Length 11;
Best Local Similarity: 100.0%; Pred. No. 0.0931;
Matches: 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
DB 3 LGRPPFETS 11

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RESULT 3
US-08-252-995D-12
; Sequence 12, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurgydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-252-995D-12
Query Match: 93.9%; Score 46; DB 1; Length 272;
Best Local Similarity: 88.9%; Pred. No. 0.34;
Matches: 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
DB 201 LGRPPFETS 209

RESULT 4
US-08-834-108-12
; Sequence 12, Application US/08834108
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,106
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3:53-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (4:6) 364-7311
; TELEFAX: (4:6) 361-1398
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; US-08-834-108-12

Query Match 93.9%; Score 46; DB 2; Length 272;
Best Local Similarity 88.9%; Pred. No. 0.34;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : LGRPPFETS 9
      |||||
Db 201 LGRPPFETT 209

RESULT 5
US-08-878-989-1
; Sequence 1, Application US/08878999
; Patent No. 5885903
; GENERAL INFORMATION:
; APPLICANT: Bandman, O-ga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surva K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Forter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/878,999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ballings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HJVENCB01
; CLONE: 39043
; US-08-878-989-1

Query Match 93.9%; Score 46; DB 2; Length 685;
Best Local Similarity 88.9%; Pred. No. 0.89;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
      |||||
Db 275 LGRPPFETT 283

RESULT 6
US-09-136-282-2
; Sequence 2, Application US/09136282
; Patent No. 6063609
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, KAREN
; APPLICANT: JACKSON, JEFFREY
; APPLICANT: HANSBURY, MICHAEL
; APPLICANT: NERURKAR, SANDHYA
; APPLICANT: ROSHAK, AMY
; APPLICANT: BOJZYK, MARK
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,282
; FILING DATE: 20-AUG-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/056,112
; FILING DATE: 20-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-136-282-2

Query Match 93.9%; Score 46; DB 3; Length 685;

```

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Best Local Similarity 88.9%; Pred. No. C.89;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
Db 275 LGRPPFFET 283

US-09-272-796-1
; Sequence 1, Application US/09272796
; Patent No. 6245544
; GENERAL INFORMATION:
; APPLICANT: Bardman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tocyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF 032; US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4566
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 685 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVENB01
; CLONE: 39043
US-09-272-796-1

Query Match: 93.9%; Score 46; DB 1; Length 685;
Best Local Similarity 88.9%; Pred. No. C.89;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
Db 275 LGRPPFFET 283

US-09-505-744-2
; Sequence 2, Application US/09505744
; Patent No. 6245544
; GENERAL INFORMATION:
; APPLICANT: Karen M. Anderson
; APPLICANT: Mark M. Bouzyk
; APPLICANT: Michael J. Hansbury
; APPLICANT: Jeffrey R. Jackson
; APPLICANT: Sandhya S. Nerurkar
; APPLICANT: Amy K. Roshak
; TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (SNK)
; FILE REFERENCE: GH-70231-D1
; CURRENT APPLICATION NUMBER: US/09/505,744
; CURRENT FILING DATE: 2003-02-16
; EARLIER APPLICATION NUMBER: 09/136,282
; EARLIER FILING DATE: 1998-08-20
; EARLIER APPLICATION NUMBER: 60/056,112
; EARLIER FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 685
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-505-744-2

Query Match: 93.9%; Score 46; DB 3; Length 685;
Best Local Similarity 88.9%; Pred. No. C.89;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
Db 275 LGRPPFFET 283

US-08-861-338-6
; Sequence 6, Application US/08861338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,338
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-861-338-6
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Query Match 87.8%; Score 43; DB 3; Length 20;
 Best Local Similarity 77.8%; Pred. No. 0.033; Indels 0;
 Matches 7; Conservative 2; Mismatches 0; Gaps 0;

QY 1 LGRPFFETS 9
 : : : : :
 DB 5 VGKPPFFETS 13

RESULT 1:
 US-08-252-995D-14
 ; Sequence 14, Application US/08252995D
 ; Patent No. 5653501
 ; GENERAL INFORMATION:
 ; APPLICANT: Dennis, James W
 ; APPLICANT: Heffernan, Mike
 ; APPLICANT: Fode, Carol
 ; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BERESKIN & PARR
 ; STREET: 40 King Street West
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5H 3Y2
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/252-995D
 ; FILING DATE: 02-JUN-1994
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kurdydyk, Linda M
 ; REGISTRATION NUMBER: 34,971
 ; REFERENCE/DOCKET NUMBER: 3153-96
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 364-7311
 ; TELEFAX: (416) 364-1398
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 272 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; ORIGINAL SOURCE:
 ; ORGANISM: Mus musculus
 ; US-08-252-995D-14

Query Match 87.8%; Score 43; DB 3; Length 272;
 Best Local Similarity 77.8%; Pred. No. 1.2;
 Matches 7; Conservative 2; Mismatches 0; Indels 0;

QY 1 LGRPFFETS 9
 : : : : :
 DB 20: VGKPPFFETS 209

RESULT 1:
 US-08-834-108-14
 ; Sequence 14, Application US/08834108
 ; Patent No. 5976893
 ; GENERAL INFORMATION:
 ; APPLICANT: Dennis, James W
 ; APPLICANT: Heffernan, Mike
 ; APPLICANT: Fode, Carol
 ; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 ; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BERESKIN & PARR
 ; STREET: 40 King Street West
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5H 3Y2
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/834,108
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kurdydyk, Linda M
 ; REGISTRATION NUMBER: 34,971
 ; REFERENCE/DOCKET NUMBER: 3153-210
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 364-7311
 ; TELEFAX: (416) 361-1398
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 272 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; ORIGINAL SOURCE:
 ; ORGANISM: Mus musculus
 ; US-08-834-108-14

Query Match 87.8%; Score 43; DB 2; Length 272;
 Best Local Similarity 77.8%; Pred. No. 1.2;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPFFETS 9
 : : : : :
 DB 201 VGKPPFFETS 209

RESULT 12
 US-09-198-122-2
 ; Sequence 2, Application US/09198122
 ; Patent No. 6180380
 ; GENERAL INFORMATION:
 ; APPLICANT: Strebhardt, Klaus; Rubsamen-Waigmann, Helga;
 ; APPLICANT: Holtrich, Uwe
 ; TITLE OF INVENTION: CLONING OF A MEMBER OF THE SERINE-
 ; TITLE OF INVENTION: THREONINE-KINASE FAMILY
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SPRUNG HORN KRAMER & WOODS
 ; STREET: 660 White Plains Road
 ; CITY: Tarrytown
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10591-5144
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
 ; MEDIUM TYPE: storage
 ; COMPUTER: NEC Powermate SX-20
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/198,122
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/601,014
 ; FILING DATE: 23-FEB-1996

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1 APPLICATION NUMBER: PCT/EP94/02863
2 FILING DATE: 30-AUG-1994
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: DE 4329177
5 FILING DATE: 30-AUG-1993
6 ATTORNEY/AGENT INFORMATION:
7 NAME: Kurt G. Briscoe
8 REGISTRATION NUMBER: 33,141
9 REFERENCE/DOCKET NUMBER: Payer 9514 KGB
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (914) 332-1700
12 TELEFAX: (914) 332-1844
13 TELEX:
14 INFORMATION FOR SEQ ID NO: 2:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 603 amino acids
17 TYPE: amino acid
18 TOPOLOGY: linear
19 MOLECULE TYPE: Protein
20 US-09 198 122-2

Query Match 87.8%; Score 43; DB 3; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPFFTS 9
DB 246 VGRPPFTS 254

RESULT 13
US-09-311-311C 26
1 Sequence 26, Application US/0901131C
2 Patent No. 6399736
3 GENERAL INFORMATION:
4 APPLICANT: Erikson, et al.
5 TITLE OF INVENTION: POLO BOX THERAPEUTIC COMPOSITIONS,
6 FILE REFERENCE: 1874/117
7 CURRENT APPLICATION NUMBER: US/09/311,311C
8 PRIOR FILING DATE: 1999-05-13
9 PRIOR FILING DATE: 1998-05-13
10 NUMBER OF SEQ ID NOS: 27
11 SOFTWARE: FastSeq for Windows Version 4.0
12 SEQ ID NO 26
13 LENGTH: 603
14 TYPE: PPT
15 ORGANISM: Mus musculus
16 FEATURE:
17 NAME/KEY: DOMAIN
18 LOCATION: 11...1663
19 OTHER INFORMATION: Plk protein
20 US-09-311-311C 26

Query Match 87.8%; Score 43; DB 4; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPFFTS 9
DB 246 VGRPPFTS 254

RESULT 14
US-08-861-338-15
1 Sequence 15, Application US/080861338
2 Patent No. 6174993
3 GENERAL INFORMATION:
4 APPLICANT: Ben-Sasson, Shmuel A.
5 TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
6 MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
7 NUMBER OF SEQUENCES: 22

```

```

1 CORRESPONDENCE ADDRESS:
2 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
3 STREET: Two Militia Drive
4 CITY: Lexington
5 STATE: Massachusetts
6 COUNTRY: USA
7 ZIP: 02173
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC compatible
11 OPERATING SYSTEM: PC DOS/MS-DOS
12 SOFTWARE: Patent In Release #1.0, Version #1.30
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/861,338
15 FILING DATE: 21-MAY-1997
16 CLASSIFICATION: 514
17 ATTORNEY/AGENT INFORMATION:
18 NAME: Brook, David E.
19 REGISTRATION NUMBER: 22,592
20 REFERENCE/DOCKET NUMBER: CMCC-590
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: (781) 861-6240
23 TELEFAX: (781) 861-9540
24 INFORMATION FOR SEQ ID NO: 15:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 9 amino acids
27 TYPE: amino acid
28 STRANDEDNESS: not relevant
29 TOPOLOGY: not relevant
30 MOLECULE TYPE: peptide
31 FEATURE:
32 NAME/KEY: Modified-site
33 LOCATION: 1
34 OTHER INFORMATION: /note= "N-Acetyl Methionine"
35 FEATURE:
36 NAME/KEY: Modified site
37 LOCATION: 9
38 OTHER INFORMATION: /note= "Gamma Benzyl Ester of
39 OTHER INFORMATION: Glutamic Acid-NH2"
40 US-08-861-338-15

Query Match 81.6%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPFPE 7
DB 3 LGRPFPE 9

RESULT 15
US-08-252-995D-10
1 Sequence 10, Application US/08252995D
2 Patent No. 5650501
3 GENERAL INFORMATION:
4 APPLICANT: Dennis, James W
5 APPLICANT: Heffernan, Mike
6 APPLICANT: Fode, Carol
7 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
8 NUMBER OF SEQUENCES: 14
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: BERESKIN & PARR
11 STREET: 40 King Street West
12 CITY: Toronto
13 STATE: Ontario
14 COUNTRY: Canada
15 ZIP: M5H 3Y2
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Patent In Release #1.0, Version #1.30
21 CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/08/252-995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34, 971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-252-995D-10

Query Match 81.6%; Score 40; DB 1; Length 273;
Best Local Similarity 75.0%; Pred. No. 4.6;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFET 8
DB 202 IGRPPFDT 209

RESULT 16
US-08-834-108-10
Sequence 10, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834-108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34, 971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-834-108-10

Query Match 81.6%; Score 40; DB 2; Length 273;
Best Local Similarity 75.0%; Pred. No. 4.6;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFET 8
DB 202 IGRPPFDT 209

RESULT 17
US-08-252-995D-2
Sequence 2, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252-995D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34, 971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-252-995D-2

Query Match 81.6%; Score 40; DB 1; Length 416;
Best Local Similarity 75.0%; Pred. No. 7.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFET 8
DB 206 IGRPPFDT 213

RESULT 18
US-08-834-108-2
Sequence 2, Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West

CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/834,108
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-08-834-108-2

Query Match 81.6%; Score 40; DB 2; Length 416;
Best Local Similarity 75.0%; Pred. No. 7.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFT 8
DB 206 IGRPPFT 213

RESULT 19
US-08-252-9950-6
Sequence 6, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 02-JUN-1994
APPLICATION NUMBER: US/08/252,995D
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-252-995D-6

Query Match 81.6%; Score 40; DB 1; Length 464;
Best Local Similarity 75.0%; Pred. No. 7.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFT 8
DB 206 IGRPPFT 213

RESULT 20
US-08-834-108-6
Sequence 6, Application US/08834108
Patent No. 5976933
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-834-108-6

Query Match 81.6%; Score 40; DB 2; Length 464;
Best Local Similarity 75.0%; Pred. No. 7.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFT 8
DB 206 IGRPPFT 213

RESULT 21
US-08-252-995D-4
Sequence 4, Application US/08252995D
Patent No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE


```

; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 925 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US 08-252-995D-4

Query Match 81.6%; Score 40; DB 1; Length 925;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGPPPET 8
DB 206 IGRPPFDT 213

RESULT 22
US-08-834-108-4
; Sequence 11, Application US/08834108
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,108
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELEPHONE: (416) 364-7311

```

```

; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 925 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-834-108-4

Query Match 81.6%; Score 40; DB 2; Length 925;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGPPPET 8
DB 206 IGRPPFDT 213

RESULT 23
US-08-252-995D-11
; Sequence 11, Application US/08252995D
; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
; US-08-252-995D-11

Query Match 77.6%; Score 38; DB 1; Length 271;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGPPPET 8
DB 200 VGGPPFET 237

RESULT 24
US-08-834-108-11

```

Sequence 11, Application US/C8834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent'n Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/C8/834,108
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydk, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLGY: linear
ORIGINAL SOURCE:
ORGANISM: *Esosiphila melanogaster*
US-08 634-108-11

Query Match 77.6% Score 140 DB 20 Length 271
Best Local Similarity 75.0% Pred. No. 107
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGPPPE 8
DB 200 VGGPPPE 207

RESULT 25
US-08-861-118-17
Sequence 17, Application US/06861316
Patent No. 6174993
GENERAL INFORMATION:
APPLICANT: Ben Sasson, Shmuel A
TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent'n Release #1.0, Version #1.05
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/C8/861,338
FILING DATE: 21-MAY-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CMCC-590
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "N-Acetyl Methionine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: /note= "Gamma Benzyl Ester of
Glutamine Acid-NH2"
US-08-861-338-17

Query Match 75.5% Score 37; DB 3; Length 9;
Best Local Similarity 85.7% Pred. No. 2.5e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPPE 7
DB 3 LGKEPPE 9

RESULT 26
US-08-233-146-2
Sequence 2, Application US/08233146
Patent No. 5648256
GENERAL INFORMATION:
APPLICANT: BEPPU, TERUHIKO
APPLICANT: YAMADA, HIDEAKI
APPLICANT: NAGASAWA, TORU
APPLICANT: HORINOUCHI, SUEHARU
APPLICANT: NISHIYAMA, MAKOTO
TITLE OF INVENTION: A GENE ENCODING A POLYPEPTIDE HAVING
N-TRIPLE HYDRATASE ACTIVITY, A TRANSFORMANT CONTAINING THE
TITLE OF INVENTION: GENE AND A PROCESS FOR THE PRODUCTION OF AVIDES USING THE
TITLE OF INVENTION: TRANSFORMANT
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: N.Y.
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent'n Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,146
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/694,746
FILING DATE: 02-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE

REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-024-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 969-9741
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Pseudomonas chlororaphis
STRAIN: B23 (FERM BP 187)
US-08-233-146-2

Query Match 73.5%; Score 36; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPPE 7
Db 120 GRPPE 125

RESULT 27
US-08-463-470-2
Sequence 2, Application US/08463470
Patent No. 5789211
GENERAL INFORMATION:
APPLICANT: BEPPU, TERUHIKO
APPLICANT: YAMADA, HIDEAKI
APPLICANT: NAGASAWA, TORU
APPLICANT: HORINOUCHI, SUEHARU
APPLICANT: NISHIYAMA, MAKOTO
TITLE OF INVENTION: A GENE ENCODING A POLYPEPTIDE HAVING
TITLE OF INVENTION: NITRILE HYDROLASE ACTIVITY, A TRANSFORMANT CONTAINING THE
TITLE OF INVENTION: GENE AND A PROCESS FOR THE PRODUCTION OF AMIDES USING THE
TITLE OF INVENTION: TRANSFORMANT
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & ECKMOS
STREET: 1155 AVENUE OF THE AMERICANS
CITY: NEW YORK
STATE: N.Y.
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,470
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,146
FILING DATE: 22-APR-1994
APPLICATION NUMBER: US 07/694,746
FILING DATE: 02-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7005-024-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 969-9741
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Pseudomonas chlororaphis
STRAIN: B23 (FERM BP-187)
US-08-463-470-2

Query Match 73.5%; Score 36; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPPE 7
Db 120 GRPPE 125

RESULT 28
US-08-878-989-15
Sequence 15, Application US/08878989
Patent No. 5885803
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Survi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-945-4166
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 607 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1827450
US-08-878-989-15

Query Match 73.5%; Score 36; DB 2; Length 607;
Best Local Similarity 75.0%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSPFFETS 9
| | | | |
Db 217 GSPFFETA 224

RESULT 29

US-09-272-796-15
; Sequence 15, Application US/09272796
; Patent No. 6207149

GENERAL INFORMATION:

; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,949
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-032; US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:

INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 607 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 1827450

; US-09-272-796-15

Query Match 73.5%; Score 36; DB 3; Length 607;

Best Local Similarity 75.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSPFFETS 9

| | | | |

Db 217 GSPFFETA 224

RESULT 30

US-09-134-001C-3742
; Sequence 3742, Application US/09134001C
; Patent No. 6380370

GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-037
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3742
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3742

Query Match

71.4%; Score 35; DB 4; Length 182;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPF 6

| | | | |

Db 177 LGRPPF 182

RESULT 31

US-08-755-728-4
; Sequence 4, Application US/08755728
; Patent No. 5962312
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,728
; FILING DATE: No. 5962312;ember 25, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 499-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-974-655-4

Query Match 71.4%; Score 35; DB 2; Length 403;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LGRPPFETS 9

Db 324 VGKPPFEAN 332

RESULT 32
US-08-974 655-4
Sequence 4, Application US/08974655
Patent No. 5972676
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Mossie, Kevin
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR 1
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,655
FILING DATE: August 14, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/755,728
FILING DATE: January 22, 1998
APPLICATION NUMBER: 08/755,728
FILING DATE: No. 6207401ember 25, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
APPLICATION NUMBER: 60/021,543
FILING DATE: August 14, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-974-655-4

Query Match 71.4%; Score 35; DB 2; Length 403;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LGRPPFETS 9

Db 324 VGKPPFEAN 332

RESULT 33
US-09-283-011-4
Sequence 4, Application US/09283011
Patent No. 6207401
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Mossie, Kevin
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/283,011
FILING DATE: August 14, 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/012,135
FILING DATE: January 22, 1998
APPLICATION NUMBER: 08/755,728
FILING DATE: No. 6207401ember 25, 1996
APPLICATION NUMBER: 60/021,943
FILING DATE: August 14, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 231/282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-283-011-4

Query Match 71.4%; Score 35; DB 3; Length 403;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LGRPPFETS 9

Db 324 VGKPPFEAN 332

RESULT 34
US-09-134-001C-5260
Sequence 5260, Application US/09134001C
Patent No. 6380370

```

; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5260
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5260

Query Match      69.4%; Score 34; DB 4; Length 226;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGPPPET 8
   |||||
DQ 54 LGNPPPAT 61

RESULT 35
US-09-252-991A-24255
; Sequence 24255; Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 137196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/374,799
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/294,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24255
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24255

Query Match      69.4%; Score 34; DB 4; Length 254;
Best Local Similarity 85.7%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGPPPE 7
   |||||
DQ 34 LGPPPE 40

RESULT 36
US-08-755-728-3
; Sequence 3; Application US/08755728
; Patent No. 5962312
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,729
; FILING DATE: No. 5962312member 25, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/008,939
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-755-728-3

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Query Match      69.4%; Score 34; DB 2; Length 344;
Best Local Similarity 55.6%; Pred. No. 77;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 1 LGPPPFETS 9
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DQ 268 VGNPPFESA 276

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RESULT 37
US-08-974-655-3
; Sequence 3; Application US/08974655
; Patent No. 5972676
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: D:AGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,655
; FILING DATE:

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1 CLASSIFICATION: 435
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: 08/755,728
4 FILING DATE: No. 5972676eember 25, 1996
5 APPLICATION NUMBER: 60/008,809
6 FILING DATE: December 18, 1995
7 APPLICATION NUMBER: 60/023,943
8 FILING DATE: August 14, 1996
9 ATTORNEY/AGENT INFORMATION:
10 NAME: Warburg, Richard C.
11 REGISTRATION NUMBER: 32,127
12 REFERENCE/DOCKET NUMBER: 23/113
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE: (213) 489-1600
15 TELEFAX: (213) 955-0440
16 TELEX: 67-3510
17 INFORMATION FOR SEQ ID NO: 3:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 344 amino acids
20 TYPE: amino acid
21 STRANDEDNESS: single
22 TOPOLOGY: linear
23 MOLECULE TYPE: protein
24 HYPOTHETICAL: NO
25 ANTI-SENSE: NO
26 US 08-974 655-3
27
28 Query Match 69.4%; Score 34; DB 2; Length 344;
29 Best Local Similarity 55.6%; Pred. No. 77;
30 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
31
32 QY 1 LGPPPPETS 9
33 DB 268 VGNPPFESA 276
34
35 RESULT 38
36 US 08-283 011-3
37 Sequence 3, Application US/09253011
38 Patent No. 6207401
39 GENERAL INFORMATION:
40 APPLICANT: Plowman, Gregory
41 APPLICANT: Nossie, Kevin
42 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF ADP
43 TITLE OF INVENTION: AND/OR ADP-2 RELATED DISORDERS
44 NUMBER OF SEQUENCES: 39
45 CORRESPONDENCE ADDRESS:
46 ADDRESSEE: LYON & LYON
47 STREET: 631 West Fifth Street
48 CITY: Los Angeles
49 STATE: California
50 COUNTRY: U.S.A.
51 ZIP: 90071-2066
52 COMPUTER READABLE FORM:
53 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
54 MEDIUM TYPE: Storage
55 COMPUTER: IBM Compatible
56 OPERATING SYSTEM: IBM P.C. DOS 5.0
57 SOFTWARE: FastSeq for Windows 2.0
58 CURRENT APPLICATION DATA:
59 APPLICATION NUMBER: US/09/283,011
60 FILING DATE:
61 CLASSIFICATION:
62 PRIOR APPLICATION DATA:
63 APPLICATION NUMBER: 09/012,135
64 FILING DATE: January 22, 1998
65 APPLICATION NUMBER: 08/755,728
66 FILING DATE: No. 6207401eember 25, 1996
67 APPLICATION NUMBER: 60/023,943
68 FILING DATE: August 14, 1996
69 APPLICATION NUMBER: 60/008,809
70 FILING DATE: December 18, 1996

```

```

1 ATTORNEY/AGENT INFORMATION:
2 NAME: Warburg, Richard C.
3 REGISTRATION NUMBER: 32,127
4 REFERENCE/DOCKET NUMBER: 23/282
5 TELECOMMUNICATION INFORMATION:
6 TELEPHONE: (213) 489-1600
7 TELEFAX: (213) 955-0440
8 TELEX: 67-3510
9 INFORMATION FOR SEQ ID NO: 3:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 344 amino acids
12 TYPE: amino acid
13 STRANDEDNESS: single
14 TOPOLOGY: linear
15 MOLECULE TYPE: protein
16 HYPOTHETICAL: NO
17 ANTI-SENSE: NO
18 US-09-283-011-3
19
20 Query Match 69.4%; Score 34; DB 3; Length 344;
21 Best Local Similarity 55.6%; Pred. No. 77;
22 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
23
24 QY 1 LGPPPPETS 9
25 DB 268 VGNPPFESA 276
26
27 RESULT 39
28 US-09-016-000-1
29 Sequence 1, Application US/090:6000
30 Patent No. 5962232
31 GENERAL INFORMATION:
32 APPLICANT: Hillman, Jennifer L.
33 APPLICANT: Lal, Preeti
34 APPLICANT: Bardman, Olga
35 APPLICANT: Akerblom, Ingrid E.
36 APPLICANT: Shah, Purvi
37 APPLICANT: Corley, Neil C.
38 APPLICANT: Guegler, Karl G.
39 TITLE OF INVENTION: PROTEIN KINASE MOLECULES
40 NUMBER OF SEQUENCES: 12
41 CORRESPONDENCE ADDRESS:
42 ADDRESSEE: Incyte Pharmaceuticals, Inc.
43 STREET: 3174 Porter Drive
44 CITY: Palo Alto
45 STATE: CA
46 COUNTRY: USA
47 ZIP: 94304
48 COMPUTER READABLE FORM:
49 MEDIUM TYPE: Diskette
50 COMPUTER: IBM Compatible
51 OPERATING SYSTEM: DOS
52 SOFTWARE: FastSeq for Windows Version 2.0
53 CURRENT APPLICATION DATA:
54 APPLICATION NUMBER: US/09/016,000
55 FILING DATE: HEREWITH
56 CLASSIFICATION:
57 PRIOR APPLICATION DATA:
58 APPLICATION NUMBER:
59 FILING DATE:
60 ATTORNEY/AGENT INFORMATION:
61 NAME: Billings, Lucy J.
62 REGISTRATION NUMBER: 36,749
63 REFERENCE/DOCKET NUMBER: PF-0465 US
64 TELECOMMUNICATION INFORMATION:
65 TELEPHONE: 650-855-0555
66 TELEFAX: 650-845-4166
67 TELEX:
68 INFORMATION FOR SEQ ID NO: 1:
69 SEQUENCE CHARACTERISTICS:
70 LENGTH: 347 amino acids
71 TYPE: amino acid

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STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: HMC:NOTC1
 CLONE: 294C
 US-09-016-000-1

Query Match: 69.4%; Score 147 DB 2; Length 147;
 Best Local Similarity 55.6%; Pred. No. 77;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY : LGRPPFETS 9
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 DB 271 VGNPPESA 279

RESULT 40
 US-09-252-991A-24417
 : Sequence 24417, Application US/09252991A
 : Patent No. 6551795
 : GENERAL INFORMATION:
 : APPLICANT: Marc J. Rubenfield et al.
 : TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 : FILE REFERENCE: 207196.136
 : CURRENT APPLICATION NUMBER: US/09/252,991A
 : CURRENT FILING DATE: 1999-02-18
 : PRIOR APPLICATION NUMBER: US 60/074,788
 : PRIOR FILING DATE: 1998-02-19
 : PRIOR APPLICATION NUMBER: US 60/094,199
 : PRIOR FILING DATE: 1998-07-27
 : NUMBER OF SEQ ID NOS: 33:42
 : SEQ ID NO 24417
 : LENGTH: 1019
 : TYPE: PR
 : ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-24417

Query Match: 69.4%; Score 147 DB 4; Length 1019;
 Best Local Similarity 62.5%; Pred. No. 2,4e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 2 GPPPFETS 9
 : |||||
 DB 417 GKPPFEA 424

Search completed: November 14, 2003, 13:59:52
 Job time: 11.6286 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: November 14, 2003, 13:28:05 : Search time 22.3714 Seconds
(without alignment)
/3.443 Million cell updates/sec

Title: US-09-736-076 15

Perfect score: 49

Sequence: 1 LGRPPFETS 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 566188

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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3: /cgn2_6/ptodata/1/pubpaa/US66_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US66_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*

Pred. No. is the number of results returned by search to have a score greater than or equal to the score of the hit being printed, and is derived by analysis of the index with the distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	9	US-09-736-076-18
2	49	100.0	11	9	US-09-736-076-19
3	46	93.9	400	15	US-10-026-021-5
4	46	93.9	469	15	US-10-059-585-14
5	46	93.9	685	10	US-09-771-161A-243
6	46	93.9	685	10	US-09-771-161A-250
7	46	93.9	685	10	US-09-771-161A-251
8	46	93.9	685	12	US-10-024-298A-111
9	46	93.9	685	12	US-09-769-970-1
10	46	93.9	685	12	US-10-042-211A-101
11	43	87.8	20	9	US-09-736-076-6
12	43	87.8	329	10	US-09-925-300-1268
13	43	87.8	367	15	US-10-026-021-6
14	43	87.8	516	15	US-09-771-161A-123
15	43	87.8	603	10	US-09-771-161A-214

16	43	87.8	603	15	US-10-171-311-186	Sequence 186, App
17	40	81.6	9	9	US-09-736-076-15	Sequence 15, Appl
18	40	81.6	10	9	US-09-736-076-57	Sequence 57, Appl
19	40	81.6	379	15	US-10-026-021-3	Sequence 3, Appl
20	40	81.6	970	15	US-10-026-021-2	Sequence 2, Appl
21	37	75.5	9	9	US-09-736-076-17	Sequence 17, Appl
22	36	73.5	373	15	US-10-026-021-4	Sequence 4, Appl
23	36	73.5	505	15	US-10-156-761-14310	Sequence 14310, A
24	36	73.5	607	12	US-09-769-970-15	Sequence 15, Appl
25	36	73.5	607	12	US-10-204-041-16	Sequence 16, Appl
26	36	73.5	607	15	US-10-108-580-2	Sequence 2, Appl
27	36	73.5	899	12	US-10-318-906A-48	Sequence 48, Appl
28	36	73.5	899	12	US-10-319-216A-48	Sequence 48, Appl
29	36	73.5	210	9	US-09-922-217-692	Sequence 692, App
30	36	73.5	210	10	US-09-833-263-692	Sequence 692, App
31	36	73.5	210	14	US-10-025-380-692	Sequence 692, App
32	36	73.5	1548	9	US-09-922-217-1095	Sequence 1095, Ap
33	36	73.5	1548	14	US-10-025-380-1095	Sequence 1095, Ap
34	36	73.5	1551	12	US-10-318-906A-46	Sequence 46, Appl
35	36	73.5	1551	12	US-10-319-216A-46	Sequence 46, Appl
36	35	71.4	403	9	US-09-012-135A-4	Sequence 4, Appl
37	35	71.4	403	15	US-10-026-021-7	Sequence 7, Appl
38	35	71.4	403	15	US-10-059-585-33	Sequence 33, Appl
39	35	71.4	403	15	US-10-209-324-2	Sequence 2, Appl
40	35	71.4	633	11	US-09-934-455-186	Sequence 186, App
41	34	69.4	200	12	US-09-882-227-124	Sequence 124, App
42	34	69.4	309	15	US-10-128-714-3051	Sequence 3051, Ap
43	34	69.4	326	10	US-09-925-300-1605	Sequence 1605, Ap
44	34	69.4	344	9	US-09-012-135A-3	Sequence 3, Appl
45	34	69.4	344	15	US-10-059-585-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-736-076-18
; Sequence 18, Application US/09736076
; Patent No. US2002004931A
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015.009
; CURRENT APPLICATION NUMBER: US/09/736,076
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(9)
; OTHER INFORMATION: position 7 is benzyloester
; NAME/KEY: AMIDATION
; LOCATION: (10)...(19)
; OTHER INFORMATION: J45
US-09-736-076-18

Query Match 100.0%, Score 49; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.9e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9

Db 1 LGRPPFETS 9

RESULT 2

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US-09-736-076-19
; Sequence 19, Application US/09736076
; Patent No. US2002049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736.076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(6)
; OTHER INFORMATION: position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: (3)...(11)
; OTHER INFORMATION: J46
US-09-736-076-19

Query Match 100.0%; Score 49; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
DB 3 LGRPPFFETS 11

RESULT 3
US-10-026-021-5
; Sequence 5, Application US/10026021
; Publication No. US20030027758A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasunichi
; APPLICANT: Demo, Susan
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; FILE REFERENCE: 021044-00121003
; CURRENT APPLICATION NUMBER: US/10/026.021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 62/303,430
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(400)
; OTHER INFORMATION: human SNK mitotic kinase kinase domain
US-10-026-021-5

Query Match 93.9%; Score 46; DB 15; Length 400;
Best Local Similarity 88.9%; Pred. No. 2.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
DB 275 LGRPPFFET 283

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RESULT 4
US-10-059-585-14
; Sequence 14, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Toroyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Furubashi, Shin-Ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-Ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: US/10/059.585
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-585-14

Query Match 93.9%; Score 46; DB 15; Length 469;
Best Local Similarity 88.9%; Pred. No. 3.4;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
DB 59 LGRPPFFET 67

RESULT 5
US-09-771-161A-249
; Sequence 249, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 249
; LENGTH: 685

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-249

Query Match          93.9%; Score 46; DB 10; Length 685;
Best Local Similarity 88.9%; Pred. No. 4.9;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPFETS 9
      |||||:
Db      275 LGRPPFT 283

RESULT 6
US-09-771-161A-250
; Sequence 250, Application US/09771161A
; Publication No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 250
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-250

Query Match          93.9%; Score 46; DB 10; Length 685;
Best Local Similarity 88.9%; Pred. No. 4.9;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPFETS 9
      |||||:
Db      275 LGRPPFT 283

RESULT 7
US-09-771-161A-251
; Sequence 251, Application US/09771161A
; Publication No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 251
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-251

Query Match          93.9%; Score 46; DB 10; Length 685;
Best Local Similarity 88.9%; Pred. No. 4.9;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPFETS 9
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Db      275 LGRPPFT 283

RESULT 8
US-10-024-298A-101
; Sequence 101, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAMI KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0-91P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2003-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 101
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-101

Query Match          93.9%; Score 46; DB 12; Length 685;
Best Local Similarity 88.9%; Pred. No. 4.9;
Matches      8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPPFETS 9
      |||||:
Db      275 LGRPPFT 283

RESULT 9
US-09-769-970-1
; Sequence 1, Application US/09769970
; Publication No. US2003070219A
; GENERAL INFORMATION:
; APPLICANT: Bandman, Oiga
; Hillman, Jennifer L.
; Corley, Neil C.
; Guegler, Karl G.
; Lai, Preeti
; Gai, Surya K.
; Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
```

```
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-Seq for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/769,970
  FILING DATE: 24-Jan-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/272,796
  FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
  NAME: Billings, Lucy J.
  REGISTRATION NUMBER: 36,744
  REFERENCE/SOCKET NUMBER: PP-0321 US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 415-853-0555
  TELEFAX: 415-845-4166
  TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 685 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  IMMEDIATE SOURCE:
    LIBRARY: HUVENB01
    CLONE: 39C43
  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US 09 769 970-1

Query Match      93.9%  Score 46; DB 12; Length 685;
Best Local Similarity 88.9%  Pred. No. 4.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPFFETS 9
      |||||
DB      275 LGRPFFET 283

RESULT 10
US-10-042-211A-101
; Sequence 101, Application US/1004221A
; Publication No. US2003070719A
; GENERAL INFORMATION:
; APPLICANT: MACSUDA, ARIO et al.
; TITLE OF INVENTION: NFKB ACTIVATION GENE
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US 1004221A
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402,890
; PRIOR FILING DATE: 2002-12-28
; PRIOR APPLICATION NUMBER: JP 2001-288071
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254014
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,395
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-101

Query Match      93.9%  Score 46; DB 12; Length 685;
Best Local Similarity 88.9%  Pred. No. 4.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-Seq for Windows Version 2.0
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/769,970
  FILING DATE: 24-Jan-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/272,796
  FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
  NAME: Billings, Lucy J.
  REGISTRATION NUMBER: 36,744
  REFERENCE/SOCKET NUMBER: PP-0321 US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 415-853-0555
  TELEFAX: 415-845-4166
  TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 685 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  IMMEDIATE SOURCE:
    LIBRARY: HUVENB01
    CLONE: 39C43
  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US 09 769 970-1

Query Match      93.9%  Score 46; DB 12; Length 685;
Best Local Similarity 88.9%  Pred. No. 4.9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPFFETS 9
      |||||
DB      275 LGRPFFET 283

RESULT 11
US-09-736-076-6
; Sequence 6, Application US/C9736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Samuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242 1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/961,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PPT
; ORGANISM: Unknown
; FEATURES:
; OTHER INFORMATION: POLO
US-09-736-076-6

Query Match      87.8%  Score 43; DB 9; Length 20;
Best Local Similarity 77.8%  Pred. No. 0.54;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LGRPFFETS 9
      |||||
DB      5 VGRPPFFETS 13

RESULT 12
US-09-925-300-1268
; Sequence 1268, Application US/C9925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Roper,
; APPLICANT: Steve Roper,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/C5988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1268
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (59)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (307)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (308)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (314)
```

```

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (317)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (323)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (327)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (328)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (329)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-925-300-1268

```

```

Query Match      87.8%; Score 43; DB 10; Length 329;
Best Local Similarity 77.8%; Pred. No. 8.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LGRPPFETS 9
Db 262 VGKPPFETS 270

```

```

RESULT 13
US-10-026-021-6
; Sequence 6, Application US/10026021
; Publication No. US20030027756A;
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi;
; APPLICANT: Demo, Susan
; APPLICANT: Cenkins, Yonchu
; APPLICANT: Rige Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026-021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (17...367)
; OTHER INFORMATION: human PLK1 mitotic kinase kinase domain
; US-10-026-021-6

```

```

Query Match      87.8%; Score 43; DB 15; Length 367;
Best Local Similarity 77.8%; Pred. No. 9.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LGRPPFETS 9
Db 246 VGKPPFETS 254

```

```

RESULT 14
US-09-771-161A-123
; Sequence 123, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A

```

```

; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 123
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-771-161A-123

```

```

Query Match      87.8%; Score 43; DB 10; Length 516;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LGRPPFETS 9
Db 159 VGKPPFETS 167

```

```

RESULT 15
US-09-771-161A-214
; Sequence 214, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 214
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-771-161A-214

```

```

Query Match      87.8%; Score 43; DB 10; Length 603;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 LGRPPFETS 9
Db 246 VGKPPFETS 254

```

```

RESULT 16
US-10-171-311-186
; Sequence 186, Application US/0171311
; Publication No. US2003087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, Cohn
; APPLICANT: Kamatkar, Shubhargi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER

```

FILE REFERENCE: MRI-035
 ; CURRENT APPLICATION NUMBER: US/10/171,311
 ; PRIOR FILING DATE: 2002-06-12
 ; PRIOR APPLICATION NUMBER: US 60/298,159
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/298,155
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/335,916
 ; PRIOR FILING DATE: 2001-11-14
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 196
 ; LENGTH: 603
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-171-311-196

Query Match 87.8% Score 43; DB 15; Length 603;
 Best Local Similarity 77.8%; Pred. No. 15;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LGRPPEFS 9
 |||||
 Db 246 VGRPEFS 254

RESULT 17

US-09-736-076-15
 ; Sequence 15, Application US/59736076
 ; Patent No. US2002004931A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ben-Sasson, Shmuel A.
 ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 ; FILE REFERENCE: 1242.1015-009
 ; CURRENT APPLICATION NUMBER: US/09/736-076
 ; CURRENT FILING DATE: 2000-12-13
 ; PRIOR APPLICATION NUMBER: US 08/861,436
 ; PRIOR FILING DATE: 1997-05-21
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 15
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: ACTIVATION
 ; LOCATION: (1)...(10)
 ; OTHER INFORMATION: position 1 is Ser 736076
 ; NAME/KEY: ACTIVATION
 ; LOCATION: (1)...(19)
 ; OTHER INFORMATION: J42
 ; US-09-736-076-15

Query Match 81.6% Score 40; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 599-027

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LGRPPE 7
 |||||
 Db 3 LGRPPE 9

RESULT 18

US-09-736-076-57
 ; Sequence 57, Application US/59736076
 ; Patent No. US2002004931A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ben-Sasson, Shmuel A.
 ; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
 ; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
 ; FILE REFERENCE: 1242.1015-009
 ; CURRENT APPLICATION NUMBER: US/09/736-076

; CURRENT FILING DATE: 2000-12-13
 ; PRIOR APPLICATION NUMBER: US 08/861,338
 ; PRIOR FILING DATE: 1997-05-21
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 57
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: MYRISTATE
 ; LOCATION: (1)...(10)
 ; OTHER INFORMATION: position 10 is benzylester
 ; NAME/KEY: ACTIVATION
 ; LOCATION: (1)...(10)
 ; OTHER INFORMATION: SNK
 ; US-09-736-076-57

Query Match 81.6% Score 40; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.93;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LGRPPE 7
 |||||
 Db 4 LGRPPE 10

RESULT 19

US-10-026-021-3
 ; Sequence 3, Application US/10026021
 ; Publication No. US2003027756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hitoshi, Yasumichi
 ; APPLICANT: Demo, Susan
 ; APPLICANT: Rigel Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
 ; TITLE OF INVENTION: Treatment of Cancer
 ; FILE REFERENCE: 021044-00121005
 ; CURRENT APPLICATION NUMBER: US/10/026,021
 ; CURRENT FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/309,632
 ; PRIOR FILING DATE: 2001-08-01
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 379
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: DOYAIN
 ; LOCATION: (1)...(379)
 ; OTHER INFORMATION: SAK serine/threonine kinase kinase domain
 ; US-10-026-021-3

Query Match 81.6% Score 40; DB 15; Length 379;
 Best Local Similarity 75.0%; Pred. No. 32;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 1 LGRPPE 8
 |||||
 Db 206 LGRPPE 213

RESULT 20

US-10-026-021-2
 ; Sequence 2, Application US/10026021
 ; Publication No. US2003027756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hitoshi, Yasumichi
 ; APPLICANT: Demo, Susan
 ; APPLICANT: Rigel Pharmaceuticals, Inc.

```

; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 97C
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(373)
; OTHER INFORMATION: human SAK serine/threonine kinase
US-10-026-021-2

```

```

Query Match      81.6%   Score 40; DB 15; Length 970;
Best Local Similarity 75.0%   Pred. No. 78;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

Cq 1 LGPPPEF 8
Db 206 IGRPPPEF 213

```

```

RESULT 21
US-09-736-076-17
; Sequence 17, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)..(9)
; OTHER INFORMATION: position 9 is benzyl ester
; NAME/KEY: AMIDATION
; LOCATION: (0)..(9)
; OTHER INFORMATION: J43.1
US-09-736-076-17

```

```

Query Match      75.5%   Score 37; DB 9; Length 9;
Best Local Similarity 85.7%   Pred. No. 5;9e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Cq 1 LGPPPEF 7
Db 3 LGKPPPE 9

```

```

RESULT 22
US-10-026-021-4
; Sequence 4, Application US/10026021
; Publication No. US20030027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Demo, Susan
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for

```

```

; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(373)
; OTHER INFORMATION: human FNK mitotic kinase domain
US-10-026-021-4

```

```

Query Match      73.5%   Score 36; DB 15; Length 373;
Best Local Similarity 75.0%   Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Cq 2 GRPPFFETS 9
Db 256 GSPFFETA 263

```

```

RESULT 23
US-10-156-761-14310
; Sequence 14310, Application US/10156761
; Publication No. US2003019018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14310
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14310

```

```

Query Match      73.5%   Score 36; DB 15; Length 505;
Best Local Similarity 100.0%   Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Cq 2 GRPPFFE 7
Db 305 GRPPFFE 310

```

```

RESULT 24
US-09-769-970-15
; Sequence 15, Application US/09769970
; Publication No. US20030170219A1
; GENERAL INFORMATION:
; APPLICANT: Bandmar, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti

```

Geli, Surya K.
Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA: US/09/769,970
APPLICATION NUMBER: US/09/769,970
FILING DATE: 24-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/272,796
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy C.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 607 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1827450
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-769-970-15

Query Match 73.5%; Score 36; DB 12; Length 607;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPPEETS 9
DB 217 GSPPFETA 224

RESULT 25
US-10-204-041-16
Sequence 16, Application US/10204041
Publication No. US20030176443A;
GENERAL INFORMATION:
APPLICANT: STEIN-GERSLACH, MATTHIAS
APPLICANT: SALASIDIS, KONSTANTINOS
APPLICANT: BACHER, GERALD
APPLICANT: MULLER, STEFAN
TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Prid
FILE REFERENCE: AXM-007.1P US
CURRENT APPLICATION NUMBER: US/10/204,041
CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: EP 01111854.5
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: PCT/EP02/05420
PRIOR FILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patent in version 3.1

SEQ ID NO 16
LENGTH: 607
TYPE: PRT
ORGANISM: Homo sapiens
US-10-204-041-16

Query Match 73.5%; Score 36; DB 12; Length 607;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPPEETS 9
DB 217 GSPPFETA 224

RESULT 26
US-10-108-580-2
Sequence 2, Application US/10108580
Publication No. US2003007768A1
GENERAL INFORMATION:
APPLICANT: Cogswell, John
TITLE OF INVENTION: PLK3 PROTEIN-PROTEIN INTERACTIONS
FILE REFERENCE: PU4458
CURRENT APPLICATION NUMBER: US/10/108,580
CURRENT FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patent in version 3.1
SEQ ID NO 2
LENGTH: 607
TYPE: PRT
ORGANISM: homo sapiens
US-10-108-580-2

Query Match 73.5%; Score 36; DB 15; Length 607;
Best Local Similarity 75.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPPEETS 9
DB 217 GSPPFETA 224

RESULT 27
US-10-318-906A-48
Sequence 48, Application US/10318906A
Publication No. US20030157678A1
GENERAL INFORMATION:
APPLICANT: Lambeth, J. David
APPLICANT: Griendling, Kathy
APPLICANT: Lassegue, Bernard
APPLICANT: Arnold, Rebecca S.
APPLICANT: Cheng, Guangjie
TITLE OF INVENTION: Mitogenic Oxygenases
FILE REFERENCE: 05501-0221
CURRENT APPLICATION NUMBER: US/10/318,906A
CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: US 09/437,568
PRIOR FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 48
LENGTH: 899
TYPE: PRT
ORGANISM: Homo sapiens
US-10-318-906A-48

Query Match 73.5%; Score 36; DB 12; Length 899;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPPE 7
DB 842 GRPPE 847


```

RESULT 28
US-10-319-236A-48
; Sequence 48, Application US/10319236A
; Patent No. US20030166798A1
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griending, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: Antibodies to Mitogenic Oxygenases
; FILE REFERENCE: 05501-0220 (43:50-28:75)
; CURRENT APPLICATION NUMBER: US/10319-236A
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 09/437,568
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 899
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-319-236A-48

Query Match: 73.5%; Score 36; DB 12; Length 899;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPFFE 7
DB 842 GRPFFE 847

RESULT 29
US-09-922-217-692
; Sequence 692, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Yeager, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922-217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 692
; LENGTH: 1210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-217-692

Query Match: 73.5%; Score 36; DB 3; Length 1210;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPFFE 7
DB 1153 GRPFFE 1156

RESULT 30
US-09-833-263-692
; Sequence 692, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 692
; LENGTH: 1210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-263-692

Query Match: 73.5%; Score 36; DB 10; Length 1210;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPFFE 7
DB 1153 GRPFFE 1158

RESULT 31
US-10-025-380-692
; Sequence 692, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 692
; LENGTH: 1210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-025-380-692

Query Match: 73.5%; Score 36; DB 14; Length 1210;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPFFE 7
DB 1153 GRPFFE 1156

```

US-10-025-380-1095

Query Match 73.5% Score 36; DB 14; Length 1548;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPPE 7
DB 1491 GRPPE 1496

RESULT 34

US-10-318-906A-46
; Sequence 46, Application US/10318906A
; Publication No. US20030157678A1
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griendling, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: Mitogenic Oxygenases
; FILE REFERENCE: 05501-0221
; CURRENT APPLICATION NUMBER: US/10/318,906A
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 09/437,568
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-906A-46

Query Match 73.5% Score 36; DB 12; Length 1551;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPPE 7
DB 1494 GRPPE 1499

RESULT 35

US-10-319-236A-46
; Sequence 46, Application US/10319236A
; Publication No. US20030166198A1
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griendling, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: Antibodies to Mitogenic Oxygenases
; FILE REFERENCE: 05501-0220 (43150-281176)
; CURRENT APPLICATION NUMBER: US/10/319,236A
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 09/437,568
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 46
; LENGTH: 1551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-319-236A-46

Query Match 73.5% Score 36; DB 12; Length 1551;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPPE 7

RESULT 32

US-09-922-217-1095
; Sequence 1095, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Weagter, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Liang, Yugu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1295
; LENGTH: 1348
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-217-1095

Query Match 73.5% Score 36; DB 3; Length 1548;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPPE 7
DB 1491 GRPPE 1496

RESULT 33

US-10-025-380-1095
; Sequence 1095, Application US/10025380
; Publication No. US20030182191A1
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Weagter, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Liang, Yugu
; APPLICANT: Smith, Carole E.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Farger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1095
; LENGTH: 1548
; TYPE: PRT
; ORGANISM: Homo sapiens

```

Db          1494 GRPPE 1499
|||||
US-09-012-135A-4
; Sequence 4, Application US/09012135A
; Patent No. US20020081576A1
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossaie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AIR-1
; TITLE OF INVENTION: AND/OR AIR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE:
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,135A
; FILING DATE: January 22, 1998
; CLASSIFICATION: 435
; PRICE APPLICATION DATA:
; APPLICATION NUMBER: 09/035,269
; FILING DATE: January 9, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. US20020081576A1-Enter 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/038,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 677951C
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-09-012-135A-4
Query Match 71.4%; Score 35; DB 15; Length 403;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy          1 LGRPFETS 9
|||
Db          324 VGRPFPEAN 332

RESULT 37
US-10-026-021-7
; Sequence 7, Application US/10026021
; Publication No. US2003027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Demo, Susan
; APPLICANT: Jenkins, Yonchu
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human ARK mitotic kinase
US-10-026-021-7
Query Match 71.4%; Score 35; DB 15; Length 403;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy          1 LGRPFETS 9
|||
Db          324 VGRPFPEAN 332

RESULT 38
US-10-059-585-33
; Sequence 33, Application US/10059585
; Publication No. US20030082776A1
; GENERAL INFORMATION:
; APPLICANT: Ota, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Sugiyama, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Keiichi
; APPLICANT: Otsuki, Tetsuji
; APPLICANT: Funahashi, Shin-ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06501-098001
; CURRENT APPLICATION NUMBER: PCT/JP00/05060
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/05060
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-06-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens

```

US-10-059 595-33

Query Match 71.4%; Score 35; DB 15; Length 403;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
DB 324 VGRPPFEAN 332

RESULT 39

US-10-209-324-2
Sequence 2, Application US/10209324
Publication No. US200301089:0A1
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF CALIFORNIA SAN FRANCISCO
APPLICANT: TOLAND, Amanda E.
APPLICANT: BALMAIN, Allan
TITLE OF INVENTION: STK15 (STK6) GENE POLYMORPHISM AND METHODS OF DETERMINING CANCER
FILE REFERENCE: UCSF1120-2
CURRENT APPLICATION NUMBER: US/10/209,324
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/334,146
PRIOR FILING DATE: 2002-11-28
PRIOR APPLICATION NUMBER: US 60/308,911
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: NISC FEATURE
LOCATION: (31)-(31)
OTHER INFORMATION: Xaa is Ile or Phe
US-10-209-324-2

Query Match 71.4%; Score 35; DB 15; Length 403;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
DB 324 VGRPPFEAN 332

RESULT 40

US-09 534 455-186
Sequence 156, Application US/09934455
Publication No. US2003021270A:
GENERAL INFORMATION:
APPLICANT: Adam, Luc
APPLICANT: Creelman, Robert
APPLICANT: Dubell, Arnold
APPLICANT: Heard, Jacqueline
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Keddle, James
APPLICANT: Pilgrim, Marsha
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reuber, Lynne
APPLICANT: Riechmann, Jose Luis
APPLICANT: Yu, Guo-Liang
APPLICANT: Pineda, Omaida
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: MB-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: PatentIn version 3.1
SEQ ID NO 186
LENGTH: 633
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-934-455-186

Query Match 71.4%; Score 35; DB 11; Length 633;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPF 6
DB 382 LGRPPF 387

Search completed: November 14, 2003, 13:43:27
Job time : 22.3714 secs

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OM Protein - protein search, using sw mode:

Run on: November 14, 2003, 13:20:05 : Search time 10.8 Seconds

'without alignments'

80.141 Million cell updates/sec

Title: US-09-736-076-18

Perfect score: 49

Sequence: 1 LGRPFFETS 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 3.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum EB seq length: 0

Maximum EB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	46	93.9	682	2	A4493	serum-inducible ki
2	43	87.8	603	2	S34130	serine/threonine-s
3	43	87.8	603	2	A47545	protein kinase (EC
4	43	87.8	603	2	A54596	protein kinase - m
5	41	83.7	521	2	D99640	Protein F5A8.2 [i
6	40	81.6	465	2	B57248	protein kinase (EC
7	40	81.6	925	2	A57248	protein kinase (EC
8	39	79.6	153	2	E71526	hypothetical prote
9	39	79.6	389	2	S52242	protein kinase (EC
10	39	79.6	407	2	S52243	p46Eg265 protein -
11	38	77.6	576	2	S22127	protein kinase pol
12	38	77.6	656	2	D96831	hypothetical prote
13	36	73.5	179	2	H81682	conserved hypothet
14	36	73.5	220	1	B47275	triple hydratase
15	36	73.5	256	2	A81354	glutamine-binding
16	36	73.5	631	2	A57286	probable serine/th
17	35	71.4	217	2	AD3132	hypothetical prote
18	35	71.4	217	2	H91155	probable perase
19	35	71.4	403	2	JC5974	aurora-related kin
20	35	71.4	445	2	A60488	histidine-rich gly
21	35	71.4	558	2	JC2004	nuclear factor-kap
22	35	71.4	589	2	JG0196	protein kinase DNR
23	35	71.4	629	2	JG0195	protein kinase DNR
24	35	71.4	633	2	C85010	hypothetical prote
25	35	71.4	1044	2	T31072	heterocyst differe
26	35	71.4	1044	2	AR2158	heterocyst differe
27	34	69.4	162	2	D26802	hypothetical prote
28	34	69.4	177	2	D83727	RNA polymerase ECF
29	34	69.4	202	2	B64621	conserved hypothet

30	34	69.4	200	2	A71895	hypothetical prote
31	34	69.4	221	2	A89825	conserved hypothet
32	34	69.4	227	2	H84864	hypothetical prote
33	34	69.4	242	2	AE3528	flagellar m-ring p
34	34	69.4	252	2	E83469	hypothetical prote
35	34	69.4	256	2	F72421	iron(III) ABC tran
36	34	69.4	303	2	G71109	hypothetical prote
37	34	69.4	305	2	T43221	serine/threonine-s
38	34	69.4	320	2	AI2393	hypothetical prote
39	34	69.4	329	2	B87790	protein B0207.4 [i
40	34	69.4	359	2	F87524	histidinol-phospha
41	34	69.4	370	2	C75268	carboxypeptidase G
42	34	69.4	426	2	AP2663	hypothetical prote
43	34	69.4	426	2	E97445	nitrate transport
44	34	69.4	1018	2	E83699	probable RND efflu
45	34	69.4	1100	2	T42260	guanylate cyclase

ALIGNMENTS

RESULT 1

A44493

serum-inducible kinase - mouse

C:Species: Mus musculus (house mouse)

C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 10-Sep-1997

C:Accession: A44493

R:Simmons, D.L.; Neel, B.G.; Stevens, R.; Evett, G.; Eriksen, R.L.

Mol. Cell. Biol. 12, 4164-4169, 1992

A:Title: Identification of an early-growth-response gene encoding a novel putative pr

A:Reference number: A44493; MJID:92375085; PMID:1508211

A:Accession: A44493

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-682 <SIM>

A:Experimental source: F-2 cells

A>Note: sequence extracted from NCBI backbone (NCBIN:111721, NCBI:P:111722)

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

C:Keywords: ATP

F:77-331/Domain: protein kinase homology <KIN>

Query Match 93.9% Score 46; DB 2; Length 682;
Best Local Similarity 88.9% Pred. No. 0.79;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPFFETS 9

DB 272 LGRPFFETT 280

RESULT 2

S34130

serine/threonine-specific protein kinase PLK (EC 2.7.1.1) - human

N:Alternate names: polo-like protein kinase; protein kinase plk-1

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999

C:Accession: S34130; I38123; S61543

R:Golsteyn, R.M.; Schultz, S.C.; Bartek, J.; Ziemiecki, A.; Ried, T.; Nigg, E.A.

submitted to the EMBL Data Library, June 1993

A:Description: Cloning and characterization of a novel human protein kinase plk-1 a p

through mitosis.

A:Reference number: S34130

A:Accession: S34130

A:Molecule type: mRNA

A:Residues: 1-603 <GOL>

A:Cross-references: EMBL:X73458; NID:g312997; PIDN:CAA51837.1; PID:g312998

A:Experimental source: nasopharyngeal carcinoma

R:Holtrich, U.; Wolf, G.; Brauning, A.; Karn, T.; Bohme, B.; Rubsamen-Waigmann, H.;

Proc. Natl. Acad. Sci. U.S.A. 91, 1736-1740, 1994

A:Title: Induction and down-regulation of PLK, a human serine/threonine kinase expres

A:Reference number: A53134; MJID:94173904; PMID:8127874

A:Accession: I38123

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-140, P:142-226, E:228-633 <RES>
A:Cross-references: EMBL:X75932; NID:9460768; PIDN:CAAS4536.1; PID:9460769
A:Experimental source: lung tumor
K:Bräutinger, A.; Strebnadt, K.; Ruebsamen-Waigmann, H.
Oncogene 11, 1793-1803, 1995
A:Title: Identification and functional characterization of the human and murine polo-like kinase 1
A:Reference number: S61543; MUID:96068956; PMID:7478467
A:Accession: S61543
A:Molecule type: DNA
A:Residues: 1-122, T:124-136 <BRA>
A:Cross-references: EMBL:X90725; NID:91561143; PIDN:CAAC02260.1; PID:91061144
A:Experimental source: placenta
A:Note: the authors translated the codon AAG for residue 107 as Met
C:Genetics:
A:Gene: GDB:PLK
A:Cross-references: GDB:331003
A:Map position: 17pter:17p12
C:Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolog
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:51-305/Domain: protein kinase homology <KIN>
Query Match 87.8%; Score 43; DB 2; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGRPPFFETS 9
:|||||
DB 246 VGRPPFFETS 254

RESULT 3
A47545
protein kinase (EC 2.7.1.37) Plk mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C:Accession: A47545
R:Clay, F.J.; McEwen, S.J.; Bertencelot, I.; Wilks, A.F.; Dunn, A.R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4982-4986, 1993
A:Title: Identification and cloning of a protein kinase encoding mouse gene, Plk, related to the human and murine polo-like kinase
A:Reference number: A47545; MUID:93281660; PMID:8099445
A:Accession: A47545
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-603 <CLA>
A:Cross-references: GDB:331003; NID:9460768; PIDN:CAAS4536.1; PID:9460769
C:Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolog
C:Keywords: ATP; phosphotransferase
F:51-305/Domain: protein kinase homology <KIN>
Query Match 87.8%; Score 43; DB 2; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGRPPFFETS 9
:|||||
DB 246 VGRPPFFETS 254

RESULT 4
A54596
protein kinase - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 01-Jul-1996 #text_change 24-Sep-1999
C:Accession: A54596
R:Lake, R.C.; Jein, W.R.
Mol. Cell. Biol. 13, 7793-7801, 1993
A:Title: Cell cycle- and terminal differentiation-associated regulation of the mouse mRNA
A:Reference number: A54596; MUID:94067140; PMID:7902533
A:Accession: A54596
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-603 <RES>

A:Cross-references: GB:L19558; NID:9403473; PIDN:AAA16071.1; PID:9403474
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
F:51-305/Domain: protein kinase homology <KIN>
Query Match 87.8%; Score 43; DB 2; Length 603;
Best Local Similarity 77.8%; Pred. No. 2.6;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGRPPFFETS 9
:|||||
DB 246 VGRPPFFETS 254

RESULT 5
D88640
protein F55A8.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
C:Accession: D88640
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A:Reference number: A75003; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: D88640
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-521 <STO>
A:Cross-references: GB:chr_IV; PIDN:AAC19186.1; PID:g3193148; GSPDB:GNC0022; CESP:F55A8.2
A:Gene: F55A8.2
A:Map position: 4
C:Superfamily: cGMP-dependent protein kinase; cAMP receptor protein cyclic nucleotide-gated ion channel
Query Match 83.7%; Score 41; DB 2; Length 521;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 LGRPPFFETS 9
:|||||
DB 403 LGRPPFFOAS 411

RESULT 6
B55748
protein kinase (EC 2.7.1.37) Sak-b - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 19-Dec-1997
C:Accession: B55748
R:Foddy, C.; McRob, B.; Yousefi, S.; Heffernan, M.; Dennis, J.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 6388-6392, 1994
A:Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosophila protein kinase Drosophila serine/threonine kinase
A:Reference number: A55748; MUID:94294387; PMID:8022793
A:Accession: B55748
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-465 <FO>
A:Cross-references: GS:L29480
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; phosphotransferase
F:10-265/Domain: protein kinase homology <KIN>
F:18-26/Region: protein kinase ATP-binding motif
Query Match 81.6%; Score 40; DB 2; Length 465;
Best Local Similarity 75.0%; Pred. No. 7.4;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGRPPFFET 8
:|||||
DB 286 IGRPPFFDT 213

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RESULT 7
A:5748
C:Keywords: ATP; phosphotransferase
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1995 #sequence_revision: 02 Jun-1995 #text_change 24-Sep-1999
C:Accession: A55748
C:Query Match 79.6%; Score 39; DB 2; Length 389;
Best Local Similarity 75.0%; Pred. No. 9.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
R:Roghi, C.; Le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 6389-6392, 1994
A:Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosophila
A:Reference number: A55748; MUID:94294387; PMID:822793
A:Accession: A55748
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-925 <FOD>
A:Cross-references: GB:L29479; NID:9487869; PIDN:AA037648.1; PID:9487870
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homocid
C:Keywords: ATP; phosphotransferase
F:10-265/Domain: protein kinase homology <KIN>
F:18-26/Region: protein kinase ATP-binding motif
Query Match 81.6%; Score 40; DB 2; Length 925;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGPPPPET 8
DB 206 LGPPPPET 213

RESULT 8
A:5748
C:Keywords: ATP; phosphotransferase
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision: 13-Sep-1998 #text_change 08 Oct-1999
C:Accession: E71526
C:Query Match 79.6%; Score 39; DB 2; Length 389;
Best Local Similarity 75.0%; Pred. No. 9.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
R:Stephens, R.S.; Kaiman, S.; Lamme, C.J.; Pan, J.; Marathe, R.; Atavind, L.; Mitchell,
Science 262, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trach
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: E71526
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-153 <ARN>
A:Cross-references: GB:AF001307; GB:AE001203; NID:93329757; PIDN:AA069933.1; PID:9332879
A:Experimental source: serotype D, strain CW-3/CX
C:Genetics:
A:Gene: CT388
Query Match 79.6%; Score 39; DB 2; Length 389;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGPPPPET 8
DB 11 LGPPPPET 18

RESULT 9
A:5748
C:Keywords: ATP; phosphotransferase
C:Species: Xenopus laevis (African clawed frog)
C:Date: 07-May-1995 #sequence_revision: 21-Jul-1995 #text_change 18-Jun-1999
C:Accession: S52242
C:Query Match 79.6%; Score 39; DB 2; Length 407;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
R:Roghi, C.; Le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A:Description: Eg2, selected by differential screening encodes a new Xenopus protein kin
A:Reference number: S52242
A:Accession: S52242
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-389 <ROG>
A:Cross-references: EMBL:Z17206; NID:9608274; PIDN:CAA80826.1; PID:9609280
C:Superfamily: Kinase-related transmembrane proteins; protein kinase homology

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C:Keywords: ATP; phosphotransferase
F:119-371/Domain: protein kinase homology <KIN>
F:127-135/Region: protein kinase ATP-binding motif
Query Match 79.6%; Score 39; DB 2; Length 389;
Best Local Similarity 75.0%; Pred. No. 9.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGPPPPET 8
DB 312 VGKPPPET 319

RESULT 10
A:5748
C:Keywords: ATP; phosphotransferase
C:Species: Xenopus laevis (African clawed frog)
C:Date: 07-May-1995 #sequence_revision: 03-Aug-1995 #text_change 24-Sep-1999
C:Accession: S52243; S34642; 151695
R:Roghi, C.; Le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A:Description: Eg2, selected by differential screening encodes a new Xenopus protein
A:Reference number: S52242
A:Accession: S52243
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-407 <ROG>
A:Cross-references: EMBL:Z17207; NID:9609281; PIDN:CAA78915.1; PID:9609282
R:Bouvet, P.; Omilli, F.; Arlot-Bonnemains, Y.; Legagneux, V.; Roghi, C.; Bassez, T.;
submitted to the EMBL Data Library, June 1993
A:Description: Targetted deadenylation of specific mRNAs in Xenopus embryos by a mech
A:Reference number: S34642
A:Accession: S34642
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 328-407 <BOU>
A:Cross-references: EMBL:Z24453; NID:9394756; PIDN:CAA80826.1; PID:9394757
R:Bouvet, P.; Omilli, F.; Arlot-Bonnemains, Y.; Legagneux, V.; Roghi, C.; Bassez, T.;
Mol. Cell. Biol. 14, 1893-1900, 1994
A:Title: The deadenylation conferred by the 3' untranslated region of a developmental
A:Reference number: 151695; MUID:94158861; PMID:8114721
A:Accession: 151695
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 328-407 <BO2>
A:Cross-references: EMBL:Z24453; NID:9394756; PIDN:CAA80826.1; PID:9394757
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
C:Keywords: ATP; phosphotransferase; protein kinase
F:138-390/Domain: protein kinase homology <KIN>
F:146-154/Region: protein kinase ATP-binding motif
Query Match 79.6%; Score 39; DB 2; Length 407;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGPPPPET 8
DB 331 VGKPPPET 338

RESULT 11
A:5748
C:Keywords: ATP; phosphotransferase
C:Species: Drosophila melanogaster
C:Date: 20-Feb-1995 #sequence_revision: 20-Feb-1995 #text_change 24-Sep-1999
C:Accession: S22127
R:Sunke, C.E.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22127
A:Accession: S22127
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-576 <SUN>

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A:Title: Identification by targeted differential display of an immediate early gene encoded by the human H1299 cell line
 A:Reference number: A57286; MUID:95247749; PMID:7730342

A:Accession: A57286

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-631 <DOK>

A:Cross-references: GB:U21392; GB:U24334

C:Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolog

C:Keywords: ATP; phosphotransferase

F:1-315/Domain: protein kinase homology <XK>

Query Match 73.5%; Score 16; DB 2; Length 631;

Best Local Similarity 75.0%; Pred. No. 59;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPPTTS 9

DB 257 GSPPTTA 264

RESULT 17

AD112 Hypothetical protein Atu4680 (imported) - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C:Date: 11-Jan-2002 #sequence_revision 11 Jan-2002 #text_change 18-Nov-2002

C:Accession: AD112

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Venks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavina, T.; Levy, R.; Li, M.; McCrell

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, M.; Perty, M.; Gordon-Kamm,

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743143

A:Accession: AD112

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-217 <KUP>

A:Cross-references: GB:AB008689; PIDN:AA45474.1; PID:91793180; GSPDB:GN00187

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu4680

A:Map position: linear chromosome

C:Superfamily: histidine permease protein X

Query Match 71.4%; Score 15; DB 2; Length 217;

Best Local Similarity 77.8%; Pred. No. 32;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPPTS 9

DB 82 LGWPPPTTS 90

RESULT 18

H98155 probable permease of ABC transporter PAL237 (imported) - Agrobacterium tumefaciens (stra

C:Species: Agrobacterium tumefaciens

C:Date: 22-Oct-2001 #sequence_revision 22 Oct 2001 #text_change 18-Nov-2002

C:Accession: H98155

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, M.; Blanchard, M.; Ouello, B.; Goldman,

A:Lin, F.; Williams, C.; Allinger, M.; Doughty, E.; Scott, C.; Lappas, C.; Markelz, B.

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: H98155

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-217 <KUR>

A:Cross-references: GB:AE007870; PIDN:AAK8870.1; PID:915158516; GSPDB:GN00170

C:Genetics:

A:Gene: AGR_L_403

A:Map position: linear chromosome

C:Superfamily: histidine permease protein M

Query Match 71.4%; Score 35; DB 2; Length 217;

Best Local Similarity 77.8%; Pred. No. 30;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGRPPPTS 9

DB 82 LGWPPPTTS 90

RESULT 19

JC5974

aurora-related kinase 2 (EC 2.7.1.1) - human

C:Species: Homo sapiens (man)

C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jan-2000

C:Accession: JC5974

R:Shindo, M.; Nakano, H.; Kuroyanagi, H.; Shirasawa, T.; Mihara, M.; Gilbert, D.J.; J

Biochem. Biophys. Res. Commun. 244, 285-292, 1998

A:Title: cDNA cloning, expression, subcellular localization, and chromosomal assignm

A:Reference number: JC5974; MUID:98183439; PMID:9514916

A:Accession: JC5974

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-403 <SHI>

A:Cross-references: GB:AF028551

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

C:Keywords: phosphotransferase

F:131-383/Domain: protein kinase homology <XIN>

Query Match 71.4%; Score 35; DB 2; Length 403;

Best Local Similarity 55.6%; Pred. No. 57;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPPTS 9

DB 324 VGKPPPEAN 332

RESULT 20

A60488

histidine-rich glycoprotein - bovine (fragments)

N:Alternate names: autorosette inhibition factor

C:Species: Bos primigenius taurus (cattle)

C:Date: 19-Mar-1993 #sequence_revision 23-Mar-1995 #text_change 07-Jul-1995

C:Accession: S35687; JC2196; A60488

R:Sorensen, C.B.; Krogh-Pedersen, H.; Petersen, T.E.

FEBS Lett. 328, 285-290, 1993

A:Title: Determination of the disulphide bridge arrangement of bovine histidine-rich

A:Reference number: S35687; MUID:93351678; PMID:8348977

A:Accession: S35687

A:Molecule type: protein

A:Residues: 1-25;26-52;57-75;82-88;95-119;146-173;175-206;210-309;313-445 <SOR>

A>Note: 355-Gln and 368-Tyr were also found

R:Halkier, T.; Andersen, H.; Vestergaard, A.; Magnusson, S.

Biochem. Biophys. Res. Commun. 200, 78-82, 1994

A:Title: Bovine histidine-rich glycoprotein is a substrate for bovine plasma factor X

A:Reference number: JC2196; MUID:94220160; PMID:7909439

A:Accession: JC2196

A:Molecule type: protein

A:Residues: 1-23;35-54;57-101;116;118;120-136;137-145;150

A:Experimental source: plasma

R:Vestergaard, A.B.; Andersen, H.F.; Magnusson, S.; Halkier, T.

Thromb. Res. 60, 385-390, 1990

A:Title: Histidine-rich glycoprotein inhibits contact activation of blood coagulation

A:Reference number: A60488; MUID:91196010; PMID:2084959

A:Accession: A60488

A:Molecule type: protein

A:Residues: 1-6; X 18-15 <VES>

C:Comment: This protein is a single-chained plasma protein which participates in tran

C:Superfamily: histidine-rich glycoprotein; cystatin homology

C:Keywords: glycoprotein; plasma

F:2-113/Domain: cystatin homology <CY>

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F:122-207/Domain: cystatin homology (fragments) <C2>
F:7-424,60-75,87-108,165-346,180-203,258-288/D:disulfide bonds: #status experimental
F:74,107,164,266/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Vatch
Best Local Similarity 71.4%; Score 35; DB 2; Length 445;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPPPFETS 9
      |||||
DB 235 GRPPPFKPS 242

RESULT 21
JC2004
nuclear factor kappa B p65 chain - chicken
C:Species: Gallus gallus (chicken)
C:Date: 14-Jul-1994 #sequence,revision: 14-Jul-1994 #text_change 20-Jun-2000
C:Accession: JC2004
R:Ikeda, T.; Honjo, K.; Hirota, Y.; Orodera, T.
Gene 133, 237-242, 1993
A:Title: Isolation of the chicken NF-kappaB p65 subunit-encoding cDNA and characterization
A:Reference number: JC2004; MUID:9404C8.7; PMID:7516720
A:Accession: JC2004
A:Molecule type: mRNA
A:Residues: 1-558 <K>E>
A:Cross-references: GB:D1372; NID:9455463; P:CN:BAA02874.1; P:D:Q46C974
C:Comment: This protein contains the Rel homology domain in its amino-terminal 286 amino
C:Superfamily: rel transforming protein; rel homology
C:Keywords: DNA binding; transforming protein; phosphoprotein
F:25-310/Domain: rel homology <REL>
F:236-309/Region: nuclear location signal
F:281/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match
Best Local Similarity 71.4%; Score 35; DB 2; Length 458;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGPPPFET 8
      |||||
DB 429 LGPPPFET 436

RESULT 22
JG0196
protein kinase DYRK1B (EC 2.7.1.1) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Jul-1994 #sequence,revision: 23-Jul-1994 #text_change 14-May-2000
C:Accession: JG0196
R:Keder, S.; Weber, Y.; Altafaj, A.; Estroff, X.; Jaffe, H.; Becker, W.
Biochem Biophys Res Commun 254, 474-479, 1999
A:Title: Cloning and characterization of DYRK1B, a novel member of the DYRK family of p
A:Reference number: JG0195; MUID:99119316; PMID:9918863
A:Accession: JG0196
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-559 <LED>
A:Cross-references: GB:Y18280
C:Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homolo
C:Keywords: phosphotransferase

Query Match
Best Local Similarity 71.4%; Score 35; DB 2; Length 589;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGPPPFETS 9
      |||||
DB 509 LGPPPFETS 517

RESULT 23
JG0195
protein kinase DYRK1B (EC 2.7.1.1) - human

```

```

Query Match      71.4%; Score 35; DB 2; Length 1044;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
    | . . . . .
Db 444 LSRPQFETS 452

RESULT 26
AB2158
heterocyst differentiation protein [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2000; #sequence_revision 14 Dec 2001; #text_change 09-Dec-2002
C:Accession: AB2158
R:Kanehisa, T.; Nakamura, Y.; Woik, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi,
Nakazaki, N.; Shimo, S.; Sugimoto, Y.; Takazawa, M.; Yanada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen fixing Cyanobacterium Anabaena
b:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB2158
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1044 <KUR>
A:Cross-references: GB:BA000019; FIDN:BAH74516.1; PID:g101319.1; GSPDB:GN02179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: hnfC
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match      71.4%; Score 35; DB 2; Length 1044;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGRPPFETS 9
    | . . . . .
Db 444 LSRPQFETS 452

RESULT 27
hypothetical protein Y41C4A.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999; #sequence_revision 15-Oct-1999; #text_change 18-Aug-2000
C:Accession: T26802
R:Steward, C.
submitted to the EMBL Data Library, October 1998
A:Reference number: T20269
A:Accession: T26802
A:Status: preliminary; translated from GB:U00000.EMBL
A:Molecule type: DNA
A:Residues: 1-162 <WIL>
A:Cross-references: EMBL:AL032627; PIDN:CAA21546.1; CESP:Y41C4A.3
A:Experimental source: C. elegans Y41C4A
A:Gene: CESP:Y41C4A.3
C:Superfamily: Caenorhabditis elegans hypothetical protein Y41C4A.3

Query Match      69.4%; Score 34; DB 2; Length 162;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPPE 7
    | . . . . .
Db 125 LSRPPE 131

RESULT 28
D83727
RNA polymerase ECF-type sigma factor sigv [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000; #sequence_revision 01-Dec-2000; #text_change 15-Jun-2001

C:Accession: D83727
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: AB3650; MUID:20512582; PMID:11058132
A:Accession: D83727
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-177 <STO>
A:Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04339.1; GSPDB:GI
A:Experimental source: strain C-125
C:Genetics:
A:Gene: sigv

Query Match      69.4%; Score 34; DB 2; Length 177;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPPE 7
    | . . . . .
Db 11 LSRPPE 17

RESULT 29
B64621
conserved hypothetical protein HP0810 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C>Date: 09-Aug-1997; #sequence_revision 09-Aug-1997; #text_change 24-Nov-1999
C:Accession: B64621
R:Tomb, J.F.; White, C.; Kerlavang, A.R.; Clayton, R.A.; Sutton, R.G.; Fleischmann, R
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khatalak, H.G.; Glodek, A.; McKe
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey,
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: B64621
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-200 <TOM>
A:Cross-references: GB:AE000592; GB:AE000511; NID:g2313929; PIDN:AAD07856.1; PID:g231
C:Superfamily: Escherichia coli hypothetical 21.7K protein (ftsY-nika intergenic regi

Query Match      69.4%; Score 34; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPFETS 9
    | . . . . .
Db 134 PPFETS 139

RESULT 30
A71895
hypothetical protein jhp0746 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C>Date: 12-Feb-1999; #sequence_revision 12-Feb-1999; #text_change 24-Nov-1999
C:Accession: A71895
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric P
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: A71895
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-200 <ARN>
A:Cross-references: GB:AE001505; GB:AE001439; NID:g4155295; PIDN:AAD06318.1; PID:g415
A:Experimental source: strain J99
C:Genetics:
A:Gene: jhp0746
C:Superfamily: Escherichia coli hypothetical 21.7K protein (ftsY-nika intergenic regi

```


C:Genetics:
A:Gene: TM007A
C:Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 69.4%; Score 34; DB 2; Length 256;
Best Local Similarity 77.8%; Pred. No. 55;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 LGRPPEFS 9
|||
Db 63 LGRPPEFS 71

RESULT 36
G71109
hypothetical protein PH0646 - *Pyrococcus horikoshii*
C:Species: *Pyrococcus horikoshii*
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 18-Aug-2000
C:Accession: G71109
P.Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
Y.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kishida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A7000; MUID:93344137; PMID:9679194
A:Accession: G71109
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-363 <RAW>
A:Cross-references: GB:AP000003; NID:g1236110; PIDN:BA297371; PID:di010680; PID:g32570
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0646
C:Superfamily: *Pyrococcus horikoshii* hypothetical protein PH0646

Query Match 69.4%; Score 34; DB 2; Length 303;
Best Local Similarity 75.0%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

QY 2 GRPPEFS 9
|||
Db 82 GRPPEFS 89

RESULT 37
T4322
serine/threonine specific protein kinase EC 2.7.11.1 2 *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 14-Mar-2000
C:Accession: T4322
R.Schumacher, J.M.; Golden, A.; Donovan, P.C.
J. Cell Biol. 49, 1635-1646, 1998
A:Title: Atr-2: An aurora/ipl-related protein kinase associated with chromosomes and m
A:Reference number: 222347; MUID:9069487; PMID:955156
A:Accession: T4322
A:Status: preliminary; translated from GR/EMBL/DUBJ
A:Molecule type: mRNA
A:Residues: 1-305 <SCH>
A:Cross-references: EMBL:AF071207; PIDN:AA070945.1
C:Genetics:
A:Gene: Atr-2
A:Map position: 1
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: phosphotransferase

Query Match 69.4%; Score 34; DB 2; Length 305;
Best Local Similarity 71.4%; Pred. No. 66;
Matches 5; Conservative 2; Mismatches 0; Gaps 0;

QY 1 LGRPPEFS 7
|||
Db 221 VGRPPEFS 227

RESULT 38
AI2393
hypothetical protein all4705 [imported] - *Nostoc* sp. (strain PCC 7120)
C:Species: *Nostoc* sp. PCC 7120
A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AI2393
R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 9, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1607; MUID:21595285; PMID:11759840
A:Accession: AI2393
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-320 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA76404.1; PID:g17133842; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all4705

Query Match 69.4%; Score 34; DB 2; Length 320;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPEFS 7
|||
Db 122 LGRPPEFS 128

RESULT 39
B87790
protein B0207.4 [imported] - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: B87790
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating bio
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/Celegans/ and www.sanger.ac.uk/projects/C-
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: B87790
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-329 <SC>
A:Cross-references: GB:chr_1; PIDN:AA852459.1; PID:g1943805; GSPDB:GN00019; CESP:B020
C:Genetics:
A:Gene: B0207.4
A:Map position: 1
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 69.4%; Score 34; DB 2; Length 329;
Best Local Similarity 71.4%; Pred. No. 72;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPEFS 7
|||
Db 245 VGRPPEFS 251

RESULT 40
F87524
histidinol-phosphate aminotransferase [imported] - *Caulobacter crescentus*
C:Species: *Caulobacter crescentus*
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: F87524
R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; Deboy, R.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Shapiro, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.

A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: F87524
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-159 <STC>
 A:Cross-references: GB:AE005673; MID:313423728; PID:AAK24134.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC2223
 C:Superfamily: probable histidinol-phosphate transaminase

 Query Match 69.4%; Score 34; DB 2; Length 359;
 Best Local Similarity 85.7%; Pred. No. 79;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 3 RPFETS 9
 ||| ||
 Db 242 RPPNTS 248

 Search completed: November 14, 2003, 13:59:52
 Job time: 11.8 secs

FT BINDING 108 108 ATP (BY SIMILARITY).
FT ACT_SITE 202 202 BY SIMILARITY.
FT DOMAIN 507 570 POLO BOX 1.
FT DOMAIN 603 674 POLO BOX 2.
SQ SEQUENCE 682 AA; 77811 MW; 586DEARFD7209A3D CRC64;

Query Match: 93.9%; Score 46; DB 1; Length 682;
Best Local Similarity 88.9%; Pred. No. 0.26;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
DB 272 LGRPPFFETT 280

RESULT 2

SNK_RAT
ID SNK_RAT STANDARD; PRT; 682 AA.
AC Q9R512, 2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase SNK (EC 2.7.1.-) (Serum inducible kinase).
GN SNK.
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX MBE; TaxID:10116;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=99452760; PubMed=10531297;
RA Kausemann G., Weiler M., Wulff P., Jessberger S., Konietzko U., Scaife J., Staebli U., Beretner-Hahn J., Streibardt K., Kuhl D.;
RT "The polo-like protein kinases Psk and Snk associate with a Ca(2+)- and integrin-binding protein and are regulated dynamically with synaptic plasticity".
RL ENBCJ128-5528-5539(1999).
CC -!- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS, WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.

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CC -----
DR EMBL AF136583; AAF08166.1; -
DR InterPro: IPR000959; POLO box.
DR InterPro: IPR000719; Prot_Kinase
DR InterPro: IPR002290; Ser_Thr_kinase.
DR Pfam: PF00369; pkinase; 1.
DR Pfam: PF00659; POLO box; 2.
DR ProDom: PD00030; Prot_kinase; 1.
DR SMART: SM00223; S_TKc; 1.
DR PROSITE: PS50078; POLO BOX; 2.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS50011; PROTEIN KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE_ST; 1.
KW transferase; Serine/threonine-protein kinase; ATP binding; Repeat.
FT DOMAIN 54 59 POLY-HIS.
FT DOMAIN 79 93 PROTEIN KINASE
FT NP_BIND 85 93 ATP (BY SIMILARITY)
FT BINDING 108 108 ATP (BY SIMILARITY)
FT ACT_SITE 202 202 BY SIMILARITY
FT DOMAIN 507 570 POLO BOX 1.
FT DOMAIN 603 674 POLO BOX 2.

SQ SEQUENCE 682 AA; 77919 MW; 58C50DEBDE81D5F3 CRC64;
Query Match: 93.9%; Score 46; DB 1; Length 682;
Best Local Similarity 88.9%; Pred. No. 0.26;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRPPFFETS 9
DB 272 LGRPPFFETT 280

RESULT 3

SNK_HUMAN
ID SNK_HUMAN STANDARD; PRT; 685 AA.
AC Q9NY33; O60679; Q96CV7; Q9UE61;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase SNK (EC 2.7.1.-) (Serum inducible kinase).
GN SNK.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX MBE; TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RA Ouyang B., Dai W.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Anderson K.M., Nerurkar S.S., Hansbury M.J., Fornwald J., Scott G., Bouzyk M., Mai F., Imbruglia C.S., Carlson K., Marshall L.A., Roshak A.K.;
RT "Identification and characterization of human serum-inducible kinase (SNK), a novel member of the polo-kinase family of cell cycle regulators: potential implication for regulation of vascular smooth muscle proliferation.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN 13;
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G., Stausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.J., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stapleton M., Soares V.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman C.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein C.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 14;
RP SEQUENCE OF 110-408 FROM N.A.
RA Fidler C., Boultonwood J., Wang Jabs E., Waincoat J.S.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS, WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.

CC -!- SIMILARITY: Contains 2 POLO box domains.
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 CC -----
 DR EMBL: AF059617; AAC4573.1; -
 DR EMBL: AF223574; AAF62897.1; -
 DR EMBL: J95755; AAD00575.1; -
 DR EMBL: BC013879; AAH13879.1; -
 DR MIM: 607033; -
 DR InterPro: IPR000359; POLO_box.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR022290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00659; POLO_box; 2.
 DR ProDom: PDC02001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00378; POLO_BOX; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00311; PROTEIN_KINASE_DCM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW Transfrase: Serine/threonine-protein kinase; ATP-binding; Repeat.
 FT DOMAIN 57 64 POLY-HIS.
 FT DQAIN 92 334 PROTEIN KINASE.
 FT BLIND 88 96 ATP (BY SIMILARITY).
 FT BINDING 111 111 ATP (BY SIMILARITY).
 FT ACT SITE 225 205 BY SIMILARITY.
 FT DQAIN 310 573 POLO_BOX 1.
 FT DQAIN 606 677 POLO_BOX 2.
 FT CONFLICT 28 28 A -> G (IN REF. 1).
 SQ SEQUENCE 695 AA: 78236 MW: 6429F6EPD83B33 CRC64;
 Query Match 93.9%; Score 46; DB 1; Length 695;
 Best local similarity 89.9%; Pred. No. 0.27;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LGRPFETS 9
 DB 275 LGRPFETT 283
 RESULT 4
 ID PLK1 HUMAN STANDARD; PRT; 283 AA.
 AC P53350.
 DT 01-OCT-1996 (Rel. 34, Created;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Serine/threonine-protein kinase PLK (EC 2.7.1.-) (Serine-
 DE threonine protein kinase 13) (STPK13).
 GN PLK OR PLK1.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TSSJEP; Placenta;
 RX MEDLINE=94289253; PubMed=8018557;
 RA Hamanaka R., Maloic S., Smith M.R., O'Connell C.D., Longo D.L.,
 RA Fertis D.K.;
 RT Cloning and characterization of human and murine homologues of the
 RT Drosophila polo serine-threonine kinase.
 RL Cell Growth Differ. 5:249-257(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94267140; PubMed=7922533;
 RA Lake R.J., Celisnek W.R.;

RT "Cell cycle- and terminal differentiation-associated regulation of
 RT the mouse mRNA encoding a conserved mitotic protein kinase."; Mol.
 RL Mol. Cell. Bio. 13:7793-7801(1993).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95051109; PubMed=7962193;
 RA Golsteyn R.M., Schultz S.J., Bartek J., Ziemiecki A., Ried T.,
 RA Nigg E.A.;
 RT "Cell cycle analysis and chromosomal localization of human Plk1, a
 RT putative homologue of the mitotic kinases Drosophila polo and
 RT J. Cell Sci. 107:1509-1517(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=94173904; PubMed=8127874;
 RA Holtrich U., Wolf G., Braeuninger A., Karn T., Boehme B.,
 RA Ruebsaamen-Waigmann H., Streibhardt K.;
 RT "Induction and down-regulation of PLK, a human serine/threonine
 RT kinase expressed in proliferating cells and tumors."; Proc. Natl. Acad. Sci. U.S.A. 91:1736-1740(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon, and Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Viallaid D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL -!- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
 CC DURING G1 OR S PHASE.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: PLACENTA AND COLON.
 CC -!- DEVELOPMENTAL STAGE: ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
 CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
 CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
 CC DURING S PHASE.
 CC -!- INDUCTION: BY GROWTH-STIMULATING AGENTS.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDC5/POLO SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 POLO box domains.
 CC -----
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 CC -----
 DR EMBL: U01038; AAA56634.1; -
 DR EMBL: J13559; AAA36659.1; -
 DR EMBL: X73458; CAA51837.1; -
 DR EMBL: X75932; CAA53536.1; -
 DR EMBL: BC002369; AAH02369.1; -
 DR EMBL: BC003002; AAH03002.1; -
 DR EMBL: BC014846; AAH14846.1; -

```

DR PIR: S34330; S34130.
DR Genew: HGNC:9077; PLK.
DR GK: P53350; -.
DR Q3: G0200674; P:protein serine/threonine kinase activity; TAS.
DR Q3: G0200674; P:mitosis; TAS.
DR Q3: G0200674; P:proliferation; TAS.
DR Q3: G0200674; P:regulation of cell cycle; TAS.
DR InterPro: IPR000959; POLO box.
DR InterPro: IPR000719; Prot kinase.
DR Pfam: PF000659; Pkinase; 1.
DR Pfam: PF00659; POLO box; 2.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00078; POLO BOX; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Nuclear protein.
FT DOMAIN 53 305 PROTEIN_KINASE.
FT NP_BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 415 480 POLO BOX 1.
FT DOMAIN 515 584 POLO BOX 2.
FT CONFLICT 2 2 S -> T (IN REF. 1).
FT CONFLICT 11 11 A -> F (IN REF. 1).
FT CONFLICT 58 58 F -> S (IN REF. 1).
FT CONFLICT 60 60 G -> S (IN REF. 1).
FT CONFLICT 73 73 A -> V (IN REF. 2).
FT CONFLICT 141 141 L -> P (IN REF. 4).
FT CONFLICT 227 227 G -> E (IN REF. 4).
FT CONFLICT 301 301 N -> G (IN REF. 2).
FT CONFLICT 495 495 A -> G (IN REF. 2).
FT CONFLICT 501 501 E -> C (IN REF. 2).
SQ SEQUENCE 623 AA; 68254 MW; 17832F1C15E826 CR; 64,
Query Match 87.8% Score 43; DB 1; Length 603;
Best Local Similarity 77.8%; Evid. 0.0;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGRRPPETS 9
DB 246 VKRRPPETS 254
RESULT 6
BLK1_MOUSE STANDARD; INT: 1 3 AA
AC Q07842;
DT 01 FEB 1995 (Rel. 31, Created:
DT 01 OCT 1996 (Rel. 34, Last sequence update:
DT 16 OCT 2001 (Rel. 40, Last annotation update:
DE Serine/threonine-protein kinase PLK (EC 2.7.1.1) (P-K-1) (serine-
DE threonine protein kinase 13) (STPK) [1]
GN PLK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
GX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Bone marrow.
RX MEDLINE=93281660; PubMed=8099445;
RA Clay P., McEwen S.J., Bertorello L., Walks A.P., Dang A.R.
RT Identification and cloning of a protein kinase encoding mouse gene,
RT Plk, related to the polo gene of Drosophila.
RL Proc. Natl. Acad. Sci. U.S.A. 90:4842-4846(1993).
RN 2;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus.

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RX MEDLINE=94289293; PubMed=8018557;
RA Hananaka R., Malold S., Smith M.R., O'Connell C.D., Longo D.L.,
RA Ferris D.K.;
RT "Cloning and characterization of human and murine homologues of the
RT Drosophila polo serine-threonine kinase.";
RL Cell Growth Differ. 5:249-257(1994).
RN 3;
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=94067140; PubMed=7902533;
RA Lake R.J., Jelinek W.R.;
RT "Cell cycle- and terminal differentiation-associated regulation of
RT the mouse mRNA encoding a conserved mitotic protein kinase.";
RL Mol. Cell. Biol. 13:7793-7801(1993).
CC -!- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: NEWBORN AND ADULT SPLEEN, FETAL AND NEWBORN
CC KIDNEY, LIVER, BRAIN, THYMUS AND ADULT BONE MARROW, THYMUS,
CC OVARY AND TESTES.
CC -!- DEVELOPMENTAL STAGE: IN THE THYMUS, LEVELS INCREASED DURING FETAL
CC DEVELOPMENT, WERE HIGHEST IN NEWBORN ANIMALS AND DECREASED IN THE
CC ADULT. IN THE TESTES, THE PLX LEVELS WERE HIGHER IN THE ADULT THAN
CC IN PREPUBESCENT MICE WHILE IN THE OVARY, THE LEVELS WERE HIGHER IN
CC THE PREPUBESCENT MICE. ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
CC DURING S PHASE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC -!- SIMILARITY: Contains 2 POLO box domains.
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CC or send an email to license@isb-sib.ch).
CC EMBL: L06144; AAA19948.1;
CC EMBL: U01063; AAA56635.1;
CC EMBL: L19558; AAA16071.1;
CC PIR: A47545; A47545.
CC PIR: A54596; A54596.
CC MGD: MGI:97621; Plk.
CC InterPro: IPR000959; POLO box.
CC InterPro: IPR000719; Prot_Kinase.
CC InterPro: IPR024901; Ser_thr_kinase.
CC Pfam: PF00069; Pkinase; 1.
CC Pfam: PF00659; POLO box; 2.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00220; S_TKc; 1.
CC PROSITE: PS00078; POLO BOX; 2.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Nuclear protein.
FT DOMAIN 53 305 PROTEIN_KINASE.
FT NP_BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 415 480 POLO BOX 1.
FT DOMAIN 515 584 POLO BOX 2.
FT CONFLICT 4 4 A -> V (IN REF. 1).
FT CONFLICT 15 15 A -> T (IN REF. 1).
FT CONFLICT 23 23 P -> L (IN REF. 1).
FT CONFLICT 27 27 V -> A (IN REF. 1).
FT CONFLICT 29 29 G -> S (IN REF. 1).
FT CONFLICT 41 41 P -> L (IN REF. 1).
FT CONFLICT 54 54 V -> I (IN REF. 1).
FT CONFLICT 495 495 A -> R (IN REF. 1).

```

SQ SEQUENCE 603 AA; 68300 MW; 1B9806463665FA10 CRC64;

Query Match 87.8%; Score 43; DB 1; Length 603;

Best Local Similarity 77.8%; Pred. No. 0.9;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRRPPFETS 9

DB 246 VGRPPFETS 254

RESULT 6

ID PLK1 RAT STANDARD; PRT; 603 AA.
AC Q62673.
DT 16-OCT-2001 (Rel. 40, Created;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase PLK (EC 2.7.1.1) (PDK-1).
GN PLK
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1.
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Astrup J., Hansen J.A., Hvirilis Nielsen J.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBE databases.
CC ! FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE (BY SIMILARITY).
CC ! SUBCELLULAR LOCATION: Nuclear (By similarity).
CC ! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC GCS/POLO SUBFAMILY.
CC ! SIMILARITY: Contains 2 POLO box domains.
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EMBL: J01088; AAA18895.1;
DR InterPro: IPR000959; POLO_box
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR022290; Ser_thr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00659; POLO_box; 2.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00223; S_TKc; 1.
DR PROSITE: PS00678; POLO_BOX; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase, ATP binding; Repeat;
KW Nuclear protein.
FT DOMAIN 53 305 PROTEIN KINASE.
FT NP_BIND 59 67 ATP (BY SIMILARITY).
FT BINDING 82 82 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 417 480 POLO BOX 1.
FT DOMAIN 515 584 POLO BOX 2.
SQ SEQUENCE 603 AA; 68313 MW; 1C7AFF53B7EDCC02 CRC64;

Query Match 87.8%; Score 43; DB 1; Length 603;

Best Local Similarity 77.8%; Pred. No. 0.9;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRRPPFETS 9

DB 246 VGRPPFETS 254

RESULT 7

ID STKD_MOUSE STANDARD; PRT; 282 AA.
AC O88445; Q9CLC2;
DT 28-FEB-2003 (Rel. 41, Created;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine-protein kinase 13 (EC 2.7.1.37) (Aurora/p11/Eg2
DE protein 1) (Aurora-C).
GN STK13 OR AIE1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1.
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=99025676; PubMed=9809744;
RA Tseng T.C., Chen S.H., Hsu Y.P., Tang T.K.;
RT "Protein kinase profile of sperm and eggs: cloning and
RT characterization of two novel testis-specific protein kinases (AIE1;
RT AIE2) related to yeast and fly chromosome segregation regulators.";
RL DNA Cell Biol. 17:823-833(1998).
RN 12.
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=20551164; PubMed=11098217;
RA Hu H.M., Chuang C.K., Lee M.J., Tseng T.C., Tang T.K.;
RT "Genomic organization, expression, and chromosome localization of a
RT third aurora-related kinase gene, Aie1.";
RL DNA Cell Biol. 19:679-688(2000).
CC !- FUNCTION: May play a part in organizing microtubules in relation
CC to the function of the centrosome/spindle pole during mitosis.
CC !- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated
CC !- SUBCELLULAR LOCATION: Localized to spindle pole from anaphase to
CC cytokinesis (By similarity).
CC !- TISSUE SPECIFICITY: Expressed only in testis.
CC !- DEVELOPMENTAL STAGE: Expressed on day 14 dpc in prepubertal
CC testis, expression reached its plateau on day 21 dpc and remained
CC at a high level in adult.
CC !- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.

EMBL: AF054620; AAC25954.1;
DR EMBL: AF195272; AAF25838.1;
DR HSP: Q63450; A006
DR MGD: MGI:1321119; Stk13.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR022290; Ser_thr_kinase.
DR InterPro: IPR01245; Tyr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00223; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 16 266 PROTEIN KINASE.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT CONFLICT 74 74 R -> P (IN REF. 2).

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EMBL: AF054620; AAC25954.1;
DR EMBL: AF195272; AAF25838.1;
DR HSP: Q63450; A006
DR MGD: MGI:1321119; Stk13.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR022290; Ser_thr_kinase.
DR InterPro: IPR01245; Tyr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00223; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 16 266 PROTEIN KINASE.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT CONFLICT 74 74 R -> P (IN REF. 2).

```
SQ SEQUENCE 282 AA; 32907 MW; 7CBA8E4984E7853 CRC64;
Query Match 79.6%; Score 39; DB 1; Length 282;
Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 1 LGPPFFETS 9
DB 207 VGKPPFFET 215

RESULT 8
ST6L_XENLA STANDARD; PRT; 408 AA.
ID ST6L_XENLA
AC Q91820;
DT 28-FEB-2003 (Rel. 41, Created);
DI 28-FEB-2003 (Rel. 41, Last sequence update);
DE 28-FEB-2003 (Rel. 41, Last annotation update);
DE Serine/threonine protein kinase Eg2 (EC 2.7.1.37) (p46Eg265).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Egg;
RA MEDLINE=98122845; PubMed=9454730;
RA Roghi C., Giet R., Uzbekov R., Morin N., Chartrain I., Le Guellec R.,
RA Couturier A., Doree M., Philippe M., Prigent C.;
RT "The Xenopus protein kinase p62g associates with the centrosome in a
RT cell cycle-dependent manner, binds to the spindle microtubules and is
RT involved in bipolar mitotic spindle assembly.";
RL J. Cell Sci. 111:557-572(1998).
CC -!- FUNCTION: Associates with the centrosome in a cell-cycle dependent
CC manner and invades the microtubules at the poles of the spindle
CC during mitosis suggesting that it may be involved in the correct
CC formation of bipolar mitotic spindles.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis
CC especially from prophase through anaphase. Partially colocalised
CC with gamma tubulin in the centrosome, from S to M phase.
CC -!- TISSUE SPECIFICITY: Highly expressed in ovary and testis.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC
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CC
CC EMBL; Z17207; CAA78915.1;
CC PIR; S52243; S52243.
CC HSP; P24941; IAK1.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC SMART; SM00219; TTKc; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS0108; PROTEIN_KINASE_ST; 1.
CC Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding;
CC Phosphorylation.
CC DOMAIN 140 390 PROTEIN_KINASE.
CC NP_BIND 146 154 ATP (BY SIMILARITY).
CC BINDING 169 169 ATP (BY SIMILARITY).
CC ACT_SITE 263 263 BY SIMILARITY.
CC
CC Query Match 79.6%; Score 39; DB 1; Length 408;
CC Best Local Similarity 75.0%; Pred. No. 3.6;
CC Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 1 LGPPFFET 8
DB 311 VGKPPFFET 338

RESULT 9
ST6L_XENLA STANDARD; PRT; 408 AA.
ID ST6L_XENLA
AC Q91819;
DT 28-FEB-2003 (Rel. 41, Created);
DI 28-FEB-2003 (Rel. 41, Last sequence update);
DE 28-FEB-2003 (Rel. 41, Last annotation update);
DE Serine/threonine protein kinase Eg2-like (EC 2.7.1.37) (p46XlEg22).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Egg;
RA Roghi C., Le Guellec R., Paris J., Couturier A., Philippe M.;
RT "Eg2, selected by differential screening encodes a new Xenopus protein
RT kinase family.";
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localizes to the spindle pole during mitosis
CC especially from prophase through anaphase. Partially colocalised
CC with gamma tubulin in the centrosome, from S to M phase (By
CC similarity).
CC -!- PTM: Phosphorylated (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC
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CC
CC EMBL; Z17206; CAA78914.1; ALT_INIT.
CC HSP; P24941; IAK1.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_kinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC SMART; SM00219; TTKc; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS0108; PROTEIN_KINASE_ST; 1.
CC Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding;
CC Phosphorylation.
CC DOMAIN 140 390 PROTEIN_KINASE.
CC NP_BIND 146 154 ATP (BY SIMILARITY).
CC BINDING 169 169 ATP (BY SIMILARITY).
CC ACT_SITE 263 263 BY SIMILARITY.
CC
CC Query Match 79.6%; Score 39; DB 1; Length 408;
CC Best Local Similarity 75.0%; Pred. No. 3.6;
CC Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 1 LGPPFFET 8
DB 311 VGKPPFFET 338
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DB 331 VGKPPFET 338
RESULT 13
PC POLO DROME STANDARD: PRT: 576 AA.
AC P52304; Q9VW32;
DT 11-OCT-1996 (Rel. 34, Created);
DT 16-OCT-2001 (Rel. 40, Last sequence update);
DE 16-OCT-2001 (Rel. 40, Last annotation update);
DE Protein kinase polo [EC 2.7.1.1];
GN POLO OR CG12306;
OS Drosophila melanogaster (Fruit fly);
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Eterysteta;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Ephydroidea; Drosophilidae; Drosophila;
OX NCBI_TaxID=7227;
RN [1];
RN SEQUENCE FROM N.A.;
RC STRAIN=Cantor-S;
RX MEDLINE=92084390; PubMed=1660828;
RA J. Amarares S., Moreira A., Tavares A., Girdham C., Spruce B.A.,
RA Gonzalez C., Karsch R.E., Glover D.M., Sunkel C.E.;
RT "Polo encodes a protein kinase homolog required for mitosis in
RT Drosophila.";
RL Genes Dev. 5:2163-2165 (1991);
RN [2];
RN SEQUENCE FROM N.A.;
RC STRAIN=Berkley;
RX MEDLINE=20196036; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaralides F.G., Scherz S.E., Li P.W., Hoskins A.A., Galle R.F.,
RA Burton R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman G.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazer V.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbavani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Baylarkregu L., Beasley B.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokva S., Botchan M.R., Bouck J.J., Brockstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadley E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davison L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann M.,
RA Fodler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorell C.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.B., Houch J.,
RA Hostin D., Houston K.A., Howland T., Wei M.H., Hwang S.,
RA Jalali M., Kalush F., Karpen G.H., Keane J., Kesterson D.A., Ketchum K.A.,
RA Kimrei B.B., Kodira C.D., Kraft M., Krawitz S., Kuhl D., Lai Z.,
RA Lasko P., Lee Y., Levitsky A.A., Li C.H., Lin Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Nodary C., Norris C., Voshrefi A.,
RA Mount S.M., Xoy M., Murphy B., Murphy D., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet C.M.,
RA Parazolo M., Pittman G.S., Pan S., Rollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Schroeder F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svyrkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000);
CC -!- FUNCTION: MAY PLAY A ROLE IN REGULATING BOTH NUCLEAR AND
CC CYTOPLASMIC ASPECTS OF THE MITOTIC CYCLE.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: LARVAL DISCS. BRAIN AND TESTIS.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

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CC CDC5/POLO SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 POLO box domains.
 CC
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 CC
 CC EMBL; X63361; CAA44963.1; .
 CC EMBL; A5003514; AAF49036.1; .
 CC PIR; S22127; S22127.
 CC HSP; Q63450; IAO6.
 CC FlyBase; FBgn3003124; polo.
 CC GO; GO:0005813; C:centrosome; IDA.
 CC GO; GO:0005819; C:spindle; IDA.
 CC GO; GO:004674; F:protein serine/threonine kinase activity; IDA.
 CC GO; GO:0007140; P:meiotic cell cycle; IMP.
 CC GO; GO:0007067; P:mitosis; IMP.
 CC InterPro; IPR000959; POLO_box.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR002290; Ser_thr_kinase.
 CC Pfam; PF00069; pkinase; 1.
 CC Pfam; PF00659; POLO_box; 2.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC SMART; SMC0220; S_TKC; 1.
 CC PROSITE; PS00078; POLO_BOX; 2.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 CC PROSITE; PS00117; PROTEIN_KINASE_DOM; 1.
 CC PROSITE; PS00138; PROTEIN_KINASE_ST; 1.
 CC Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
 CC DOMAIN 25 277 PROTEIN KINASE.
 CC NP_BIND 31 39 ATP (BY SIMILARITY).
 CC BINDING 54 54 ATP (BY SIMILARITY).
 CC ACT_SITE 148 148 BY SIMILARITY.
 CC DOMAIN 398 461 POLO_BOX 1.
 CC DOMAIN 496 564 POLO_BOX 2.
 CC CONFLICT 187 197 P -> A (IN REF. 1).
 CC SEQUENCE 576 AA; 66973 MW; 5022B9AC0E888FAD CRC64;
 CC
 CC Query Match 77.6%; Score 38; DB 1; Length 576;
 CC Best Local Similarity 75.0%; Pred. No. 8.1;
 CC Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1:IGKPPFET 8
 CC Db 218 VGQPPFET 225
 CC
 CC RESULT 11
 CC NHAB_PSECL STANDARD; PRT: 220 AA.
 CC ID NHAB_PSECL STANDARD; PRT: 220 AA.
 CC AC P27763;
 CC DT 01-AUG-1992 (Rel. 23, Created)
 CC DT 01-AUG-1992 (Rel. 23, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Nitrate hydratase subunit beta [EC 4.2.1.84] (Nitrilase) (NHase).
 CC GN NTHB.
 CC OS Pseudomonas chlororaphis (Pseudomonas aureofaciens).
 CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 CC OC Pseudomonadaceae; Pseudomonas.
 CC OX NCBI_TaxID=333;
 CC [1]
 CC RNC SEQUENCE FROM N.A., AND SEQUENCE OF 1-23 AND 158-170.
 CC RC STRAIN=B23;
 CC RX MEDLINE=91193202; PubMed=20135568;
 CC RA Nishiyama M., Horinouchi S., Kobayashi M., Nagasawa T., Yamada H.,
 CC RA Beppu T.;
 CC RT "Cloning and characterization of genes responsible for metabolism of
 CC RT nitrile compounds from Pseudomonas chlororaphis B23";
 CC RL J. Bacteriol. 173:2465-2472 (1991).

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EMBL: AF136984; AAF08367.1; InterPro: IPR000959; PLOQ box.
InterPro: IPR000719; Prot_kinase.
InterPro: IPR002290; Ser_thr_pkinase.
Pfam: PF00069; pkinase; 1.
Pfam: PF00653; PLOQ_box; 2.
ProDom: PD060001; Prot_kinase; 1.
SMART: SMO022C; S_TKc; 1.
PROSITE: PS50378; PLOQ_BOX; 2.
PROSITE: PS06107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS50321; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
Transfaser: Serine/threonine-protein kinase; ATP-binding; Repeat; Phosphorylation.
KW NON_TER 1 1
FT DOMAIN 31 283 PROTEIN KINASE
FT NP_BIND 37 45 ATP (BY SIMILARITY).
FT BINDING 60 60 ATP (BY SIMILARITY).
FT ACT_SITE 154 154 BY SIMILARITY.
FT DOMAIN 440 503 PLOQ_BOX 1.
FT DOMAIN 537 607 PLOQ_BOX 2.
FT NON_TER 615 615
SQ SEQUENCE 615 AA; 68800 MW; 06584C229B5D71BD CRC64;

Query Match 73.5% Score 36; DB 1; Length 615;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 GRPPFETS 9
| | | | | :
DB 225 GSPPPEA 232

RESULT 13
CNK MOUSE
ID CNK_MOUSE STANDARD; PRT; 631 AA.
AC Q60806; Q60822; Q9R309;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 4.; Last annotation update)
DE Cytokine-inducible serine/threonine-protein kinase (EC 2.7.1.37) [PGF-inducible kinase].
DE CNK OR FNK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN:NH Swiss.
RX MEDLINE=95247749; PubMed=7730342;
RA Donohue P.J., Alberts G.F., Guo Y., Winkles J.A.;
RI "Identification by targeted differential display of an immediate early
RL gene encoding a putative serine/threonine kinase.";
RL J. Biol. Chem. 270:10351-10357(1995).
RN [2]
RP SEQUENCE OF 333-437 FROM N.A. (ISOFORM 2).
RC STRAIN:NH Sw:ss;
RA Kauselmann G., Weiler M., Kuhl D.;
RL Submitted (Nov-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RN FUNCTION, AND PHOSPHORYLATION.
RX MEDLINE=98343954; PubMed=9677325;
RA Chase D., Feng Y., Hanstew B., Winkles J.A., Longo D.L., Ferris D.K.;
RI "Expression and phosphorylation of fibroblast-growth-factor-inducible
RL protein kinase."
RN [4]

```

RT kinase (Pnk) during cell-cycle progression." ;
RL Biochem. J. 333:655-660(1998);
CC -!- FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN REGULATING M
CC PHASE FUNCTIONS DURING THE CELL CYCLE. MAY ALSO BE PART OF THE
CC SIGNALING NETWORK CONTROLLING CELLULAR ADHESION. IN VITRO, IS ABLE
CC TO PHOSPHORYLATE CDC25C AND CASEIN (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
CC -!- SUBUNIT: BINDS TO THE CALCIUM/INTEGRIN-BINDING PROTEIN (CIB). THIS
CC INTERACTION PROBABLY OCCURS VIA THE POLO-BOX DOMAIN (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Membrane-associated (By similarity).
CC ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC Name=2;
CC IsoId=Q60806-1; Sequence=Displayed;
CC IsoId=Q60806-2; Sequence=VSP_004927;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN SKIN.
CC -!- PTM: PHOSPHORYLATED AS CELLS ENTER MITOSIS AND DEPHOSPHORYLATED AS
CC CELLS EXIT MITOSIS.
CC ! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC
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CC
DR EMBL: U21492; AAC52191.1;
DR EMBL: U22434; AAC52192.1;
DR EMBL: AF136586; AAF08369.1;
DR EMBL: AF27286; A57286.
DR MISC: XGI109604; Crk.
DR InterPro: IPR000359; POLO box.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR Pfam: PF00069; Kinase; 1
DR Pfam: PF00859; POLO_box; 2.
DR ProDom: PDC00001; Prot_Kinase; 1.
DR SMART: SM0220; S_TK; 1.
DR PROSITE: PS00078; POLO_BOX; 2.
DR PROSITE: PS01077; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS02111; PROTEIN_KINASE_DFG; 1.
DR PROSITE: PS01094; PROTEIN_KINASE_ST; 1.
DR Transferase: Serine/threonine protein kinase. All binding. Repeat:
KW Phosphorylation; Alternative splicing.
FT DOMAIN 53 315 PROTEIN KINASE
FT NP_BIND 63 77 ATP (BY SIMILARITY)
FT BINDING 92 92 ATP (BY SIMILARITY)
FT ACT_SITE 186 186 BY SIMILARITY.
FT DOMAIN 455 518 POLO_BOX_1
FT DOMAIN 552 622 POLO_BOX_2
FT VARSPCIC 373 373 L -> SVSCGKSTSGHEVRL (in isoform 2).
FT FTID=VSP_004927.
FT CONFLICT 386 386 1 -> V (IN REF. 2).
SQ SEQUENCE 631 AA; 700.2 MW; 2285741870CB1D2 C9764;
Query Match 73.5% Score 67 DB 1; Length 631;
Best Local Similarity 75.0% Pred. MS 22;
Matches 6; Conservative 1; Mismatches 1; Gaps 0;
QY 2 GAPPFETS 9
DB 257 GAPPFETA 264
RESULT 14
ONE HUMAN
ID ONE HUMAN STANDARD; PRT; 346 AA

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AC Q9H4B4; Q15767;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytokine-inducible serine/threonine-protein kinase (EC 2.7.1.37) (PGF-
DE inducible kinase) (Proliferation-related kinase).
GN CNK OR FNK OR PRK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=20493044; PubMed=1039900;
RA Holtrich U., Wolf G., Yuan J., Bereiter-Hahn J., Karn T., Weiler M.,
RA Kauselmann G., Rehli M., Andreesen R., Kaufmann M., Kuhl D.,
RA Strebhardt K.;
RT "Adhesion induced expression of the serine/threonine kinase Pnk in
RT human macrophages." ;
RL Oncogene 19:4832-4839(2000).
RN [2]
RP SEQUENCE OF 28-646 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96325053; PubMed=9702627;
RA Li B., Ouyang B., Pan H., Reissmann P.T., Slamon D.J., Arcaci R.,
RA Lu L., Dai W.;
RT "Prk, a cytokine-inducible human protein serine/threonine kinase whose
RT expression appears to be down-regulated in lung carcinomas." ;
RL J. Biol. Chem. 271:19402-19408(1996).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=98019242; PubMed=935331;
RA Ouyang B., Pan H., Li J., Stambrook P., Li B., Dai W.;
RT "Human Prk is a conserved protein serine/threonine kinase involved in
RT regulating M phase functions." ;
RL J. Biol. Chem. 272:28646-28651(1997).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=20027391; PubMed=10557092;
RA Ouyang B., Li W., Pan H., Meadows J., Hoffmann I., Dai W.;
RT "The physical association and phosphorylation of Cdc25C protein
RT phosphatase by Prk." ;
RL Oncogene 18:6329-6336(1999).
CC -!- FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN REGULATING M
CC PHASE FUNCTIONS DURING THE CELL CYCLE. MAY ALSO BE PART OF THE
CC SIGNALING NETWORK CONTROLLING CELLULAR ADHESION. IN VITRO, IS ABLE
CC TO PHOSPHORYLATE CDC25C AND CASEIN.
CC -!- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
CC -!- SUBUNIT: BINDS TO THE CALCIUM/INTEGRIN-BINDING PROTEIN (CIB). THIS
CC INTERACTION PROBABLY OCCURS VIA THE POLO-BOX DOMAIN.
CC -!- SUBCELLULAR LOCATION: Membrane-associated.
CC -!- TISSUE SPECIFICITY: TRANSCRIPTS ARE HIGHLY DETECTED IN PLACENTA,
CC LUNG, FOLLOWED BY SKELETAL MUSCLE, HEART, PANCREAS, OVARIES AND
CC KIDNEY AND WEAKLY DETECTED IN LIVER AND BRAIN. MAY HAVE A SHORT
CC HALF-LIFE. IN CELLS OF HEMATOPOIETIC ORIGIN, STRONGLY AND
CC EXCLUSIVELY DETECTED IN TERMINALLY DIFFERENTIATED MACROPHAGES.
CC TRANSCRIPTS EXPRESSION APPEARS TO BE DOWN-REGULATED IN PRIMARY
CC LUNG TUMOR.
CC -!- INDUCTION: CYTOKINE AND CELLULAR ADHESION TRIGGER FNK INDUCTION.
CC -!- PTM: PHOSPHORYLATED AS CELLS ENTER MITOSIS AND DEPHOSPHORYLATED AS
CC CELLS EXIT MITOSIS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC -!- SIMILARITY: Contains 2 POLO box domains.
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CC EMBL: A2293866; CAC10659.1; ACT_INIT.
CC EMBL: J66998; AAC50637.1; ACT_INIT.
CC Genbank: HGNC:2154; CNK.
CC GR: Q9H4B4.
CC YIM: 602913.
CC GO: GO:0004674; P:protein serine/threonine kinase activity; TAS.
CC GO: GO:0004688; P:protein amino acid phosphorylation; TAS.
CC GO: GO:0005374; P:regulation of cell cycle; TAS.
CC InterPro: IPR000959; POLO_BOX.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_Thr_kinase.
CC Pfam: PF00069; pkinase.
CC Pfam: PF00659; POLO_BOX; 2.
CC ProDom: PDC00001; Prot_kinase.
CC SMART: SMC0220; S_TKC; 1.
CC PROSITE: PS50078; POLO_BOX; 2.
CC PROSITE: PS50107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC TRANSFERASE; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW Phosphorylation.
FT DOMAIN 62 314 PROTEIN_KINASE.
FT NP_BIND 68 76 ATP (BY SIMILARITY).
FT BINDING 91 91 ATP (BY SIMILARITY).
FT ACT_SITE 185 185 BY SIMILARITY.
FT DOMAIN 470 537 POLO_BOX_1.
FT DOMAIN 567 637 POLO_BOX_2.
FT CONFLICT 99 99 V -> A (IN REF. 2).
FT CONFLICT 353 353 V -> G (IN REF. 2).
FT CONFLICT 419 419 H -> D (IN REF. 2).
FT CONFLICT 464 470 ESEWVG -> VSKWVDY (IN REF. 2).
FT CONFLICT 522 522 R -> P (IN REF. 2).
SQ SEQUENCE 646 AA; 71789 MW; C201470DFCBA9B4 CRC64;

Query Match 73.5%; Score 16; DB 1; Length 646;
Best Local Similarity 75.0%; Pred. No 23;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRPFFTS 9
DB 256 GSPFFETA 263

RESULT 16
PKNI COREF STANDARD; FRT; 160 AA
AC GRPFI5;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable serine/threonine protein kinase (G30643 (Ref. 2, 3, 1, 37)).
GN CE2033.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteriales;
CC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
CX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11159;
RA Kawarabayashi Y., Yamazaki J., Hiro Y., Kikuchi H., Nakamura Y.,
RA Ikeg K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RL The entire genomic sequence of Corynebacterium efficiens YS-314."
RL Submitted (MAY-2002) to the EMBL/GenBank/CCRC databases.
CC CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC SIMILARITY: Contains 3 PASTA domains.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: APO5214; BAC16843.1; -.
CC InterPro: IPR005543; PASTA.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_Thr_kinase.
CC InterPro: IPR001445; Tyr_kinase.
CC Pfam: PF03793; PASTA; 3.
CC Pfam: PF00069; pkinase; 1.
CC ProDom: PDC00001; Prot_kinase; 1.
CC SMART: SM00740; PASTA; 3.
CC SMART: SM00223; S_TKC; 1.
CC SMART: SM00219; TyrcK; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW ATP-binding; Repeat; Complete proteome.
FT DOMAIN 9 278 PROTEIN_KINASE.
FT DOMAIN 377 443 PASTA_1.
FT DOMAIN 444 512 PASTA_2.
FT DOMAIN 513 577 PASTA_3.
FT NP_BIND 15 23 ATP (BY SIMILARITY).
FT BINDING 38 38 ATP (BY SIMILARITY).
FT ACT_SITE 136 136 BY SIMILARITY.
SQ SEQUENCE 660 AA; 69646 MW; D33D797EB02D44B1 CRC64;

Query Match 73.5%; Score 36; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPFFE 7
DB 210 GRPFFE 215

RESULT 16
HRG_BOVIN STANDARD; FRT; 396 AA.
ID HRG_BOVIN
AC P33433;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histidine-rich glycoprotein (Histidine-proline rich glycoprotein)
DE (HRG); (Fragments).
GN HRG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
CX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=93351678; PubMed=8348977;
RA Soerensen C.B., Krogh-Pedersen H., Petersen T.E.;
RT Determination of the disulphide bridge arrangement of bovine
RT histidine-rich glycoprotein."
RL FEBS Lett. 328:285-290(1993).
CC FUNCTION: THE PHYSIOLOGICAL FUNCTION IS NOT YET KNOWN. IT BINDS
CC HEME, DYES AND DIVALENT METAL IONS. IT CAN INHIBIT ROSETTE
CC FORMATION AND IS KNOWN TO INTERACT WITH HEPARIN, THROMBOSPONDIN,
CC AND THE LYSINE-BINDING SITE OF PLASMINOGEN. ON THE BASIS OF ITS
CC HOMOLOGUE WITH HMW KININOGEN, THE HIS-RICH REGION OF THIS PROTEIN
CC MAY MEDIATE THE CONTACT ACTIVATION PHASE OF INTRINSIC BLOOD
CC COAGULATION CASCADE.
CC SUBCELLULAR LOCATION: Secreted.
CC TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
CC DOMAIN: IN ADDITION TO HAVING A HIGH HIS AND PRO CONTENT, THIS
CC PROTEIN HAS MANY INTERNAL REPEATS. 12 TANDEM REPEATITIONS OF A 5-
CC RESIDUE SEQUENCE (GHPH, CONSENSUS) FORM A HISTIDINE-RICH REGION.
CC SIMILARITY: Contains 2 cystatin-like domains.

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Glycoprotein; Heparin-binding; Repeat.
 KW DOMAIN 1 102 CYSTATIN-LIKE 1.
 FT DOMAIN 103 169 CYSTATIN-LIKE 2.
 FT DOMAIN 191 238 PRO-RICH.
 FT DOMAIN 243 368 PRO/HIS-RICH.
 FT DISULFID 7 375
 FT DISULFID 56 67
 FT DISULFID 77 92
 FT DISULFID 123 297
 FT DISULFID 137 160
 FT DISULFID 212 242
 FT NON_CONS 52 53
 FT CARBOHYD 70 70
 FT NON_CONS 71 72
 FT NON_CONS 78 79
 FT CARBOHYD 91 94
 FT NON_CONS 103 104
 FT CARBOHYD 122 122
 FT NON_CONS 163 164
 FT CARBOHYD 220 220
 FT NON_CONS 263 264
 FT NON_CONS 303 304
 FT VARIANT 86 86
 FT VARIANT 309 309
 FT VARIANT 322 322
 SC SEQUENCE 396 AA; 44470 MW; 128AE23459DE6FC CRC64;
 Query Match 71.4%; Score 35; DB 1; Length 396;
 Best Local Similarity 75.0%; Pred. No. 21;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 CY 2 GRPFKPS 9
 DE 189 GRPFKPS 196
 RESULT 17
 STK6 HUMAN STANDARD; PRT; 403 AA.
 AC G14965; On0445; 075873; Q9BCD6; Q9JFJ5;
 DT 29-FEB-2003 (Rel. 41, Created)
 DT 15-FEB-2003 (Rel. 42, Last sequence update)
 DS Serine/threonine kinase 6 (EC 2.7.1.37) (Serine/threonine kinase 15)
 DE (Aurora-A) (Breast-tumor-amplifying kinase)
 GN STK6 OR STK15 OR AIK OR ARK1 (P. ABRA OR BTAK)
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catartida; Homalida; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Blood;
 RC MEDLINE=97298283; PubMed=91513211;
 RA Kimura Y., Korani S., Hattori T., Sugi K., Yoshioke T., Tachikoro K.,
 RA Okano Y.,
 RA "Cell cycle-dependent expression and spindle pole localization of a
 RT novel novel protein kinase, Aik, related to Aurora of Drosophila and
 RT yeast Ipi1.";
 RL J. Biol. Chem. 272:13766-13771(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98183439; PubMed=9514926;
 RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
 RA Gilbert D.J., Jenkins N.A., Cepelland N.G., Yagita H., Okumura K.,
 RC "cDNA cloning, expression, subcellular localization, and chromosomal
 RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)
 RT 1 and 2.";
 RL Biochem. Biophys. Res. Commun. 244:285-292(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 PC TISSUE=Breast;

RX MEDLINE=98442657; PubMed=9771714;
 RA Zhou H., Kuang J., Zhong L., Kuo W.-L., Gray J.W., Sahin A.,
 RA Brinkley B.R., Sen S.,
 RT "Tumour amplified kinase STK15/BTAK induces centrosome amplification,
 RT aneuploidy and transformation.";
 RL Nat. Genet. 20:199-193(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Wang L., Thibodeau S.,
 RT "Mutational analysis of the STK15 gene in human tumors.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.B., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,
 RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.T., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharialho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.B., McConachie L.J., McKay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin R., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.,
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Cervix, Colon, Kidney, and Muscle;
 RC MEDLINE=2238257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., USCIN T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Yadan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP CELL-CYCLE REGULATION.
 RX MEDLINE=21895866; PubMed=11790771;
 RA Tanaka M., Ueda A., Kanamori H., Ideguchi H., Yang J., Kitajima S.,
 RA Ishigatsubo Y.,
 RT "Cell-cycle-dependent regulation of human aurora A transcription is
 RT mediated by periodic repression of E4TF1.";
 RL J. Biol. Chem. 277:10719-10726(2002).

RN [8]
 RP REVIEW.
 RX MEDLINE=21306577; PubMed=11413462;
 RA Nigg E.A.;
 RT "Mitotic kinases as regulators of cell division and its checkpoints.";
 RJ Nat. Rev. Mol. Cell Biol. 2:121-12(2001).
 CC -!- FUNCTION: May play a role in cell cycle regulation during anaphase
 CC and/or telophase, in relation to the function of the
 CC centrosome/spindle pole region during chromosome segregation.
 CC May be involved in microtubule formation and/or stabilization. May
 CC play a key role during tumor development and progression.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated protein.
 CC -!- SUBCELLULAR LOCATION: Localizes on centrosomes in interphase cells
 CC and at each spindle pole in mitosis.
 CC -!- TISSUE SPECIFICITY: Highly expressed in testis and weakly in
 CC skeletal muscle, thymus and spleen. Also highly expressed in
 CC colon, ovarian, prostate, neuroblastoma, breast and cervical
 CC cancer cell lines. Expression is cell-cycle regulated, low in
 CC G1/S, accumulates during G2/M, and decreases rapidly after.
 CC -!- PTM: phosphorylated.
 CC -!- DISEASE: Defects in STK6 are responsible for numerical centrosome
 CC aberrations including aneuploidy.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC AURORA SUBFAMILY.
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
 CC in positions 105, 125, 129, 235 and 241.
 CC -!- CAUTION: Although authors have considered STK6 and STK15 as two
 CC different proteins, it is clear that they are the same protein.
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 CC
 DR EMBL: D84212; BAA23592.1; ALT FRAM.
 DR EMBL: AF088551; AAC2708.1; .
 DR EMBL: AF011467; AAC23448.1; .
 DR EMBL: AF011468; AAC6392.1; .
 DR EMBL: AF195947; AAF29508.1; .
 DR EMBL: AF195942; AAF29508.1; JOINED.
 DR EMBL: AF195943; AAF29508.1; JOINED.
 DR EMBL: AF195944; AAF29508.1; JOINED.
 DR EMBL: AF195945; AAF29508.1; JOINED.
 DR EMBL: AF195946; AAF29508.1; JOINED.
 DR EMBL: AL21214; CAC127.1; .
 DR EMBL: BC001280; AAC1280.1; .
 DR EMBL: BC002499; AAC32499.1; .
 DR EMBL: BC006423; AAC06423.1; .
 DR EMBL: BC027464; AAC27464.1; .
 DR EMBL: C14945; .
 DR MIM: 602487; .
 DR MIM: 603572; .
 DR HSP: P24941; IBUH.
 DR Genew: HGNC:11409; STK6.
 DR Genew: HGNC:11391; STK15.
 DR GO: GO:003634; C:nucleus; TAS.
 DR GO: GO:003587; C:spindle; TAS.
 DR GO: GO:0007657; P:mitosis; TAS.
 DR GO: GO:0036468; P:protein amino acid phosphorylation; TAS.
 DR InterPro: IPR003719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD00001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TyrKc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE: PS00211; PROTEIN KINASE TCM; 1.
 KW Cell cycle; transferase; Serine/threonine-protein kinase; ATP-binding.

KW Phosphorylation. 383
 FT DOMAIN 133 PROTEIN KINASE.
 FT NP_BIND 139 ATP (BY SIMILARITY).
 FT BINDING 162 ATP (BY SIMILARITY).
 FT ACT_SITE 256 BY SIMILARITY.
 FT CONFLICT 31 F -> I (IN REF. 3).
 FT CONFLICT 57 V -> I (IN REF. 2).
 SQ SEQUENCE 403 AA; 45809 MW; 125F3594834CD157 CRC64;
 Query Match 71.4%; Score 35; DB 1; Length 403;
 Best Local Similarity 55.6%; Pred. No. 21;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LGRPPFETS 9
 DB 324 VGKPPFEAN 332
 RESULT 18
 TF65 CHICK STANDARD; PRT: 558 AA.
 ID P98152;
 DT 01-OCT-1996 [Rel. 34, Created]
 DT 01-OCT-1996 [Rel. 34, Last sequence update]
 DT 28-FEB-2003 [Rel. 41, Last annotation update]
 DE Transcription factor p65 (Nuclear factor NF-kappa-B p65 subunit).
 GN RELA.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN [1];_TaxID=9031;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Sp.teen;
 RX MEDLINE=94040817; PubMed=7916720;
 RA Ikeda T., Honjo K., Hirota Y., Onodera T.;
 RT "Isolation of the chicken NF-kappa B p65 subunit-encoding cDNA and
 RT characterization of its products";
 RL Gene 133:237-242(1993).
 CC -!- FUNCTION: P65 IS A SUBUNIT OF THE NUCLEAR FACTOR KAPPA-B, A SECOND
 CC MESSENGER, WHICH ACTIVATES THE TRANSCRIPTION OF A NUMBER OF GENES
 CC IN MULTIPLE TISSUES. THE INHIBITORY EFFECT OF I-KAPPA-B UPON
 CC NF-KAPPA-B IN THE CYTOPLASM IS EXERTED PRIMARILY THROUGH THE
 CC INTERACTION WITH P65. P65 SHOWS A WEAK DNA-BINDING SITE WHICH
 CC COULD CONTRIBUTE DIRECTLY TO DNA BINDING IN THE NF-KAPPA-B
 CC COMPLEX.
 CC -!- SUBUNIT: ACTIVE NF-KAPPA-B IS A HETERODIMER OF AN ABOUT 50 kDa
 CC DNA-BINDING SUBUNIT AND THE WEAK DNA-BINDING SUBUNIT P65. TWO
 CC HETERODIMERS MIGHT FORM A LABILE TETRAMER.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR, BUT ALSO FOUND IN THE CYTOPLASM
 CC IN AN INACTIVE FORM COMPLEXED TO AN INHIBITOR (I-KAPPA-B).
 CC -!- TISSUE SPECIFICITY: SPLEEN; LOWER LEVEL IN BRAIN.
 CC -!- SIMILARITY: BELONGS TO THE REL/DORSAL FAMILY.
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 CC
 CC EMBL: D13721; BAA02874.1; .
 DR PIR: JC2004; JC2004.
 DR HSSP: Q04207; 1IKN.
 DR InterPro: IPR002909; IPT_TIG
 DR InterPro: IPR000451; NF_Rel_dor_fam.
 DR Pfam: PF00554; RHD; 1.
 DR Pfam: PF01833; TIG; 1.
 DR PRINTS: PR00057; NFkBNSCPCT.
 DR SMART: SM00429; IPT; 1.
 DR PROSITE: PS01204; REL_1; 1.

DR PROSITE: PS0254; REL 2; 1.
 KW DNA-binding; Transcription regulation; Activator; Nuclear protein;
 FT Phosphorylation.
 FT DOMAIN 25 312 REL-LIKE (RHD).
 FT DOMAIN 306 329 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD RES 281 281 PHOSPHORYLATION (BY PKA) (POTENTIAL).
 SQ SEQUENCE 558 AA; 60071 MW; 0528D159A4D47B36 CRC64;

Query Match 71.4%; Score 35; DB 1; Length 558;
 Best Local Similarity 75.0%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRRPPFT 8
 DB 429 LGRRPPFT 436

RESULT 19
 DYRB MOUSE
 ID DYRB MOUSE STANDARD; PRT; 589 AA.
 AC Q92188;
 DT 16-OCT-2001 (Rel. 40; Created).
 DT 16-OCT-2001 (Rel. 40; Last sequence update).
 DE Dual specificity tyrosine-phosphorylation regulated kinase 1B
 DE (EC 2.7.1.1).
 GN DYRK1B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1].
 RP SEQUENCE FROM N.A.
 RC STRAIN:NMRL; TISSUE:Testis;
 RX MEDLINE=99119336; PubMed=9918863;
 RA Leder S., Weber Y., Altafaj X., Estivill X., Joost H.-G., Becker W.;
 RT "Cloning and characterization of DYRK1B, a novel member of the DYRK
 family of protein kinases";
 RL Biochem. Biophys. Res. Commun. 254:474-479 (1999).
 CC -1- PTM: PHOSPHORYLATED BY MAP KINASE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MNB/DYRK SUBFAMILY.

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DR EMSL; Y18280; CAA77101.2;
 DR HSP; P24941; ICKP.
 DR MGD; MGI:1330302; Dyk1b.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR002230; Ser_Thr_Kinase.
 DR Pfam; PF00669; pkinase; 1.
 DR ProDom; PD000001; Prot_Kinase; 1.
 DR SMART; SM0220; S_TKc; 1.
 DR PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00211; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; Tyrosine protein kinase;
 KW ATP-binding; Nuclear protein; Phosphorylation.
 FT DOMAIN 69 86 BIPARTITE NUCLEAR LOCALIZATION SIGNAL
 (POTENTIAL).
 FT DOMAIN 111 391 PROTEIN KINASE
 FT NP_BIND 117 125 ATP (BY SIMILARITY).
 FT BINDING 140 140 ATP (BY SIMILARITY).
 FT ACT_SITE 239 239 POLY-PYC.
 FT DOMAIN 518 521 POLY-PYC.
 FT DOMAIN 537 544 POLY-PYC.

SQ SEQUENCE 589 AA; 64914 MW; 48B4242AD6E8401E CRC64;

Query Match 71.4%; Score 35; DB 1; Length 589;
 Best Local Similarity 77.8%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGRRPPFTS 9
 DB 509 LGRRPPFTS 517

RESULT 20
 DYRB HUMAN
 ID DYRB HUMAN STANDARD; PRT; 629 AA.
 AC Q9Y463; O75258; O75788; O75789;
 DT 16-OCT-2001 (Rel. 40; Created).
 DT 16-OCT-2001 (Rel. 40; Last sequence update).
 DT 28-FEB-2003 (Rel. 41; Last annotation update).
 DE Dual-specificity tyrosine-phosphorylation regulated kinase 1B
 DE (EC 2.7.1.1) (Mirk protein kinase).
 GN DYRK1B OR Mirk.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1].
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC TISSUE=Testis;
 RX MEDLINE=99119336; PubMed=9918863;
 RA Leder S., Weber Y., Altafaj X., Estivill X., Joost H.-G., Becker W.;
 RT "Cloning and characterization of DYRK1B, a novel member of the DYRK
 family of protein kinases";
 RL Biochem. Biophys. Res. Commun. 254:474-479 (1999).
 RN [2].
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Colon carcinoma;
 RX Lee K., Deng X., Friedman E.;
 RT "Mirk protein kinase is a MAP kinase substrate";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [3].
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Sperm;
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,
 RA Burkhardt-Schulz K.J., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
 RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
 RA Liu S., Attix C., Andreise T., Frankheim M., Amico-Keller G.,
 RA Czeftel J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
 RA Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
 RA Kobayashi A., Oisen A.S., Garrano A.V.;
 RA "Sequence analysis of a 2.2 Mb region in 19q13.1 containing the RYR
 gene";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS.
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=Q9Y463-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9Y463-2; Sequence=VSP_004925;
 CC Name=3;
 CC IsoId=Q9Y463-3; Sequence=VSP_004926;
 CC -1- TISSUE SPECIFICITY: HIGH LEVELS IN TESTIS AND SKELETAL MUSCLE, LOW
 LEVELS IN BRAIN.
 CC -1- PTM: PHOSPHORYLATED BY MAP KINASE.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MNB/DYRK SUBFAMILY.

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RN SEQUENCE FROM N.A.
 RP TISSUE: Liver, and Spleen;
 RC MEDLINE=99077433; PubMed=9859806;
 RA Kimura M., Matsuda Y., Yoshioaka T., Sumi N., Okano Y.;
 RT "Identification and characterization of STK12/AiK2, a human gene
 related to aurora of Drosophila and yeast IPL1";
 RL Cytogenet. Cell Genet. 82:147-152(1998).
 RV [4]
 RW SEQUENCE FROM N.A.
 RX MEDLINE=21364697; PubMed=11471245;
 RA Prigent C., Gill R., Tower M., Sansom P.;
 RT "In silico cloning of a new protein kinase, AiK2, related to
 Drosophila aurora using the new tool EST Blast";
 RL In Silico Bio. 1:123-128(1999).
 RV [5]
 RW SEQUENCE FROM N.A.
 RP Zhang Q., Yu L., Bi A.;
 RA "Cloning of a novel human gene homologous to mouse STK-1";
 RT Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RV [6]
 RW SEQUENCE FROM N.A.
 RP TISSUE: Lung, Lymph, and Muscle;
 RX MEDLINE=2238257; PubMed=12477532;
 PA Strausberg R.L., Feingold E.A., Grouse L.H., Berger L.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Sherman C.V., Schuler G.D.,
 AL-Schul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S., Wang C., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong J.,
 RA Stapleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein V.C., Usdin T.B., Toshiyuki S., Carrino P., Prange C.,
 RA Rala S.S., Lequellano N.A., Peters G.J., Abramson K.D., Mullahy S.C.,
 RA Bosak S.A., Lequellano N.A., McKernan K.J., Malek S.A., Gunaratne P.H.,
 RA Richards S., Wootley K.C., Hale S., Garcia A.M., Gay L.J., Huily S.W.,
 RA Villalón D.K., Mazny D.M., Sodergren E., Lu X., Gibbs R.A.,
 RA Farcy C., Helton E., Ketteran M., Yadan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Yadan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchran J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.N.,
 RA Sauterford V.S.N., Krzywinski M., Skalska J., Sallus D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA Human and mouse cDNA sequences";
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16689-16693(2002).
 RV [7]
 RW REVIEW
 RA MEDLINE=21304497; PubMed=1141462;
 RA Nigg E.A.;
 RT "Mitotic Kinases as regulators of cell division and its checkpoints.";
 RL Nat. Rev. Mol. Cell Biol. 2:21-32(2001).
 CC -1- FUNCTION: May be directly involved in regulating the cleavage of
 polar spindle microtubules and is a key regulator for the onset of
 cytokinesis during mitosis.
 CC -2- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -3- SUBCELLULAR LOCATION: Localized to the midzone of central spindle
 in late anaphase and concentrated into the midbody in telophase
 and cytokinesis. Colocalized with gamma tubulin in the mid-body.
 CC -4- TISSUE SPECIFICITY: High level expression seen in the thymus. It
 is also expressed in the spleen, lung, testis, colon, placenta and
 fetal liver. Expressed during S and G2/M phase and expression is
 upregulated in cancer cells during M phase.
 CC -5- DISEASE: Disruptive regulation of expression is a possible
 mechanism of the perturbation of chromosomal integrity in cancer
 cells through its dominant-negative effect on cytokinesis.
 CC -6- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC AURORA SUBFAMILY.
 CC
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 CC -----
 DR EMBL: AF008552; AAC12709.1;
 DR EMBL: AB011450; BAA32136.1;
 DR EMBL: AB011446; BAA82709.1;
 DR EMBL: AF004022; AAB65786.1;
 DR EMBL: AF015254; AAC98891.1;
 DR EMBL: BC000442; AAH00442.1;
 DR EMBL: BC009751; AAH09751.1;
 DR EMBL: BC033300; AAH13300.1;
 DR HSSP: Q63450; IAO6.
 DR Genew: HGNC:11390; STK12.
 DR GK: Q96GD4;
 DR MIM: 604970;
 DR InterPro: IPR002032; N6_Mtase.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; pkinase_1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TyKc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
 KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 77 327 PROTEIN KINASE.
 FT NF_BIND 83 91 ATP (BY SIMILARITY).
 FT BINDING 106 106 ATP (BY SIMILARITY).
 FT ACT_SITE 200 200 BY SIMILARITY.
 FT CONFLICT 14 15 RQ -> DK (IN REF. 5).
 FT CONFLICT 70 70 E -> RR (IN REF. 6; AAH13300).
 FT CONFLICT 161 161 E -> M (IN REF. 4 AND 5).
 FT CONFLICT 167 169 QKS -> HKT (IN REF. 4).
 FT CONFLICT 179 180 T -> TVRR (IN REF. 4).
 FT CONFLICT 180 183 I -> VRVV (IN REF. 5).
 FT CONFLICT 226 226 P -> T (IN REF. 3).
 FT CONFLICT 249 250 MH -> ID (IN REF. 3).
 FT CONFLICT 271 271 MISSING (IN REF. 3).
 FT CONFLICT 298 298 T -> M (IN REF. 6; AAH09751/AAH13300).
 SQ SEQUENCE 344 AA; 39280 MW; 8325E3BF5A1FB170 CRC64;
 Query Match 69.4%; Score 34; DB 1; Length 344;
 Best Local Similarity 55.6%; Pred. No. 28;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LGKPPFETS 9
 DB 268 VGNPFESA 276
 RESULT 23
 ID H181 CAUCR STANDARD; PRT; 359 AA.
 AC Q9A671;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Histidinol-phosphate aminotransferase 1 (EC 2.6.1.9) (Imidazole
 acetol-phosphate transaminase 1).
 GN HSC1 OR CC223.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
 OC Caulobacteraceae; Caulobacter.
 OC NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19389 / CB15;
 RX MEDLINE=21173698; PubMed=11259647;
 RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen C., Heidelberg C.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.C., Durkin A.S., Gwinn M.L., Haft D.H.,

BA Kolonay J F, Smit J, Craven M B, Khouri H, Shetty J, Berry K, Jutterback T, Tran K, Wolf A, Vamathevan C, Ermolaeva M, White O, Salberg S L, Venter J C, Shapiro A, Fraser C M, "Complete genome sequence of *Caulobacter crescentus*," Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).

CC CATALYTIC ACTIVITY: L-histidinol phosphate + 2-oxoglutarate -> L-histidol + 2-oxopropyl phosphate + L-glutamate.

CC CCFactor: Pyridoxal phosphate. By similarity.

CC PATHWAY: Histidine biosynthesis; seventh step.

CC SIMILARITY: BELONGS TO CLASS-1: OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES. HISTIDINOL-PHOSPHATE AMINOTRANSFERASES SUBFAMILY.

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CC EMBL: AEC05893; AAX24154.1; .

CC TIGR: F87524; F87524.

CC HAMAP: MF_01023; .

CC InterPro: IPR004839; Aminotransf_2.

CC InterPro: IPR005861; Hisp_aminotransf.

CC InterPro: IPR01917; NHtransf_2.

CC Pfam: PF00155; aminotran_1.2; 1.

CC TIGRfam: TIGR0114; hisC_1.

CC PROSITE: PS00599; AA_TRANSFER_CLASS_2; FALSE NEG.

CC Histidine biosynthesis; transferase, aminotransferase.

KW Pyridoxal phosphate; Complete proteome.

KW BINDING 216 216 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

FT BINDING 216 216 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

SQ SEQUENCE 359 AA; 39261 MW; A2E9E4E0A8B6C65 CQ664;

Query Match 59.4%; Score 34; DB 1; Length 359;
Best Local Similarity 95.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RPPPTS 9
DB 242 RPPPTS 248

RESULT 24

CC FLUF BRUAH STANDARD; PRT; 81 AA

CC Q5259.

DT 30-MAY-2000 (Rel. 39, Created).

DT 30-MAY-2000 (Rel. 39, Last sequence update).

DT 16-OCT-2001 (Rel. 40, Last annotation update).

DE Flagellar M-ring protein.

GN FLUF.

OS Brucella abortus.

CC Bacteria; Proteobacteria; Alphaproteobacteria; Brucellales.

CC Brucellaceae; Brucella.

CC NCBI_TaxID=215;

CC SEQUENCE FROM N.A.

CC STRAIN:544 / Biovar 1;

CC MEDLINE=20463005; PubMed=1103703;

CC Halling S X;

CC "On the presence and organization of open reading frames of the nonpathogenic *Brucella abortus* similar to genes II, III, and IV flagellar genes and to *lecD* virulence superficially," Microb. Comp. Genomics 3:21-29 (1999).

CC FUNCTION: THE M-RING MAY BE ACTIVELY INVOLVED IN ENERGY TRANSDUCTION (BY SIMILARITY).

CC SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE FLAGELLAR CRANELLE AND CONSISTS OF FIVE RINGS (FLA-E, AND MOUNTED ON A CENTRAL ROD. THE M-RING IS INTEGRAL TO THE INNER MEMBRANE OF THE CELL AND MAY BE CONNECTED TO THE FLAGELLAR ROD

CC VIA THE S RING. THE S (SUPRAMEMBRANE RING) LIES JUST DISTAL TO THE M RING. THE L AND P RINGS LIE IN THE OUTER MEMBRANE AND THE PERIPLASMIC SPACE, RESPECTIVELY (BY SIMILARITY).

CC SUBCELLULAR LOCATION: CYTOPLASMIC, MEMBRANE-ASSOCIATED (BY SIMILARITY).

CC SIMILARITY: BELONGS TO THE FLUF FAMILY.

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CC EMBL: AF019251; AAC01568.1; .

CC InterPro: IPR000067; F_gmring_FLUF.

CC InterPro: IPR003282; Sec111OMPK.

CC InterPro: IPR006182; YscJ_FLUF.

CC Pfam: PF01514; YscJ_FLUF; 1.

CC PRINTS: PR01009; FLGMR-INGFLUF.

CC PRINTS: PR01338; TYPE3OMKPROT.

CC TIGRfam: TIGR00206; flf; 1.

KW Flagella; Membrane.

SQ SEQUENCE 540 AA; 57447 MW; 43B30916B8A32492 CRC64;

Query Match 69.4%; Score 34; DB 1; Length 540;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGPPFFET H
DB 50 LGPPSYET 57

RESULT 25

CC GCL2 MOUSE STANDARD; PRT; 830 AA.

CC Q9JH52.

DT 16-OCT-2001 (Rel. 40, Created).

DT 16-OCT-2001 (Rel. 40, Last sequence update).

DT 28-FEB-2003 (Rel. 41, Last annotation update).

DE General control of amino acid synthesis protein S-like 2 (EC 2.3.1.-) (Histone acetyltransferase GCN5) (mGCN5).

DE GCN5.2.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

CC NCBI_TaxID=10090;

CC [1]_TaxID=10090;

CC SEQUENCE FROM N.A.

CC MEDLINE=98414562; PubMed=9742083;

CC Xu W., Edmondson D.G., Roth S.Y., "Mammalian GCN5 and P/CAP acetyltransferases have homologous amino-terminal domains important for recognition of nucleosomal substrates."

CC Moir Gail, Biol. 28:5659-5669 (1998).

CC FUNCTION: Functions as a histone acetyltransferase (HAT) to promote transcriptional activation. Has significant histone acetyltransferase activity with core histones, but not with nucleosome core particles (By similarity).

CC SUBUNIT: INTERACTS WITH P300, CBP AND ADA2.

CC SUBCELLULAR LOCATION: Nuclear.

CC SIMILARITY: Contains 1 bromodomain.

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DR EMBL: AF254441; AAF70497.1; --
DR HSPF: Q92831.1; LB3; --
DR MGD: MGI:134331; Gcn5L2; --
DR InterPro: IPR001487; Bromodomain;
DR InterPro: IPR00182; GCN5acetyltransf.;
DR Pfam: PF05583; Acetyltransf. 1;
DR Pfam: PF00439; bromodomain; 1;
DR SMART: SMART0297; BROMO; 1;
DR PROSITE: PS00633; BROMODOMAIN_1; FALSE_NEG;
DR PROSITE: PS0014; BROMODOMAIN_2; 1;
KW Transcription regulation; Transferase; Nuclear protein;
KW Bromodomain.
FT DOMAIN 548 621 ACETYLTTRANSFERASE.
FT DOMAIN 738 808 BROMODOMAIN.
SQ SEQUENCE 830 AA; 93391 MW; 8933C35E0E734179 CRC64;

Query Match 69.4%; Score 34; DB 1; Length 830;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : LGRPPE 7
DB 216 LGSPPE 222

RESULT 26
GC22 HUMAN
ID GC22 HUMAN STANDARD; PRT; 837 AA.
AC Q92830; Q3UCW; --
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE General control of amino acid synthesis protein 5-like 2 (GC22.2.1.2)
DE (Histone acetyltransferase GCN5) (hsGCN5).
GN GCN5L2 CR GCN5 CR HGCN5.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Rodentia; Rod-
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Liver;
RX MEDLINE=98278910; PubMed=8684459;
RA Yang X.-J., Ogryzko V.V., Nishikawa C., Howard B.H., Nakatani Y.,
RA Berger S.L., Nakatani Y., Allis C.D.
RA "Cloning of Drosophila GCN5: conserved features among metazoan GCN5
RA family members".
RT Nucleic Acids Res. 26:2948-2954(1998).
RN 2;
RP SEQUENCE OF 362-837 FROM N.A. (ISUF8M 1);
RC TISSUE=Brain;
RX MEDLINE=96300317; PubMed=8684459;
RA Yang X.-J., Ogryzko V.V., Nishikawa C., Howard B.H., Nakatani Y.,
RA Berger S.L., Nakatani Y., Allis C.D.
RA "A p300/CRP-associated factor that competes with the adenoviral
RA oncoprotein E1A".
RT Nature 392:319-324(1996).
RN 3;
RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
RC TISSUE=Testis;
RX MEDLINE=96140426; PubMed=8552087;
RA Candau R., Moore P.A., Wang L., Barlev N., Ying G.Y., Rosen C.A.,
RA Berger S.L.;
RT Identification of human proteins functionally conserved with the
RT yeast putative adaptors ADA2 and GCN5."
RL Mol. Cell. Biol. 16:593-602(1996).
CC -- FUNCTION: Functions as a histone acetyltransferase (HAT) to
CC promote transcriptional activation. Has significant histone
CC acetyltransferase activity with core histones, but not with
CC nucleosome core particles.
CC -- SUBUNIT: INTERACTS WITH p300, CRP AND ADA2.
CC -- SUBCELLULAR LOCATION: Nuclear.
CC -- ALTERNATIVE PRODUCTS:
CC Event:Alternative splicing; Named isoforms=2;

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CC Name=1; Synonyms=GCN5-L;
CC IsoId=Q92830-1; Sequence=Displayed;
CC Name=2; Synonyms=GCN5-S;
CC IsoId=Q92830-2; Sequence=VSP_000556;
CC -- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES TESTED, WITH MOST
CC ABUNDANT EXPRESSION IN OVARY.
CC -- SIMILARITY: Contains 1 bromodomain.
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CC -----
CC EMBL: AF029777; AAC39769.1; --
CC EMBL: U57316; AAC50641.1; --
CC PIR: S71789; S71789.
CC PDB: 1F68; 13-DEC-00.
CC TRANSFAC: T01686; --
CC Genew: HGNC:4201; GCN5L2.
CC MIM: 602301; --
CC GO: GO:0005679; C:nucleosome remodeling complex; TAS.
CC GO: GO:003713; F:transcription co-activator activity; TAS.
CC GO: GO:006338; P:chromatin modeling; TAS.
CC GO: GO:0006473; P:protein amino acid acetylation; TAS.
CC GO: GO:0006357; P:regulation of transcription from Pol II pro.; TAS.
CC InterPro: IPR001487; Bromodomain.
CC InterPro: IPR00182; GCN5acetyltransf.
CC Pfam: PF00583; Acetyltransf. 1.
CC Pfam: PF00439; bromodomain; 1.
CC PRINTS: PR00503; BROMODOMAIN.
CC SMART: SM00297; BROMO; 1.
CC PROSITE: PS00633; BROMODOMAIN_1; FALSE_NEG.
CC PROSITE: PS0014; BROMODOMAIN_2; 1.
KW Transcription regulation; Transferase; Nuclear protein; Bromodomain;
KW Alternative splicing; 3D-structure.
FT DOMAIN 555 628 ACETYLTTRANSFERASE.
FT DOMAIN 745 815 BROMODOMAIN.
FT VARSPPLIC 1 410 Missing (in isoform 2).
FT SEQUENCE 837 AA; 93836 MW; 96C2F67C65627C4C CRC64;
Query Match 69.4%; Score 34; DB 1; Length 837;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPE 7
DB 221 LGSPPE 227

RESULT 27
PN2A-PENVA
ID -PN2A-PENVA STANDARD; PRT; 72 AA.
AC P81057;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Penaeidin-2a precursor (Pen-2a) (Pen-2) (P2).
OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Litopenaeus.
OX NCBI_TaxID=6689;
RL [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 22-71, FUNCTION, MASS SPECTROMETRY,
RP AND AVIDATION.
RC TISSUE=Hemocyte;
RX MEDLINE=98019209; PubMed=9353298;
RA Destoumieux D., Bulet P., Loew D., van Dorsellaer A., Rodriguez J.,
RA Bachere E.;

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RT "Penaeldins, a new family of antimicrobial peptides isolated from the
RT shrimp *Penaeus vannamei* (Decapoda)";
RL J. Biol. Chem. 272:28398-28406(1997);
[2]
RP SEQUENCE OF 22-72 FROM N.A., SEQUENCE OF 22-71, AND FUNCTION.
RX MEDLINE=21060119; PubMed=10561573;
RA Destoumieux D., Bulet P., Strub C.M., van Dorsselaer A., Bache E.,
"Recombinant expression and range of activity of penaeidins,
RT antimicrobial peptides from penaeid shrimp";
RJ Eur. J. Biochem. 266:335-346(2000);
[3]
RN CHITIN-BINDING ACTIVITY, TISSUE SPECIFICITY, SUBCELLULAR LOCATION, AND
RP DEVELOPMENTAL STAGE.
RX MEDLINE=20107129; PubMed=10639333;
RA Destoumieux D., Muroz M., Cosseau C., Rodriguez C., Bulet P.,
Comps M., Bache E.,
RT "Penaeldins, antimicrobial peptides with chitin-binding activity, are
RT produced and stored in shrimp granulocytes and released after
RT microbial challenge";
RJ Cell. Sci. 113:461-469(2000);
[4]
RN REVIEW.
RX MEDLINE=20479889; PubMed=11028917;
RA Destoumieux D., Muroz M., Bulet P., Bache E.,
"Penaeldins, a family of antimicrobial peptides from penaeid shrimp";
RJ Cell. Mol. Life Sci. 57:1260-1271(2000);
[5]
RP FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST *M. LUTEUS* AND *E. COLI*
CC BACTERIA; ANTIFUNGAL ACTIVITY AGAINST *N. CRASSA* AND *F. OXYSPORIUM*.
CC PRESENTS CHITIN-BINDING ACTIVITY.
CC SUBCELLULAR LOCATION: Cytoplasmic granules of hemocytes and to a
CC lesser extent in small granules of hemocytes.
CC TISSUE SPECIFICITY: HIGHER EXPRESSION IN HEMOCYTES AND TO A LESSER
CC EXTENT IN HEART, TESTIS, GILLS, INTESTINE, LYMPHONOID ORGAN AND
CC HEPATOPANCREAS. TRACES IN EYES AND SUBCUTICULAR EPITHELIUM. NOT
CC PRESENT IN THE BRAIN.
CC DEVELOPMENTAL STAGE: EXPRESSION DECREASES 3 HOURS AFTER MICROBIAL
CC CHALLENGE TO RETURN TO CONTROL LEVELS AFTER 12 HOURS AND SLIGHTLY
CC INCREASES AFTER 24 HOURS.
CC PFM: Three disulfide bonds are present.
CC MASS SPECTROMETRY: MW=5523; METHOD=MALEI; RANGE=22-71.
CC SIMILARITY: BELONGS TO THE PENAELDIN FAMILY.
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DR EMBL; Y14925; CAA75142.1; ..
RW Antibiotic; Fungicide; Chitin-binding; Amidation; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 71 PENAELDIN-2A.
FT DOMAIN 29 43 PRO-RICH.
FT MOD RES 71 71 AMIDATION (G 72 PROVIDE AN IDE GROUP).
SQ SEQUENCE 72 AA; 7833 MW; 574DE69C94673954 CRC64;
Query Match 67.3%; Score 33; DB 1; Length 72;
Best Local Similarity 83.3%; Pred. No. 9.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGRPPPF 6
DQ 36 LGRPPF 41
RESULT 28
MSI STRCS STANDARD; PRT; 304 AA.
ID STKC RAT
AC 052692
DT 16-OCT-2001 (Rel. 40; Created;
Query Match 67.3%; Score 33; DB 1; Length 72;
Best Local Similarity 83.3%; Pred. No. 9.5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGRPPPF 6
DQ 36 LGRPPF 41
RESULT 28
MSI STRCS STANDARD; PRT; 304 AA.
ID STKC RAT
AC 052692
DT 16-OCT-2001 (Rel. 40; Created;

DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Modification methylase ScaI (EC 2.1.1.113) (N-4 cytosine-specific
DE methyltransferase ScaI) (M.ScaI);
GN SCAIM.
OS Streptomyces caespitosus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=53502;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99077292; PubMed=9862476;
RA Xu S.-Y., Xiao J.-P., Etwiller L., Holden M., Aliotta J., Poh C.L.,
Dalton M., Robinson D.P., Petronzio T.R., Moran L., Ganatra M.,
Ware J., Slatko B., Bemner J. II,
RT "Cloning and expression of the ApaLI, NspI, NspH, SacI, ScaI, and
RT SspI restriction-modification systems in *Escherichia coli*";
RJ Mol. Gen. Genet. 260:226-231(1998).
CC FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE
CC AGACT. CAUSES SPECIFIC METHYLATION ON C-5 ON BOTH STRANDS, AND
CC PROTECTS THE DNA FROM CLEAVAGE BY THE SCAI ENDONUCLEASE.
CC CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA cytosine = S-
CC adenosyl-L-homocysteine + DNA N(4)-methylcytosine.
CC SIMILARITY: BELONGS TO THE N4-METHYLTRANSFERASE FAMILY.
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CC or send an email to license@isb-sib.ch).
DR EMBL; AF044681; AAC97178.1; ..
RW REBASE; 3498; M.ScaI.
DR InterPro; IPR01091; C4 Mettransf.
DR InterPro; IPR002295; D2ING_mtfase.
DR InterPro; IPR002941; N6/N4_Mtase.
DR Pfam; PF01555; N6_N4_Mtase_1.
DR PRINTS; PRO0506; D2INGMTFRASE.
DR PRINTS; PRO0508; S2IN4MTFRASE.
DR PROSITE; PS00093; N4_MTASE; 1.
KW Transferase; Methyltransferase; Restriction system.
SQ SEQUENCE 304 AA; 34187 MW; F589CF18B62C3634 CRC64;
Query Match 67.3%; Score 33; DB 1; Length 304;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 LGRPPPF 9
DQ 41 LGRPYE:S 49
RESULT 29
STKC RAT
ID STKC RAT STANDARD; PRT; 343 AA.
AC 055099;
DT 28-FEB-2003 (Rel. 41; Created)
DT 28-FEB-2003 (Rel. 41; Last sequence update)
DT 15-SEP-2003 (Rel. 42; Last annotation update)
DE Serine/threonine protein kinase 12 (EC 2.7.1.37) (Aurora- and Ipl1-
DE like midbody-associated protein 1) (AIM-1) (Aurora-B).
GN STK12 OR AIM1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Kidney;
RW MEDLINE=98119810; PubMed=9450992;
RA Terada Y., Tatsuka Y., Suzuki F., Yasuda Y., Fujita S., Otsu Y.;

DR PROSITE: PS00108; PROTEIN KINASE ST. 1;
 KW Cell cycle; Transferase; Serine/threonine-protein kinase; ATP binding.
 FT DOMAIN 82 332 PROTEIN KINASE
 FT RP BIND 88 96 ATP (BY SIMILARITY)
 FT BINDING 111 111 ATP (BY SIMILARITY)
 FT ACT SITE 205 205 BY SIMILARITY
 FT CONFLICT 44 44 R (IN REF. 1)
 SQ SEQUENCE 345 AA; 39324 MW; C1D8B8BDBEA00A0 CRC64;
 Query Match 67.3%; Score 33; DB 1; Length 646;
 Best Local Similarity 62.5%; Pred. No. 45;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGRPPEET 8
 DB 273 VGNPPES 280

RESULT 31:
 PKN5 MYXA STANDARD; PRT; 380 AA.
 AC P54737;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Serine/threonine-protein kinase pkn5 (EC 2.7.1.37);
 GN PKN5.
 OS MYXOCOCCUS XANTHUS.
 CC Bacteria; Proteobacteria; Delta proteobacteria; Myxococcales;
 CC Cyctobacterineae; Myxococcaceae; Myxococcus.
 CX NCBI_TaxID=34;
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN=DZFI;
 RA Zhang W., Inouye V., Inouye S.;
 Z "Reciprocal regulation of the differentiation of Myxococcus xanthus
 by PKN5 and PKN6, eukaryotic-like Ser/Thr protein kinases";
 RL MOL. MICROBIOL. 20:435-447(1996);
 CC 1. FUNCTION: PKN5 and pkn6 may have reciprocal roles in growth and
 development. PKN5 may be a kinase that negatively regulates
 development.
 CC 2. CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC 3. SUBCELLULAR LOCATION: Cytoplasm.
 CC 4. DEVELOPMENTAL STAGE: Expressed transiently only during the life
 cycle. With slight increases at early stage of development.
 CC 5. PTM: Autophosphorylated at Serine residues.
 CC 6. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC
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 CC
 CC EMBL: J040566, AAB40049.1;
 CC F000564; S70964;
 CC F000564; S70964;
 CC InterPro: IPR000719; Prot kinase.
 CC Pfam: PF00069; Pkinase, 1.
 CC ProDom: P000001; Prot kinase, 2.
 CC PROSITE: PS0107; PROTEIN KINASE ATP (ALIVE NE)
 CC PROSITE: PS0108; PROTEIN KINASE ST. 1
 CC PROSITE: PS0111; PROTEIN KINASE DOM. 1
 CC Transferase; Serine/threonine-protein kinase; ATP binding;
 KW Phosphorylation.
 FT DOMAIN 9 378 PROTEIN KINASE
 FT NP BIND 15 23 ATP (BY SIMILARITY)
 FT BINDING 38 38 ATP (BY SIMILARITY)

FT ACT SITE 244 244 BY SIMILARITY
 SQ SEQUENCE 360 AA; 41924 MW; DC3ADFB824420C1F CRC64;
 Query Match 67.3%; Score 33; DB 1; Length 380;
 Best Local Similarity 83.3%; Pred. No. 49;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPPE 7
 DB 317 GRPPE 322

RESULT 32
 PKN1 CORGL STANDARD; PRT; 646 AA.
 AC OBNJ58;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Probable serine/threonine protein kinase Cgl0041 (EC 2.7.1.37).
 GN CGL0041.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 CX NCBI_TaxID=1718;
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 R "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC 1. CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC 2. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC 3. SIMILARITY: Contains 3 PASTA domains.
 CC
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 CC
 CC EMBL: APC05294; BAB37434.1;
 CC InterPro: IPR00543; PASTA.
 CC InterPro: IPR000189; Prot kinase.
 CC InterPro: IPR002290; Ser/thr_pkinase.
 CC Pfam: PF03793; PASTA, 1.
 CC Pfam: PF00069; Pkinase, 1.
 CC ProDom: P000001; Prot kinase, 1.
 CC PROSITE: PS0107; PROTEIN KINASE ATP, 1.
 CC PROSITE: PS00011; PROTEIN KINASE DOM, 1.
 CC PROSITE: PS0108; PROTEIN KINASE ST, 1.
 CC KW Hypothetical protein; Transferase; Serine/threonine-protein kinase;
 KW ATP-binding; Repeat; Complete proteome.
 FT DOMAIN 9 278 PROTEIN KINASE
 FT DOMAIN 365 431 PASTA 1.
 FT DOMAIN 432 500 PASTA 2.
 FT DOMAIN 501 565 PASTA 3.
 FT NP BIND 15 23 ATP (BY SIMILARITY).
 FT BINDING 38 38 ATP (BY SIMILARITY).
 FT ACT SITE 136 136 BY SIMILARITY.
 SQ SEQUENCE 646 AA; 68237 MW; CF3B4980ECF3BFB CRC64;

Query Match 67.3%; Score 33; DB 1; Length 646;
 Best Local Similarity 83.3%; Pred. No. 87;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRPPE 7
 DB 210 GRPPE 215

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RESULT 33
PLK1 CASE:
ID PK1 CAEEL STANDARD: PRT: 643 AA.
AC P34331: C61662; C76763;
DT 01-FEB-1994 (Rel. 28, Created)
DI 28 FEB 2003 (Rel. 41, Last sequence update)
DI 28 FEB 2003 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase plk 1 (EC 2.7.1.1) (Polo like
kinase-1)
GN PLK1; CR PUC; CR C14B9.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Felodetiidae; Caenorhabditis.
OX NCBI_TaxID:6239;
RN 1:1; TaxID:6239;
RP SEQUENCE FROM N.A. (ISOFORM S);
RX MEFLINE=99104501; PubMed=10376213;
RA Guvanc B., Wang Y., Dai W.;
RT "Caenorhabditis elegans contains structural homologs of human plk and
RT plk";
RL DNA Seq. 10:139-113(1999);
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A), FUNCTION, AND SUBCELLULAR LOCATION
RC STRAIN=Bristol N2;
RX MEFLINE=26190108; PubMed=10665671;
RA Chase D., Serafinas C., Ashcroft N., Kosinski M., Long C.,
RA Fortis D.K., Golden A.;
RT "The polo-like kinase Plk-1 is required for nuclear envelope breakdown
RT and the completion of meiosis in Caenorhabditis elegans";
RJ Genesis 26:126-41(2000);
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEFLINE=94150118; PubMed=79556395;
RA Wilson R., Altschough R., Anderson K., Baynes C., Berks M.,
RA Penfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin P., Pavello A., Fraser A.,
RA Fullon M., Gardner A., Green P., Hawkins T., Haller L., Hoyer M.,
RA Johnston J., Jones M., Kershaw J., Kirtlen C., Laister N.,
RA LaRuelle P., Lightning C., Lloyd C., Mortimore R., O'Callaghan M.,
RA Parsons P., Percy C., Rifkin B., Roopra A., Saunders C., Showkeen M.,
RA Sims M., Shaldon N., Smith A., Smith M., Schrammer E., Staden R.,
RA Sultson J., Thiery-Mieg C., Thomas K., Vaudin M., Vaughan K.,
RA Watkinson R., Watson A., Weinstock L., Wilkinson Bryant J.,
RA Weidman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RJ Nature 368:12-34(1994);
RN [4]
RP REVIEWS, AND ALTERNATIVE SPLICING.
RA Watkinson R.;
PL Submitted (MAY-2002) to the EMBL/GenBank/DBEM databases.
CC -!- FUNCTION: Required for oocyte nuclear envelope breakdown before
CC entry of oocyte into spermatheca. In mitotic cells, plays a role
CC in spindle organization and centrosome maturation. In mitotic
CC cells, required for spindle dynamics and probably for spindle
CC attachment to the chromosomes. Zygotic role in the development of
CC the germline and nerve cord.
CC -!- SUBCELLULAR LOCATION: In mitosis, remains associated with
CC centrosomes entering prophase through to anaphase. During
CC metaphase, found at the centrosomes of the metaphase plate. In
CC meiosis, detected at centrosomes after promuclear meeting in post-
CC meiotic 1-cell embryos. Associated with chromatin during
CC chromosome segregation of anaphase and in the region between the
CC dividing chromosomes. Cytoplasmic in mature, fertilized oocytes.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Name= isoform S;
CC Name=b;
CC IsoId=P34331-1; Sequence=Displayed;
CC Name=a;
CC IsoId=P34331-2; Sequence=VSP_1429;
CC -!- SIMILARITY: BELONGS TO THE SERINE FAMILY OF PROTEIN KINASES
CC (CDC5/PCLO SUBFAMILY).

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-!- SIMILARITY: Contains 2 POLO box domains.
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CC
EXBL: AF057165; AAC14129.1;
DR EXBL: AF080581; AAC14661.1;
EXBL: L15188; AAA27947.2;
DR EXBL: L15188; AAA22025.1;
P-R: T43337; T43337;
DR HSP; Q63450; IAO6.
DR WormPep; C14B9.4a; CE26649.
DR WormPep; C14B9.4b; CE30602.
DR GO; GO:0005634; CnucLeus; EP.
DR GO; GO:0005524; F-ATP binding activity; ISS.
DR GO; GO:0004674; F-protein serine/threonine kinase activity; ISS.
DR GO; GO:0007477; P-centrosome cycle; IMP.
DR GO; GO:0007098; P-centrosome cycle; IMP.
DR GO; GO:0007052; P-mitotic spindle assembly; IMP.
DR GO; GO:0007468; P-protein amino acid phosphorylation; ISS.
DR InterPro; IPR000599; POLO box.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00659; POLO box; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00219; TyrKc_1.
DR PROSITE; PS00078; POLO BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase; Repeat;
KW Nuclear protein; Alternative splicing.
FT DOMAIN 38 290 PROTEIN_KINASE.
FT NP_BIND 45 52 ATP (BY SIMILARITY).
FT BINDING 57 67 ATP (BY SIMILARITY).
FT ACT_SITE 162 162 BY SIMILARITY.
FT DOMAIN 420 485 POLO BOX 1.
FT DOMAIN 520 589 POLO BOX 2.
FT VARSP: C 93 89 VDMERIL -> MTQEVQ (in isoform a).
FT SEQUENCE 643 AA; 73633 MW; 54D969F140D7A43B CRC64;
Query Match 67.38; Score 13; DB 1; Length 649;
Best Local Similarity 71.48; Pred No. 87;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 GRPFET 8
Db 232 GQPFES 236
RESULT 34
TOP1 SYN7
ID TOP1 SYN7 STANDARD: PRT: 839 AA.
AC P34185;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
DE (Unwinding enzyme) (Swivelase).
GN TOPA.
OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID:11140;
RN 1:1;
RP SEQUENCE FROM N.A.

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RX MEDLINE=95388763; PubMed=7659748;
RA Ronen-Tal M., Lianan-Hurwitz J., Gabay C., Orus M.I., Kapan A.;
RC "The genomic region of rbcL in Synechococcus sp. PCC 7942 contains
RT genes involved in the ability to grow under low CO2 concentration and
RL in chlorophyll biosynthesis";
RL Plant Physiol. 126:1461-1469(1995).
CC -!- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE
CC CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.
CC -!- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
CC DNA, followed by passage and rejoining.
CC -!- SUBUNIT: Monomer.
CC -!- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA
CC BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN
CC WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS
CC AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
CC -!- SIMILARITY: BELONGS TO THE PROKARYOTIC TYPE I/II TOPOISOMERASE
CC FAMILY.
CC -----
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CC -----
DR EMBL: X72381; CAAS1086.1;
DR PIR: S32159; S32158.
DR HSSP: P06612; 1EC1.
DR InterPro: IPR005733; DNA_topoI_bact.
DR InterPro: IPR000386; DNA_topoisomerase.
DR InterPro: IPR003651; DNATop_ATP_bind.
DR InterPro: IPR003632; DNATop_DNA_bind.
DR InterPro: IPR006171; Toprim_dom.
DR InterPro: IPR006154; Toprim_sub.
DR Pfam: PF01131; Topoisom_bac; 1.
DR Pfam: PF01591; Toprim; 1.
DR SMART: SM00437; TOP1AC; 1.
DR SMART: SM00436; TOP1BC; 1.
DR SMART: SM00493; TOPRIM; 1.
DR TIGRfam: TIGR010351; TOPA_bact; 1.
DR PROSITE: PS00336; TOPOISOMERASE_I_PROK; 1.
KW isomerase; Topoisomerase; DNA-binding.
LT ACT SITE 322 322 DNA CLEAVAGE (BY SIMILARITY;
SQ SEQUENCE 839 AA; 91236 MW; 078AC0E9E2A650 C5664.
Query Match 67.1% Score 137 DB:1; Length 1113;
Best Local Similarity 85.7% Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 3 RPPFFTS 9
UB 284 RPPFTTS 290
RESULT 35
PER3_MOUSE ID PER3_MOUSE STANDARD; PRT: 1113 AA.
AC Q70361.
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Period circadian protein 3 (PER3).
GN PER3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN 1.
RP SEQUENCE FROM N.A.
RA Zylka W.J., Shearman L.P., Weaver D.R., Reppert S.M.;

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RT "Three period homologs in mammals: differential light responses in the
RT suprachiasmatic circadian clock and oscillatin transcripts outside of
RL brain.";
RL Neuron 20:1103-1110(1998).
CC -!- FUNCTION: CIRCADIAN REGULATOR THAT MAY ACT AS A TRANSCRIPTION
CC FACTOR. BEHAVES AS A NEGATIVE ELEMENT IN CIRCADIAN TRANSCRIPTIONAL
CC LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING INDIRECT
CC TRANSCRIPTIONAL INHIBITION (BY SIMILARITY). EXPRESSION OSCILLATES
CC IN THE SUPRACHIASMATIC NUCLEI (SCN) AND EYES. THE EXPRESSION
CC RHYTHMS APPEAR TO ORIGINATE FROM RETINA.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED. EXPRESSED IN HEART, BRAIN,
CC LUNG, LIVER, SKELETAL MUSCLE, TESTIS, AND AT LOW LEVEL IN THE
CC SPLEEN AND KIDNEY. IN BRAIN, MAINLY FOUND IN THE SCN, HIPPOCAMPUS,
CC PIRIFORM CORTEX, AND CEREBELLUM. LOWER LEVEL OF EXPRESSION IN THE
CC NEOCORTEX. EXPRESSION EXHIBITS SYNCHRONOUS OSCILLATIONS IN LIVER,
CC SKELETAL MUSCLE AND TESTIS.
CC -!- INDUCTION: NOT ACUTELY INDUCED BY LIGHT IN SCN DURING SUBJECTIVE
CC NIGHT.
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS.
CC -!- SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
CC -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC -----
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CC -----
DR EMBL: AF505182; AAC40147.1;
DR PIR: T14260; T14260.
DR WGD: MGI:1277134; Per3.
DR InterPro: IPR031610; PAC.
DR InterPro: IPR030014; PAS_domain.
DR Pfam: PF00989; PAS; 1.
DR SMART: SM00086; PAC; 1.
DR SMART: SM00091; PAS; 1.
DR PROSITE: PS01112; PAS; 1.
KW Transcription regulation; Nuclear protein; Repeat; Biological rhythms.
FT DOMAIN 52 86 HELIX-LOOP-HELIX MOTIF.
FT DOMAIN 121 187 PAS 1.
FT DOMAIN 256 326 PAS 2.
FT DOMAIN 336 376 PAC.
FT DOMAIN 562 565 POLY-SER.
SQ SEQUENCE 1113 AA; 120939 MW; 8121E235D100A627 CRC64;
Query Match 67.3% Score 33; DB:1; Length 1113;
Best Local Similarity 75.0% Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GRPFFTS 9
DB 327 GRPFFTS 334
RESULT 36
HFM1_YEAST ID HFM1_YEAST STANDARD; PRT: 1188 AA.
AC P51979;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ATP-dependent DNA helicase MER3 (EC 3.6.1.-) (HFM1 protein).
GN HFM1 OR MER3 OR YGL251C OR NRE1046.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN 1.
RP SEQUENCE FROM N.A.

```

RC STRAIN=S288C / FY1679;
 RX MEDLINE=97127827; PubMed=8972576;
 RA Coussac E., Maillet E., Robineau S., Netter P.;
 RT "Sequence of a 39,411 bp DNA fragment covering the left end of
 chromosome VII of *Saccharomyces cerevisiae*.";
 RL Yeast 12:1555-1562(1996);
 RN 1;
 RP SEQUENCE OF 20-1188 FROM N.A.
 RA West R.W., Thomas S., Ma J.L.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RN 1;
 RP CHARACTERIZATION.
 RX MEDLINE=99452777; PubMed=10523314;
 RA Nakagawa T., Ogawa H.;
 RT "The *Saccharomyces cerevisiae* MER3 gene, encoding a novel
 helicase-like protein, is required for crossover control in meiosis.";
 RL EMBO J. 18:5714-5723(1999);
 RN 1;
 RP CHARACTERIZATION, AND MUTAGENESIS OF G.V.166.
 RX MEDLINE=21402874; PubMed=11376031;
 RA Nakagawa T., Flores-Rozas H., Kotodner R.D.;
 RT "The mer3 helicase involved in meiotic crossing over is stimulated by
 single-stranded dna-binding proteins and unwinds dna in the 3' to 5'
 direction.";
 RL J. Biol. Chem. 276:31487-31493(2001);
 RN 1;
 RP CONCEPTUAL TRANSLATION.
 RA Linder P.;
 RL Unpublished observations (AUG-2001).
 CC 1. FUNCTION: DNA-dependent ATPase. Required in the control of double
 strand breaks transition and crossover during meiosis. Unwinds DNA
 in the 3' to 5' direction. Prefers single-stranded DNA.
 CC 2. SUBCELLULAR LOCATION: Nuclear (Probable).
 CC 3. SIMILARITY: BELONGS TO THE HELICASE FAMILY. SMC2 SUBFAMILY.
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X94957; CAA64136.1; ALT SEQ.
 CC EMBL: U22773; CAA96971.1; ALT SEQ.
 CC EMBL: U22156; AAB93159.1; ALT INIT.
 CC SGD: S2003220; HFM1.
 CC GC: G0005634; Cnucleus; IDA.
 CC GC: G0001678; F1 DNA helicase activity; IIA
 CC GC: G00007126; Pmeiosis; IDA.
 CC InterPro: IPR033593; AAA_ATPase.
 CC InterPro: IPR031410; DEAD.
 CC InterPro: IPR031650; Helicase_C.
 CC InterPro: IPR004179; Sec63.
 CC Pfam: PF02270; DEAD; 1.
 CC Pfam: PF02871; Helicase_C; 1.
 CC Pfam: PF02889; Sec63; 1.
 CC SMART: SM00382; AAA; 1.
 CC SMART: SM00487; DEXDC; 1.
 CC SMART: SM00490; HELIC_C; 1.
 CC SMART: SM00611; SEC63; 1.
 KW Nuclear protein; Zinc-finger; DNA-binding; Helicase; Hydrolase;
 KW ATP-binding.
 FT NP_BIND 160 167 ATP (POTENTIAL).
 FT SITE 267 270 DEAD BOX.
 FT ZN_FING 1040 1055 CA-TYPE (POTENTIAL).
 FT MUTAGEN 165 165 G->D: DECREASE OF ACTIVITY.
 FT CONFLICT 552 553 MISSING (IN REF.).
 SQ SEQUENCE 1188 AA; 133099 MW; C43CEC893A565F8 CRC64;
 Query Match 67.3%; Score 33; DA 1; Length 1188;
 Best Local Similarity 85.7%; Pred No 1.7e-02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0;

QY 2 GRPPPET 8
 Db 493 GRPPPET 499
 RESULT 37
 ID PER3 HUMAN STANDARD; REF: 1210 AA.
 AC P66645; Q969K6; Q96S77; Q96S78; Q9C0J3; Q9NSP9; Q9UCU8;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Period circadian protein 3 (hPER3).
 GN PER3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC Tissue=Brain;
 RA Nagase T., Kikuno R., Ohara O.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN 2;
 RP SEQUENCE FROM N.A.
 RA Rhodes S., Huckle E.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN 3;
 RP SEQUENCE OF 44-1210 FROM N.A.
 RA Pearce A.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN 4;
 RP SEQUENCE OF 114-379 FROM N.A.
 RA Mistry S.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN 5;
 RP SEQUENCE OF 44-91 AND 732-890 FROM N.A., AND VARIANT ALA-864.
 RA Erisawa T., Uchiyama M., Kajimura N., Mishima K., Kamei Y., Katoh M.,
 RA Watanabe T., Sekimoto M., Shibui K., Kim K., Kudo Y., Ozeki Y.,
 RA Inoue Y., Yamada N., Nagase T., Ozaki N., Ohara O., Ishida N.,
 RA Okawa M., Takahashi K.;
 RT "Association of structural polymorphisms in human period3 gene with
 delayed sleep phase syndrome.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC 1. FUNCTION: CIRCADIAN REGULATOR THAT MAY ACT AS A TRANSCRIPTION
 FACTOR. BEHAVES AS A NEGATIVE ELEMENT IN CIRCADIAN TRANSCRIPTIONAL
 LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING INDIRECT
 TRANSCRIPTIONAL INHIBITION. THE EXPRESSION RHYTHMS APPEAR TO
 ORIGINATE FROM RETINA (BY SIMILARITY).
 CC 2. SUBCELLULAR LOCATION: Nuclear (Potential).
 CC 3. SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 TRANSCRIPTION FACTORS.
 CC 4. SIMILARITY: Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 CC 5. SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AB047686; BAB32925.1;
 CC EMBL: AL157954; CAB76084.1;
 CC EMBL: Z98884; CAB63147.1;
 CC EMBL: AB047521; BAB63250.1;
 CC EMBL: AB047530; BAB63251.1;
 CC EMBL: AB047531; BAB63252.1;
 CC EMBL: AB047532; BAB63253.1;
 CC EMBL: AB047533; BAB63254.1;
 CC EMBL: AB047534; BAB63255.1;

PA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skeaton C., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Vackart G., Aert R., Robben C., Grymponcz B.,
 RA Weijens J., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
 RA Gabel C., Fuchs M., Frizc C., Holzer E., Koesl D., Hilbert H.,
 RA Bortym K., Langer I., Beck A., Dehrach H., Reinhardt R., Pohl T.W.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Putnelli B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.C., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.P., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong S., Friesburg S.L.,
 RA Cerutti L., Lowe T., McConchie W.R., Paulsen O., Patashnik J.,
 RA Shpakowski G.V., Usery D., Barrett B.G., Nurse P.,
 RA "The genome sequence of Schizosaccharomyces pombe";
 RL Nature 415:87-93(2002).
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- DOMAIN: COMPOSED OF TWO SIMILAR DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE HELICASE FAMILY, SK12 SUBFAMILY.
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 CC
 DR EMBL: AL022600; CAA18663.1;
 DR EMBL: T39411; T39411.
 DR GeneDB: Spombe; SBBC1331 LOC.
 DR InterPro: IPR003593; AAA-ATPase.
 DR InterPro: IPR004103; DEAD.
 DR InterPro: IPR001650; Helicase C.
 DR InterPro: IPR004179; Sec63.
 DR Pfam: PF02270; DEAD; 2.
 DR Pfam: PF00271; Helicase_C; 2.
 DR Pfam: PF02889; Sec63; 2.
 DR SMART: SM00382; AAA; 2.
 DR SMART: SM00487; DEXDC; 2.
 DR SMART: SM00490; Helicase; 2.
 DR SMART: SM00611; SEC63; 2.
 KW Hypothetical protein: Hydrolase, Helicase, ATP binding.
 KW Nuclear protein: Repeat.
 FT AA: 663
 FT NP: 360
 FT SITE 441 424 DEAD R Y
 FT NP_BIND 1157 1264 ATP BINDING
 FT SITE 1261 1264 DEAD R Y
 FT SEQUENCE 1915 AA; 218563 MW; 90.504564 kDa; 54.
 SQ
 Query Match 67.3%; Score 14; DB 1; Length 1015;
 Best Local Similarity 75.0%; Pred. No. 2; E=0.2;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GRPPFETS 9
 DB 663 GRQPFSS 670
 RESULT 40
 RS8 ICTPU
 ID RS9 ICTPU STANDARD; PRT: 1915 AA
 AC Q0CYR6;
 DT 25-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 4CS ribosomal protein S8.
 GN RPS8.
 OS Tetrahymena parvulus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Echinostoma;
 OC Amphitrypa; Neopterygia; Teleostei; Characiformes; Characidae;
 OC Tetraodon; Tetraodon.

NCBI_TaxID=7998;
 [1]
 SEQUENCE FROM N.A.
 RA MEDLINE=2209550; PubMed=12095691;
 RA Karsi A., Patterson A., Feng J., Liu Z.-J.;
 R "Translational machinery of channel catfish: I. A transcriptomic
 approach to the analysis of 32 4CS ribosomal protein genes and their
 expression";
 RL Gene 291:177-186(2002).
 CC -!- SIMILARITY: BELONGS TO THE S8E FAMILY OF RIBOSOMAL PROTEINS.
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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 CC
 DR EMBL: AF042816; AAK95190.1;
 DR InterPro: IPR001047; Ribosomal_S8E.
 DR Pfam: PF01201; Ribosomal_S8E; 1.
 DR ProDom: PD005658; Ribosomal_S8E; 1.
 DR TIGRFAMs: TIGR00307; S8e; 1.
 DR PROSITE: PS01193; RIBOSOMAL_S8E; 1.
 KW Ribosomal protein.
 FT INIT MET
 FT SEQUENCE 207 AA; 23947 MW; 910649A78C38DD8 CRC64;
 BY SIMILARITY
 Query Match 65.3%; Score 32; DB 1; Length 207;
 Best Local Similarity 75.0%; Pred. No. 41;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LGPPPFET 8
 DB 28 LGPPPSNT 35
 Search completed: November 14, 2003, 13:25:59
 Job time : 7.68571 secs

GenCore version 5.1.6
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OM protein: protein search, using sw mode.

Run on: November 14, 2003, 13:18:40 / Search time 27 seconds
(without alignments)
86.018 Million cell updates/sec

Title: US-09-736-076-18

Perfect score: 49

Sequence: 1 LGRRPFETS 9

Scoring table: BLOSUM62

Gapcp 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL23:

- 1: sp_archaea:
- 2: sp_bacteria:
- 3: sp_fungi:
- 4: sp_human:
- 5: sp_invertebrate:
- 6: sp_mammal:
- 7: sp_mhc:
- 8: sp_organelle:
- 9: sp_phase:
- 10: sp_plant:
- 11: sp_rodent:
- 12: sp_virus:
- 13: sp_vertebrate:
- 14: sp_unclassified:
- 15: sp_rvirus:
- 16: sp_bacteriap:
- 17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY:

Result No.	Score	Query Match	Length	ID	Description
1	46	93.9	316	Q9BDK4	Q9BDK4 sus scrofa
2	46	93.9	372	Q8N7M6	Q8N7M6 homo sapien
3	46	93.9	666	Q90XS4	Q90XS4 xenopus lae
4	46	93.9	682	Q8K226	Q8K226 mus musculu
5	43	87.8	526	Q9BDP8	Q9BDP8 sus scrofa
6	43	87.8	598	P70032	P70032 xenopus lae
7	43	87.8	623	Q8U335	Q8U335 asterina pe
8	42	85.7	769	Q97143	Q97143 drosophila
9	41	83.7	568	Q8N7G6	Q8N7G6 caenorhabd:
10	41	83.7	749	Q8N7G7	Q8N7G7 caenorhabd:
11	41	83.7	783	Q76360	Q76360 caenorhabd:
12	40	81.6	324	Q9CV86	Q9CV86 mus musculu
13	40	81.6	925	Q8R015	Q8R015 mus musculu
14	40	81.6	925	Q64782	Q64782 mus musculu
15	40	81.6	970	Q96C95	Q96C95 homo sapien
16	40	81.6	970	Q00444	Q00444 homo sapien

17	40	81.6	970	4	Q81YFC	Q81YFC homo sapien
18	39	79.6	83	13	Q91891	Q91891 xenopus lae
19	39	79.6	153	16	Q84342	Q84342 chlamydia t
20	39	79.6	435	13	Q90XS2	Q90XS2 xenopus lae
21	39	79.6	557	13	Q90XS3	Q90XS3 xenopus lae
22	39	79.6	582	5	Q9GRB7	Q9GRB7 hemiceotrot
23	38	77.6	434	16	Q8EM12	Q8EM12 oceanobacil
24	38	77.6	605	10	Q93ZJ9	Q93ZJ9 arabidopsis
25	38	77.6	656	10	Q95770	Q95770 arabidopsis
26	38	77.6	767	5	Q15882	Q15882 trypanosoma
27	38	77.6	813	5	Q76216	Q76216 drosophila
28	38	77.6	813	5	Q9V721	Q9V721 drosophila
29	37	75.5	301	8	Q950L6	Q950L6 rhizophydu
30	37	75.5	346	13	Q8JGS8	Q8JGS8 brachydanio
31	37	75.5	582	11	Q8C1E3	Q8C1E3 mus musculu
32	37	75.5	779	11	Q8R311	Q8R311 mus musculu
33	36	73.5	123	4	Q9HAB5	Q9HAB5 homo sapien
34	36	73.5	256	16	Q9PPA6	Q9PPA6 campylobact
35	36	73.5	257	10	Q8H5W2	Q8H5W2 oryza sativ
36	36	73.5	310	16	Q8PIA4	Q8PIA4 xanthomonas
37	36	73.5	321	2	Q93179	Q93179 pseudomonas
38	36	73.5	504	11	Q8K0J7	Q8K0J7 mus musculu
39	36	73.5	646	4	Q96CV1	Q96CV1 homo sapien
40	36	73.5	660	16	Q8FJ15	Q8FJ15 corynebacte
41	36	73.5	1051	12	Q91EU4	Q91EU4 cydia pomon
42	36	73.5	1058	11	Q8B202	Q8B202 mus musculu
43	36	73.5	1207	6	Q9T798	Q9T798 sus scrofa
44	36	73.5	1210	4	Q9UHF9	Q9UHF9 homo sapien
45	36	73.5	1308	6	Q9MZ63	Q9MZ63 canis fami

ALIGNMENTS

RESULT 1

Q9BDK4	ID	Q9BDK4	PRELIMINARY:	PRT:	316 AA.
AC	Q9BDK4:				
DT	01-JUN-2001	(TREMBLrel. 17, Created)			
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)			
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)			
DE	Serum-inducible kinase (fragment).				
OS	Sus scrofa (pig).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX	NCBI_TaxID=9823.				
RK	[1]				
RP	SEQUENCE FROM N.A.				
RA	Anger M., Kues W.A., Kima J., Motlik J., Carnwath J.W., Niemann H.;				
RT	"Porcine serum-inducible kinase."				
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: AF348424; AAK27154.1; .				
DR	InterPro: IPR000959; POLO-box.				
DR	InterPro: IPR000719; Prot_kinase.				
DR	Pfam: PF00369; pk_kinase; 1.				
DR	Pfam: PF00659; POLO_box; 1.				
DR	ProDom: PD000001; Prot_kinase; 1.				
DR	PROSITE: PS00078; POLO_BOX; .				
KW	ATP-binding; Kinase; Transferase.				
FT	NON_TER 1				
FT	NON_TER 316				
SQ	SEQUENCE 316 AA; 35330 MW; F63BBE4A2691D62F CRC64;				

Query Match 93.9%, Score 46; DB 6; Length 316;
Best Local Similarity 98.9%; Pred.No. 0.7;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGRRPFETS 9

DB 27 LGRRPFETS 35


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RESULT 2
Q98D96
ID Q98D96 PRELIMINARY; PRT; 171 AA.
AC Q98D96;
DT 01-OCT-2002 (TREMBlrel. 22, Created);
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update);
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update);
DE Hypothetical protein FJ40644.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catartini; Hominidae; Homo.
GX NHI TaxID=9606;
LN [1];
PP SEQUENCE FROM N.A.
FC TSSSE-TIadoc;
RA Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,
RA Matsumoto K., Hirano M., Sano S., Morita R., Yoshikawa Y.,
RA Matsumura Y., Moriya S., Chiba E., Moriyama H., Onodawa S.,
RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka K.,
RA Kudo N., Kureda A., Satoh T., Kawata K., Takami S., Tetashira Y.,
RA Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T.,
RA Wakatsuki A., Ishii S., Yamamoto S., Iseno Y., Kawai H., Ota T.,
RA Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y.,
RA Sekine M., Kikuchi H., Kanda K., Wadatsuma Y., Murakawa K.,
RA Kurehara K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakita B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuno Y., Nagai K., Isogai T.,
RA "NIGRO human cDNA sequencing project";
FC Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DE EMBL: AK924733; SACC05247.1;
DE InterPro: IPR000719; Prot_Kinase.
DE InterPro: IPR002290; Ser_Thr_Pkinase.
DE InterPro: IPR001245; Tyr_Pkinase.
DE Pfam: PF00659; Pkinase; 1.
DE SMART: SM00220; S_TKc; 1.
DE PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DE PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
DE PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
DE Hypothetical protein; ATP-binding; Transferase.
KW HYPOTHETICAL PROTEIN; ATP-BINDING; TRANSFERASE.
SQ SEQUENCE 171 AA; 42632 MW; 75031F6320AC09 CRC64;

Query Match 93.9%; Score 46; DB 4; Length 372;
Best Local Similarity 98.9%; Pred. NO. 1.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGPPPPETS 9
DB 266 LGPPPPETT 276

RESULT 3
Q98D97
ID Q98D97 PRELIMINARY; PRT; 166 AA.
AC Q98D97;
DT 01-DEC-2001 (TREMBlrel. 19, Created);
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update);
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update);
DE Folic acid kinase 2.
OS Xenopus laevis (African clawed frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae.
GX XlaTaxID=8155;
LN [1];
PP SEQUENCE FROM N.A.
FC MEXB012148.543; PubMed=1159129;
RA Carlson P.J., Follett N., Nichols S., King E.A.;
RA "Isolation and Characterization of cDNA and cDNA; Two additional Pkcs
RA Folic Acid Kinases from Xenopus laevis";
RA EXP. Full Res. 270278 97/2001;
LN [1];
PP SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

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DE EMBL: AF357840; AAL30175.1;
DE InterPro: IPR000959; POLO_Box.
DE InterPro: IPR000719; Prot_Kinase.
DE InterPro: IPR002290; Ser_Thr_Pkinase.
DE Pfam: PF00659; Pkinase; 1.
DE Pfam: PF00659; POLO_Box; 2.
DE ProDom: PD000001; Prot_Kinase; 1.
DE SMART: SM00220; S_TKc; 1.
DE PROSITE: PS00078; POLO_Box; 2.
DE PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DE PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
DE PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 166 AA; 76322 MW; AB4D8F8BDFB5D4FC CRC64;

Query Match 93.9%; Score 46; DB 13; Length 666;
Best Local Similarity 88.9%; Pred. NO. 1.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGPPPPETS 9
DB 256 LGPPPPETT 264

RESULT 4
Q98D26
ID Q98D26 PRELIMINARY; PRT; 692 AA.
AC Q98D26;
DT 01-OCT-2002 (TREMBlrel. 22, Created);
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update);
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update);
DE Serum-inducible kinase.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
GX NCBI_TaxID=10090;
LN [1];
PP SEQUENCE FROM N.A.
RA Strausberg R.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DE EMBL: BC034513; AAH34513.1;
DE WGD: MG1:1599790; SNK.
DE InterPro: IPR000959; POLO_Box.
DE InterPro: IPR000719; Prot_Kinase.
DE InterPro: IPR002290; Ser_Thr_Pkinase.
DE InterPro: IPR001245; Tyr_Pkinase.
DE Pfam: PF00659; Pkinase; 1.
DE Pfam: PF00659; POLO_Box; 2.
DE ProDom: PD000001; Prot_Kinase; 1.
DE SMART: SM00220; S_TKc; 1.
DE SMART: SM00219; Tyr_Kc; 1.
DE PROSITE: PS00078; POLO_Box; 2.
DE PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DE PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
DE PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 692 AA; 77777 MW; 593A65C8DFAFFD95 CRC64;

Query Match 93.9%; Score 46; DB 11; Length 682;
Best Local Similarity 88.9%; Pred. NO. 1.5;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGPPPPETS 9
DB 272 LGPPPPETT 280

RESULT 5
Q98D98
ID Q98D98 PRELIMINARY; PRT; 526 AA.
AC Q98D98;
DT 01-JUN-2001 (TREMBlrel. 17, Created);

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DT 01-MAR-2003 (TRENDEL, 17, Last sequence update)
 DT 01-MAR-2003 (TRENDEL, 23, Last annotation update)
 DE Polio-like protein kinase (Fragment)
 OS Sus scrofa (pig)
 CC Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Eucaryotes
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus
 CC NCBI_TaxID:923;
 RN [1]
 RP SEQUENCE FROM N.A.
 PA Arita M., Kues W.A., Klima J., Mielenz M., Morlok J., Garwath J.W.,
 PA Muehm H.,
 PA "Expression of Polio-like Kinase in Cell Cycle Synchronized Porcine
 PA Fetal Fibroblasts",
 PT Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DB EMBL: AF39321; AAC28533; 1;
 DB HSP: C63450; 1;
 DB InterPro: IPR000959; POLQ_BOX.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; Kinase; 1;
 DR Pfam: PF00659; POLQ_BOX; 2;
 DR ProDom: PD000001; Prot_kinase; 1;
 DR SMART: SM00220; S_TKc; 1;
 DR PROSITE: PS00074; POLQ_BOX; 2;
 OS PROSITE: PS00107; PROTEIN KINASE ATP; 1;
 OS PROSITE: PS00111; PROTEIN KINASE BOX; 1;
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1;
 DR PROSITE: PS00111; PROTEIN KINASE BOX; 1;
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1;
 DR PROSITE: PS00111; PROTEIN KINASE BOX; 1;
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NPSERP 1 526 526
 FT NAME: 526 526
 FT NUMBER 1
 SQ SEQUENCE 526 AA: 60399 MW: 145155.602033 CRC64.
 Query Match 87.8% Score 43; DB 6; Length 526;
 Best Local Similarity 77.8% Pred. No. 5.3;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGPPFFETS 9
 DB 201 VGRPPFFETS 209
 RESULT 7
 Q81U35 PRELIMINARY; PR7: 623 AA.
 ID 081U35;
 AC Q81U35;
 DT 01-MAR-2003 (TRENDEL, 23, Created)
 DT 01-MAR-2003 (TRENDEL, 23, Last sequence update)
 DT 01-MAR-2003 (TRENDEL, 23, Last annotation update);
 DE Polio-like kinase.
 GN PLK.
 OS Asterina pectinifera (Starfish).
 CC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
 CC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
 CC NCBI_TaxID:7594;
 RN [1]
 RP SEQUENCE FROM N.A.
 PA Uchida T.O., Tachibana K., Kishimoto T.,
 PA "Starfish Plk.",
 PT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB084465; BAC22692.1; 1;
 DR KINASE.
 SQ SEQUENCE 623 AA: 70329 MW: 190802.724A CRC64;
 Query Match 87.8% Score 43; DB 5; Length 623;
 Best Local Similarity 77.8% Pred. No. 5.3;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DR PROSITE: PS00107; PROTEIN KINASE ATP; 1;
 DR PROSITE: PS00111; PROTEIN KINASE BOX; 1;
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1;
 DR PROSITE: PS00111; PROTEIN KINASE BOX; 1;
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 598 AA: 69211 MW: 246719591.1P225B6 CRC64;
 Query Match 87.8% Score 43; DB 13; Length 598;
 Best Local Similarity 77.8% Pred. No. 5.1;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LGPPFFETS 9
 DB 217 VGRPPFFETS 245
 RESULT 7
 Q81U35 PRELIMINARY; PR7: 623 AA.
 ID 081U35;
 AC Q81U35;
 DT 01-MAR-2003 (TRENDEL, 23, Created)
 DT 01-MAR-2003 (TRENDEL, 23, Last sequence update)
 DT 01-MAR-2003 (TRENDEL, 23, Last annotation update);
 DE Polio-like kinase.
 GN PLK.
 OS Asterina pectinifera (Starfish).
 CC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
 CC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
 CC NCBI_TaxID:7594;
 RN [1]
 RP SEQUENCE FROM N.A.
 PA Uchida T.O., Tachibana K., Kishimoto T.,
 PA "Starfish Plk.",
 PT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB084465; BAC22692.1; 1;
 DR KINASE.
 SQ SEQUENCE 623 AA: 70329 MW: 190802.724A CRC64;
 Query Match 87.8% Score 43; DB 5; Length 623;
 Best Local Similarity 77.8% Pred. No. 5.3;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGPPFFETS 9
 DB 222 VGRPPFFETS 260
 RESULT 8
 Q97143 PRELIMINARY; PR7: 769 AA.
 ID 097143;
 AC Q97143;
 DT 01-MAY-1999 (TRENDEL, 10, Created)
 DT 01-MAY-1999 (TRENDEL, 10, Last sequence update)
 DT 01-MAR-2003 (TRENDEL, 23, Last annotation update)
 DE SAK protein.
 GN SAK OR CG7186.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI_TaxID:7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 PA STRAIN-BERKELEY;
 RC MEDLINE:20196506; PubMed:10741132;
 RX Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RX Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.P., Vandal M.D., Zhang C., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazel R.G., Chapple M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Adri J.F., Agcavan A., An H.-J., Andrews-Pfannkuch C., Baldwin C.,
 RA Bailey R.W., Bass A., Baxendale J., Bayraktaroglu L., Beasley E.V.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,


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RC TISSUE=Blood;
RX MEDLINE=21486437; PubMed=11499007;
RA Yamashita Y., Kai-gaya S., Yoshida K., Ueno S., Gra J., Ohnishi K.,
QA Ueda M., Miyazato A., Ohta K., Kitamura T., Ozawa K., Mano H.;
RT "Serine-Threonine Kinase Acts as an Effector of Tec Tyrosine
RT Kinase.";
RJ G. Biol. Chem. 276:39012-39020(2001)
DR EMBL: AB006972; BAB69958.1;
DR HSSP: P24941; 1BJH
DR InterPro: IPR000959; POLO box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; pkinase.1;
DR PROSITE: PS00109; TYRKINASE
DR PROSITE: PS00001; Prot_kinase.1;
DR SMART: SM00220; S_TKc.1;
DR PROSITE: PS00078; POLO BOX; 1;
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1;
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1;
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1;
KW ATP binding; transferase.
SQ SEQUENCE 970 AA; 109584 MW; 1F41FA607A1550A CRC64;

Query Match 81.6%; Score 40; DB 4; Length 970;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGPPPT 8
DB 206 LGPPPT 213

RESULT 17
Q81YFC PRELIMINARY; PRT; 970 AA.
AC Q81YFC;
DT 01-MAR-2003 (TrEMBLrel. 21, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to serine/threonine protein kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC016023; AA036023.1;
KW Kinase; Serine/threonine-protein kinase.
SQ SEQUENCE 970 AA; 138971 MW; 4D56F5FD983211A6 CRC64;

Query Match 81.6%; Score 40; DB 4; Length 970;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGPPPT 8
DB 206 LGPPPT 213

RESULT 18
Q91891 PRELIMINARY; PRT; 80 AA.
AC Q91891;
DT 01-NOV-1996 (TrEMBLrel. 31, Created)
DT 01-NOV-1996 (TrEMBLrel. 31, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 9.4 kDa protein (fragment).
OS Xenopus laevis (African Clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Bouvet P., O'Neill F., ARLOT-BONNEVA N. Y., Legagneux V., Rogh; C.,
RA Bassez T., OSBORNE H.;
RT "Deadenylation conferred by the 3' untranslated region of a
RT polyadenylation controlled mRNA in xenopus embryos is switched to
RL Mol. Cell. Biol. 14:1893-1900(1995).
DR EMBL: Z24453; CAA80826.1;
DR InterPro: IPR000719; Prot_kinase.
DR Pfam: PF00069; pkinase.1;
DR PROSITE: PS00001; Prot_kinase.1;
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1;
KW Hypothetical protein; ATP-binding; Transferase.
FT NON_TER 1
SQ SEQUENCE 80 AA; 9398 MW; 8DFCEDBA14BE14FB CRC64;

Query Match 73.6%; Score 39; DB 13; Length 80;
Best Local Similarity 75.0%; Pred. No. 4;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LGPPPT 8

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4 GSEPFETS 11

RESULT 19

Q94942 PRELIMINARY: PRT: 153 AA.
AC 164942
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein CT138.
GN CT138
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
CX KCP_TaxID-813;
LN 11
PP STRAIN:J/WH-3/CX;
FX MEDLINE:96060809; PubMed:9784117;
FA Stephens R.S., Kaiman S.,ammel C.C., Fan J., Marathe R., Aravind L.,
FA Mitchell W.P., Olinger L., Iatsov R.M., Zhao Q., Koonin E.V.,
FA Davis R.W.,
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis".
RL Science 282:754-759(1998).
CP EMBL, AF01307; AAC67933.1;
KW Hypothetical protein, Complete proteome.
SV SEQUENCE 153 AA; 17828 MW; DA8E4E2FF9819C 84644

Query Match: 79.6%; Score 39; DB 16; Length 153;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 GSEPFETS 8

4 GSEPFETS 15

RESULT 20

Q94942 PRELIMINARY: PRT: 445 AA.
AC 164942
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Polo-like kinase 3 (Fragment).
GN PLX3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID-5155;
LN 11
PP STRAIN:AF397844; PubMed:11597129;
FA Duncan P.I., Pellet N., Nishis C., Nigg E.A.,
FA "Cloning and Characterization of Plx2 and Plx3, Two Additional Polo-
FA like Kinases from Xenopus laevis".
RL Exp. Cell Res. 270:78-87(2001).
CC 11. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL, AF397844; AAC30176.1;
DR InterPro: IPR000359; P00C_Box.
DR InterPro: IPR000719; P00C_Box.
DR InterPro: IPR002290; SerThr_Kinase.
DR Pfam: PF00069; Pkinase.
DR Pfam: PF00659; P00C_Box.
DR ProDom: PD000301; P00C_Box.
DR SMART: SM00225; S_TKc1.
DR PROSITE: PS00078; P00C_Box; 1.
DR PROSITE: PS00111; PROTEIN KINASE COM; 1.
DR PROSITE: PS00104; PROTEIN KINASE ST; 1.
KW ATP binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT MCM TER 457 507
SV SEQUENCE 445 AA; 60301 MW; 85222418FA6E678 CRC64;

Query Match: 79.6%; Score 39; DB 13; Length 557;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 GSEPFETS 9

255 GSEPFETS 262

RESULT 22

Q9G357 PRELIMINARY: PRT: 592 AA.
AC 09G357
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Polo like kinase.
GN PLK.
OS Hemionotus pulcherrimus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinozoa; Echinozoa; Echinozoa; Echinozoa; Echinozoa;
OC Hemionotus.
CX NCBI_TaxID-7450
LN 11
PP STRAIN:AF397844; PubMed:11597129;
FA Duncan P.I., Pellet N., Nishis C., Nigg E.A.,
FA "Cloning and Characterization of Plx2 and Plx3, Two Additional Polo-
FA like Kinases from Xenopus laevis".
RL Exp. Cell Res. 270:78-87(2001).
CC 11. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL, AF397844; AAC30176.1;
DR InterPro: IPR000359; P00C_Box.
DR InterPro: IPR000719; P00C_Box.
DR InterPro: IPR002290; SerThr_Kinase.
DR Pfam: PF00069; Pkinase.
DR Pfam: PF00659; P00C_Box.
DR ProDom: PD000301; P00C_Box.
DR PROSITE: PS00078; P00C_Box; 1.
DR PROSITE: PS00111; PROTEIN KINASE COM; 1.
DR PROSITE: PS00104; PROTEIN KINASE ST; 1.
KW ATP binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT MCM TER 457 507
SV SEQUENCE 592 AA; 85222418FA6E678 CRC64;

2 GSEPFETS 9

255 GSEPFETS 262

RA Yonemura I., Fujimoto H., Mabuchi I.;
 PT "Cloning of sea urchin plk.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RS 121
 RP SEQUENCE FROM N.A.
 RA Yonemura I., Fujimoto H., Mabuchi I.;
 PT "Cloning of sea urchin polo-like kinase";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC 1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AB043897; BAB18588.1;
 DR InterPro: IPR001395; Aldo/ker_red.
 DR InterPro: IPR003959; POLO_box.
 DR InterPro: IPR003719; Pro_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase.1;
 DR Pfam: PF02659; POLO_box.2;
 DR ProDom: PD000000; Prot_Kinase.1;
 DR SMART: SM00220; S_TKc.1;
 DR PROSITE: PS00633; ALDOKEO_PDECTASE_3.1;
 DR PROSITE: PS00078; POLO_BOX.2;
 DR PROSITE: PS0107; PROTEIN_KINASE_ATP.1;
 DR PROSITE: PS00311; PROTEIN_KINASE_DOM.1;
 DR PROSITE: PS00128; PROTEIN_KINASE_ST.1;
 KW ATP binding; Kinase; Serine/threonine protein kinase; Transferase.
 SQ SEQUENCE 582 AA; 66429 MW; A3774ACCAACPFDESD CRC64;
 Query Match 79.6%; Score 39; DB 5; Length 582;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LGRRPFET 8
 DB 220 VGRPFET 227
 RESULT 23
 QY QYEM12 PRELIMINARY; PRT; 414 AA
 AC QYEM12;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created).
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update).
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update).
 DE C4-dicarboxylate transporter.
 OS Oceanobacillus ankyensis.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=182710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HT831 / DSM 14371 / JCM 11173;
 RX MEDLINE=2220767; PubMed=12215476;
 RA Takaki H., Takaki Y., Uchiyama I.;
 PT "Genome sequence of Oceanobacillus ankyensis isolation from the Iheya
 RT Ridge and its unexpected adaptive capabilities to extreme
 RT environments";
 RL Nucleic Acids Res. 30:3927-3935(2002).
 DR EMBL: AP004602; BAC14816.1;
 KW Complete Proteome.
 SQ SEQUENCE 434 AA; 46689 MW; CDDAE65GDFPF54BES CRC64;
 Query Match 77.6%; Score 38; DB 16; Length 434;
 Best Local Similarity 77.8%; Pred. No. 34;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 49 LGTRPFETS 57
 DB 49 LGTRPFETS 57
 RESULT 24
 QY QYEM12 PRELIMINARY; PRT; 616 AA
 AC QYEM12;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created).
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update).
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update).
 DE Arabidopsis thaliana (Mouse-ear cress).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.C., Koesema E., Meyers M.C., Banh C.,
 RA Bowser L., Carninci P., Dale G.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones F., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.H., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY057486; AA039720.1;
 SQ SEQUENCE 605 AA; 65693 MW; 7FF6-B6C323BE41F CRC64;
 Query Match 77.6%; Score 38; DB 10; Length 605;
 Best Local Similarity 77.8%; Pred. No. 48;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LGRRPFETS 9
 DB 271 LGRRPFETS 279
 RESULT 25
 QY QY5770 PRELIMINARY; PRT; 656 AA
 AC QY5770;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created).
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update).
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update).
 DE F19K16.3 protein.
 GN F19K16.3 OR F18B13.8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia.
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
 RA Maiti R., Renning C.M., Koo H., Fujii C.Y., Osterback T.R.,
 RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RT "Arabidopsis thaliana chromosome 1 BAC F19K16 genomic sequence";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Pederspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.P.,
 RA Alcafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
 RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
 RA Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
 RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC011717; AA052246.1;
 DR EMBL: AC009322; AA055481.1;
 SQ SEQUENCE 656 AA; 71630 MW; C7FC4A188ACEA410 CRC64;
 Query Match 77.6%; Score 38; DB 10; Length 656;
 Best Local Similarity 77.8%; Pred. No. 52;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LGRRPFETS 9
 DB 271 LGRRPFETS 279


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DR 231 LGRRPFFET 279
RESULT 28
Q 5842
ID 015992 PRELIMINARY; PRT; 813 AA.
AC 015992
CT 01-JAN-1998 (TREMBLrel. 05, Created;
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 23, Last annotation update)
GN POLI-like protein kinase (fragment)
OS Trypanosoma brucei
OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Trypanosoma
OX NCBI_TaxID:5691
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN ST19247;
RX YIELD: 98172746; PubMed:9511345;
RA Graham T.N., Tait A., Hyde G.,
RT "Characterisation of a polo-like protein kinase gene homologue from an
RT evolutionarily divergent eukaryote, Trypanosoma brucei.",
RJ Gene 207:71-77 (1998).
CU --- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR FMR2_113969; CAA74301.1;
DR InterPro; IPR000959; POLO_BOX.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR022930; Ser_Thr_kinase.
DR InterPro; IPR012451; Tyr_kinase.
DR Pfam; PF02069; Kinase; 1.
DR Pfam; PF02659; POLO_box; 2.
DR PRINTS; PS01991; TYKINASE.
DR PRODOM; PDC00001; Prot_Kinase; 1.
DR SMART; SM02220; S_TKc; 1.
DR PROSITE; PS50078; POLO_BOX; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PRASITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR NEGATE; PS00108; PROTEIN_KINASE_ST; 1
KW ATP binding, Kinase, Serine/threonine-protein kinase, Transferase.
ST NCTER_147 767
SQ SEQUENCE 767 AA, 86423 MW, 8360253PIRFD041 (NCOR);
Query Match 77.6%; Score 38; DB 5; Length 813;
Best local similarity 87.5%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LGRRPFFET 8
DB 238 LGRRPFFET 215
RESULT 28
Q 9VVTZ1
ID 09VVTZ1 PRELIMINARY; PRT; 813 AA.
AC 09VVTZ1
CT 01-MAY-2000 (TrEMBLrel. 13, Created;
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE PCAF protein (GH11602p)
GN PCAF OR CG4107.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID:7227;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE:20196066; PubMed:107311132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scheier S.E., Li P.W., Hoskins R.A., Galie R.P.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wotman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.C., Champe M., Pfeiffer A.D.,
RA Wan K.H., Doyle G., Baxter B.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA Abul J.F., Astayani A., An H., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Saso A., Baxendale C., Bayraktaroglu L., Beasley R.M.,
RA Beeson K.Y., Berns P.V., Bertram H.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck C., Brokstein P., Brotter P.,
RA Burtis K.C., Busar J.A., Butler H., Cadieu E., Center A., Chandra J.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Fabros B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downs M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.C., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hustin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jarali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matte B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Par S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shet H.,
RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter R., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasmann D.A., Weinstein G.N., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye C., Ye P.F., Zaveri J.S., Zhang M., Zhang G., Zhao Q., Zheng L.,

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DR EMBL; AF029776; AAC49102.1;
DR HSSP; Q03330; 1YGH.
DR FlyBase; FBgn020388; Kcaf.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR000182; GSNAcetyltransf.
DR Pfam; PF00583; Acetyltransf; 1.
DR Pfam; PF00439; Bromodomain; 1.
DR PRINTS; PRO0593; Bromodomain.
DR SMART; SM00297; BROMC; 1.
DR PROSITE; PS00014; BROMODOMAIN_2; 1.
SQ SEQUENCE 813 AA, 92095 MW, 79831218CB9398D93 CRC64;
Query Match 77.6%; Score 38; DB 5; Length 813;
Best local similarity 87.5%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LGRRPFFET 8
DB 238 LGRRPFFET 215
RESULT 28
Q 9VVTZ1
ID 09VVTZ1 PRELIMINARY; PRT; 813 AA.
AC 09VVTZ1
CT 01-MAY-2000 (TrEMBLrel. 13, Created;
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE PCAF protein (GH11602p)
GN PCAF OR CG4107.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID:7227;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE:20196066; PubMed:107311132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scheier S.E., Li P.W., Hoskins R.A., Galie R.P.,
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RA Dodson K., Doup L.E., Downs M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.C., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hustin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jarali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matte B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Par S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shet H.,
RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter R., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasmann D.A., Weinstein G.N., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye C., Ye P.F., Zaveri J.S., Zhang M., Zhang G., Zhao Q., Zheng L.,

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RD      SEQUENCE FROM K.A.
RP      STRAIN 1367
RC      LANG F.B.F.
RA      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL      - CATALYTIC ACTIVITY: NADH + CHLOROPHENOL NAD+ + CHLOROPHENOL.
RC      - SIMILARITY: BELONGS TO THE COMPLEX : SUBUNIT : FAMILY.
RA      EMBL: AF040436; AAK84292.1; ...
RC      INTERPRO: IPR01694; Resp_NADH_dhl.
RA      Pfam: PF00146; NADHd; ...
RC      NAD: Oxidoreductase; Transmembrane; Uncharacterized; Mitochondrion.
RA      SEQUENCE 301 AA; 33286 MW; D658175535F41D5 CF364;
RD      Query Match 75.5%; Score 17; DB 8; Length 301;
RP      Near Local Similarity 85.7%; pred no 17;
RC      Matches 6; Conservative 1; Mismatches 11; Indexes 1; Gaps 0;

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DR 1401 BC024076; AAH24076.17
 KW Hypothetical protein.
 FT NON_TSR 1
 SQ SEQUENCE 582 AA; 65262 MW; 285474224/PAD69 CRC64;

Query Match 75.5%; Score 32; LR 11; Length 582;

Best Local Similarity 87.5%; Pred. No. 72;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGPPPEF 8

II II II

DB 305 LGPPPEF 312

RESULT 12

Q8H311 PRELIMINARY; PRT; 779 AA.

AC CBR111.

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Similar to meningioma expressed antigen 6 (coiled-coil proline-rich).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090.

RN [1]

RF SEQUENCE FROM N.A.

RA SUBMITTER'S FILE

RC Submitted (APR 2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; E026864; AAH26864.17

SQ SEQUENCE 777 AA; 87718 MW; 778P0983A83108 CRC64;

Query Match 75.5%; Score 32; LR 11; Length 582;

Best Local Similarity 87.5%; Pred. No. 97;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGPPPEF 8

II II II

DB 502 LGPPPEF 509

RESULT 13

Q8H311

AC CBR111 PRELIMINARY; PRT; 779 AA.

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catartida; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RN [1]

RF SEQUENCE FROM N.A.

RA SUBMITTER'S FILE

RC Submitted (APR 2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; A5021912; BAB13934.1

SQ SEQUENCE 123 AA; 13743 MW; 804C05E67E543E1P044

Query Match 73.5%; Score 19; LR 4; Length 123;

Best Local Similarity 87.5%; Pred. No. 43;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGPPPEF 8
 II II II
 DB 72 LGPPPEF 79

RESULT 34

Q9PPA6

ID Q9PPA6 PRELIMINARY; PRT; 256 AA.

AC Q9PPA6;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Glutamine-binding teicoplanin protein.

GN GNH OR C00817.

OS Campylobacter jejuni.

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;

OC Campylobacteraceae; Campylobacter.

OX NCBI_TaxID=197;

RN [1]

RF SEQUENCE FROM N.A.

RA STRAIN=NCTC 11168;

RC MEDLINE=20150912; PubMed=10669204;

RA Parkhill J., Wren B.W., Murgall K., Kettle J.M., Church C.,

Basham D., Chillingworth T., Davies R.M., Feitwell T., Hoiroyd S.,

Jagels K., Karlyshev A.V., Mole S., Paton M.G., Penn C.W.,

Quail M.A., Rajaratham V.A., Rutherford K.M., van Vleet A.H.M.,

Whitehead S., Barrett B.G.;

RT "The genome sequence of the food-borne pathogen Campylobacter jejuni

reveals hypervariable sequences."

RL Nature 403:665-669(2000);

DR EMBL; AL139076; CAB73082.1;

DR HSSP; P13344; LNDN.

DR InterPro; IPR001311; SBP/glu_receptor.

DR InterPro; IPR001638; SBP_bac_3.

DR Pfam; PF00497; SBP_bac_3.

DR SMART; SMC0062; PBfb; 1.

SW Complete proteome.

SQ SEQUENCE 256 AA; 23913 MW; 6CD44DDE6AF019DF CRC64;

Query Match 73.5%; Score 36; DB 16; Length 256;

Best Local Similarity 77.8%; Pred. No. 49;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGPPPEF 9

II II II

DB 27 LGPPPEF 35

RESULT 35

Q8H5W2

ID Q8H5W2 PRELIMINARY; PRT; 257 AA.

AC Q8H5W2;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE C01123_Bol.20 protein.

GN C01123_Bol.20.

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzaceae; Oryza.

OX NCBI_TaxID=39947;

RN [1]

RF SEQUENCE FROM N.A.

RA STRAIN=cv. Nipponbare;

RC Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa Nipponbare (GA3) genomic DNA, chromosome 7, BAC

clone:OJ1123_B01.11"

PL Submitted (JUN 2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP003745; BAB1925.11

SQ SEQUENCE 257 AA; 16262 MW; 9A1878473E265DBA CRC64;

Query Match 73.5%; Score 36; DB 10; Length 257;

CS Homo sapiens (Human)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catartini; Hominoidea; Homo
 CX KCB: TaxID=9606;
 EN 11
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strains=9
 RI Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RL 11. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC 11. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EXEL: BC013699; AAH13991.1
 DR InterPro: IPR000959; POLO_box.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR Pfam: PF00069; kinase_1.
 DR Pfam: PF00659; POLO_box; 2.
 DR ProDom: PDD00001; Prot_kinase; 1.
 DR SMART: SM0220; S_TK; 1.
 DR PROSITE: PS0078; POLO_BOX; 2.
 DR PROSITE: PS0107; PROTEIN_KINASE_ATF; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS0108; PROTEIN_KINASE_ST; 1.
 KW Hypothetical protein; ATP-binding; Kinase;
 KW Serine/threonine-protein kinase; Transferase;
 SQ SEQUENCE 646 AA; 71628 MW; 134.AL09008458.060-4.

Query Match 73.5% Score 36; DS 4; Length 646
 Best Local Similarity 75.0%; Pred. No. 134-646
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GRPFFPS 9
 DB 256 GSRFFFA 263

RESULT 4:
 QREFS
 TO QREFS PRELIMINARY; PRT; 646 AA
 AC QREFS
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative serine/threonine protein kinase.
 GN CAC33.
 GN Corynebacterium efficiens
 CC Bacteria; Actinobacteria; Acidithiobacillus; Acidithiobacillus
 CC Corynebacteriaceae; Corynebacterium; Corynebacterium
 CX KCB: TaxID=152734;
 EN 11
 RN SEQUENCE FROM N.A.
 RC STRAIN=YS-314 / AJ 12310 / DSM 4454 / JCM 11169.
 RA Kawaiyabashi Y., Yamazaki J., Hiro Y., Kikuchi H., Nakamura Y.,
 RA Ikeda K., Suzuki K., Mashima J., Itoh T., Yamahara A., Nishio Y.,
 RA Ueda Y., Sugimoto S.
 RT "The entire genomic sequence of Corynebacterium efficiens YS-314."
 RI Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RL EXBL: AP005214; BAC16843.1
 KW Kinase; Complete proteome
 SQ SEQUENCE 660 AA; 69646 MW; D31D979B02L4451.060-4;

Query Match 73.5% Score 36; DS 16; Length 660
 Best Local Similarity 100.0%; Pred. No. 134-660
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GRPFFPS 7
 DB 210 GRPFFE 215

Search completed: November 14, 2003, 13:27:58
 Job time : 28 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd

Query protein: protein search, using sw model

Run on: November 14, 2003, 14:14:16 / Search time 41 seconds
without alignment
42.561 Million cell updates/sec

Title: US-09-736-076 19

Perfect score: 58

Sequence: 1 MLGPPPPPTTS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1107563

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	length	DB ID	Description
1	58	100.0	11	20 AAW74163	H2 loop peptide J-
2	58	100.0	11	23 AAU98315	Polo kinase serine
3	55	94.8	469	22 AAB3244	Human protein seq
4	55	94.8	469	22 AAG7476	Amino acid sequenc
5	55	94.8	685	20 AAU98315	Human serine induci
6	55	94.8	685	20 AAW55413	Disease associated
7	55	94.8	685	23 ABA1414	Human NF-kB activa
8	55	94.8	753	23 ABA1414	Human ovarian anti
9	52	89.7	626	21 AAB15845	Protein involved i

10	49	84.5	9	20 AAW74162	H2 loop peptide J-
11	49	84.5	9	20 AAW74159	H2 loop peptide J-
12	49	84.5	9	23 AAU98315	Polo kinase serine
13	49	84.5	9	23 AAU98318	Polo kinase serine
14	49	84.5	10	20 AAW74213	H2 loop peptide K0
15	49	84.5	10	23 AAU98357	Polo kinase SNK se
16	49	84.5	20	20 AAW74173	H2 loop peptide PO
17	49	84.5	20	23 AAU98306	Peptide sequence o
18	49	84.5	229	21 AAB56690	Human prostate can
19	49	84.5	531	23 AAW74656	Mammalian polo-lik
20	49	84.5	603	16 AAW74620	Human lung tumour
21	49	84.5	603	23 AAU79306	Mouse polo-like k:
22	49	84.5	603	23 AAU79308	Mouse polo-like k:
23	49	84.5	603	23 AAU79309	Mouse polo-like k:
24	49	84.5	603	23 AAU79310	Mouse polo-like k:
25	49	84.5	603	23 AAU79311	Mouse polo-like k:
26	49	84.5	603	23 AAU79312	Mouse polo-like k:
27	49	84.5	603	23 AAU79313	Mouse polo-like k:
28	49	84.5	603	23 AAU79314	Mouse polo-like k:
29	49	84.5	603	23 AAU79315	Mouse polo-like k:
30	49	84.5	603	23 AAU79316	Mouse polo-like k:
31	49	84.5	603	23 AAU79317	Mouse polo-like k:
32	49	84.5	603	23 AAU79318	Mouse polo-like k:
33	49	84.5	603	23 AAU79319	Mouse polo-like k:
34	49	84.5	603	23 AAU79320	Mouse polo-like k:
35	49	84.5	603	23 ABR48196	Human bladder can
36	48	82.9	769	22 ABB53067	Drosophila melanog
37	46	79.3	9	20 AAW74161	H2 loop peptide J-
38	46	79.3	9	23 AAU98317	Polo kinase serine
39	46	79.3	416	17 AAR92176	Sak serine-threoni
40	46	79.3	464	17 AAR92214	Sak-b serine-threo
41	46	79.3	925	17 AAR92177	Sak-a serine-threo
42	46	79.3	925	23 ABB57273	Mouse ischaemic co
43	46	79.3	970	22 AAW78933	Human protein SEQ
44	46	79.3	970	22 AAW3244	Human polypeptide
45	46	79.3	980	22 AAW79817	Human protein SEQ

ALIGNMENTS

RESULT 1
AAW74163
ID AAW74163 standard, peptide: 11 AA.

AC AAW74163:

DT 25-MAY-1999 (first entry)

DE H2 loop peptide J-46.

XX

XX

KW H2 loop, serine/threonine kinase; cancer; diabetes; obesity; therapy;

KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;

KW inflammatory disorder; central nervous system disease; septic shock;

KW Parkinson's disease; hypertension.

XX Synthetic.

XX

Key location/Qualifiers

FT Modified-site 1

FT Modified-site 1 /note= "acetylated"

FT Modified-site 1

FT Modified-site 1 /note= "amidated"

XX

PN MO9853050-A2.

XX

PD 26-NOV-1998.

XX

XX

PF 20-MAY-1998; 98WG US0319.

XX

XX

PR 21-MAY-1997; 97US 386338.

XX

XX

PR (CHILD) CHILDRENS MEDICAL CENT.

PA WISS : YISSUM RES & DEV CO.
 PI Ben Sasson SA;
 XX WPI: 1999 070142/56.
 XX
 XX New peptides for modulating serine/threonine kinase activity -
 XX comprise a sequence corresponding to the HJ loop of a
 XX serine/threonine kinase, used for treating e.g. cancers,
 XX inflammatory disorders or autoimmune disorders
 XX
 XX Claim 14, Fig 4, 7opp, English.
 XX
 XX This sequence represents a peptide of the invention, and is a derivative
 XX of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 XX used for the treatment of disorders caused by overactivity or
 XX underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 XX shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 XX arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 XX hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 XX psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 XX of organ transplant rejection, multiple sclerosis, inflammatory bowel
 XX disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 XX disease, stroke and trauma), septic shock, Parkinson's disease or
 XX hypertension. The peptides can also be used to produce antibodies which
 XX can be used to identify cells expressing the STK and to study the
 XX intracellular distribution of the STK. In addition, the peptides can be
 XX used to identify and quantitate ligands which bind the HJ loop of the STK
 XX from which the peptide was derived
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 100.0%; Score 58; E# 20; Length 11;
 Best Local Similarity 100.0%; Pred No 0.00045;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 1 MLGRPPFFETS 11
 DQ 1 MLGRPPFFETS 11
 RESULT 3
 AAB94717
 ID AAB94717 standard; Peptide: 11 AA.
 AC AAB94717;
 XX AAB94719;
 XX
 XX 26-JUN 2001 (first entry)
 XX
 XX Human protein sequence SEQ ID NO:15726.
 XX
 XX Human; primer, detection; diagnosis; antisense therapy; gene therapy.
 XX
 XX Homo sapiens.
 XX
 XX SP:074617-A2.
 XX
 XX 07-FEB-2001.
 XX
 XX 28-JUL-2000; 2000EP-0116126.
 XX
 XX 29-JUL-1999; 99JP-0248036.
 XX
 XX 27-AUG-1999; 99JP-0300253.
 XX
 XX 11-JAN-2000; 2000JP-0118776.
 XX
 XX 02-MAY-2000; 2000JP-018767.
 XX
 XX 09-JUN-2000; 2000JP-0241899.
 XX
 XX (HELIX) HELIX RES INST.
 XX
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WP: 2001-316749/34.
 XX
 XX

PF 13-DEC-2000; 2000US-0736076.
 XX
 XX 21-MAY-1997; 97US-0861338.
 XX
 XX (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 XX Ben-Sasson SA;
 XX
 XX WPI: 2002-462797/49.
 XX
 XX New peptide from the HJ loop of serine threonine kinase, useful for
 XX treating e.g. cancer and for producing diagnostic antibodies .
 XX
 XX Disclosure, Fig 4; 4pp; English.
 XX
 XX The present invention relates to new peptides derived from the HJ loop
 XX of a serine/threonine kinase (STK). The peptides of the invention are
 XX used to modulate STK activity, especially for treating cancer, diabetes,
 XX obesity or a wide variety of central nervous system, inflammatory,
 XX autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 XX regulating lipid metabolism. The peptides are also used to generate
 XX antibodies that bind specifically to the parent STK, used e.g. for
 XX identifying STK-expressing cells and to study intracellular distribution
 XX of STK, and to identify or quantify ligands that bind to the HJ loop.
 XX The present amino acid sequence represents the polo kinase
 XX serine-threonine kinase HJ loop peptide J-46. This sequence is one of
 XX the short peptides of the invention that selectively modulate the
 XX activity of STK.
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 100.0%; Score 58; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred No 0.00045;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 1 MLGRPPFFETS 11
 DQ 1 MLGRPPFFETS 11
 RESULT 3
 AAB94717
 ID AAB94717 standard; Protein: 469 AA.
 AC AAB94717;
 XX AAB94717;
 XX
 XX 26-JUN 2001 (first entry)
 XX
 XX Human protein sequence SEQ ID NO:15726.
 XX
 XX Human; primer, detection; diagnosis; antisense therapy; gene therapy.
 XX
 XX Homo sapiens.
 XX
 XX SP:074617-A2.
 XX
 XX 07-FEB-2001.
 XX
 XX 28-JUL-2000; 2000EP-0116126.
 XX
 XX 29-JUL-1999; 99JP-0248036.
 XX
 XX 27-AUG-1999; 99JP-0300253.
 XX
 XX 11-JAN-2000; 2000JP-0118776.
 XX
 XX 02-MAY-2000; 2000JP-018767.
 XX
 XX 09-JUN-2000; 2000JP-0241899.
 XX
 XX (HELIX) HELIX RES INST.
 XX
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WP: 2001-316749/34.
 XX
 XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -

XX Claim 8: SEQ ID 15726; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAG3166 to AAG3168 and
 CC AAG3163 to AAG3174 represent human cDNA sequences; AAG2446 to
 CC AAG2589 represent human amino acid sequences; and AAG1629 to AAG1632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

XX Sequence 469 AA;

Query Match 94.8%; Score 55; DB 22; Length 469;
 Best Local Similarity 90.9%; Pred. No. 0.076; 0; Indels 0;
 Matches 10; Conservative 1; Mismatches 0; Gaps 0;

QY 1 MLGRPPPTT 11
 |||||
 Db 57 MLGRPPPTT 67

RESULT 5
 AAY00915
 IC AAY00915 standard; Protein: 685 AA.
 XX
 AC AAY00915;
 XX
 DT 28-MAY-1999 (first entry)
 XX
 DE Human serum inducible kinase.
 XX
 KW Serum inducible kinase; SNK protein; human; proliferative disease;
 KW leukaemia; solid tumour cancer; metastasis; chronic inflammatory;
 KW psoriasis; rheumatoid arthritis; proliferative cardiovascular disease;
 KW restenosis; ocular disorder; diabetic retinopathy; haemangioma;
 KW benign hyperproliferative disease; diagnosis.
 XX
 CS Homo sapiens.
 XX
 PN W0909146-A1.
 XX
 PC 25-FEB 1999.
 XX
 PF 20-AUG-1998; 98WO-US17248.
 XX
 PR 20-AUG-1997; 97US-0056112.
 XX
 PA (SMK) SMITHKLINE BEECHAM CORP.
 XX
 PI Anderson KM, Bouzyk M, Hansbury MJ, Jackson JR;
 PI Nerurkar SS, Roshak AK;
 XX
 DR WPI; 1999-18:027/15.
 DR N-PSDB; AAX27227.
 XX
 PT New serum inducible kinase (SNK); polypeptides and polynucleotides -
 PT useful for treating proliferative diseases
 XX
 XX Claim 1; Page 49-52; 41pp, English.
 XX
 CC This sequence is a human serum inducible kinase (SNK) of the
 CC invention. The invention relates to diagnostic assays or kits for
 CC detecting diseases associated with inappropriate SNK activity or levels.
 CC Disease states that can be diagnosed include proliferative diseases such

XX WPI; 2001-564736/63.
 DR N-PSDB; AAX78069.
 XX
 PT New genes encoding protein kinase and protein phosphatase, useful for
 PT identifying modulators which can be used to treat human or animal
 PT disorders associated with the expression or function of these enzymes -

XX Claim 2; Page 136-139; 336pp; Japanese.

XX The present sequence represents a human protein kinase/protein
 CC phosphatase. The polypeptides are expected to participate in signal
 CC transduction in cells. The kinase phosphatases are connected with
 CC intracellular signalling pathways. Antisense oligonucleotides and
 CC compounds identified by screening (agonists or antagonists) can be
 CC used to treat human or animal disorders associated with the expression
 CC or function of the protein. In addition, the polypeptides may be used
 CC as target molecules for drug development.

XX Sequence 469 AA;

Query Match 94.8%; Score 55; DB 22; Length 469;
 Best Local Similarity 90.9%; Pred. No. 0.076;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRPPPTT 11
 |||||
 Db 57 MLGRPPPTT 67

RESULT 5
 AAY00915
 IC AAY00915 standard; Protein: 685 AA.
 XX
 AC AAY00915;
 XX
 DT 28-MAY-1999 (first entry)
 XX
 DE Human serum inducible kinase.
 XX
 KW Serum inducible kinase; SNK protein; human; proliferative disease;
 KW leukaemia; solid tumour cancer; metastasis; chronic inflammatory;
 KW psoriasis; rheumatoid arthritis; proliferative cardiovascular disease;
 KW restenosis; ocular disorder; diabetic retinopathy; haemangioma;
 KW benign hyperproliferative disease; diagnosis.
 XX
 CS Homo sapiens.
 XX
 PN W0909146-A1.
 XX
 PC 25-FEB 1999.
 XX
 PF 20-AUG-1998; 98WO-US17248.
 XX
 PR 20-AUG-1997; 97US-0056112.
 XX
 PA (SMK) SMITHKLINE BEECHAM CORP.
 XX
 PI Anderson KM, Bouzyk M, Hansbury MJ, Jackson JR;
 PI Nerurkar SS, Roshak AK;
 XX
 DR WPI; 1999-18:027/15.
 DR N-PSDB; AAX27227.
 XX
 PT New serum inducible kinase (SNK); polypeptides and polynucleotides -
 PT useful for treating proliferative diseases
 XX
 XX Claim 1; Page 49-52; 41pp, English.
 XX
 CC This sequence is a human serum inducible kinase (SNK) of the
 CC invention. The invention relates to diagnostic assays or kits for
 CC detecting diseases associated with inappropriate SNK activity or levels.
 CC Disease states that can be diagnosed include proliferative diseases such

CC as leukemia, solid tumour cancers and metastases, chronic inflammatory
 CC proliferative diseases such as psoriasis and rheumatoid arthritis,
 CC proliferative cardiovascular diseases such as restenosis, proliferative
 CC ocular disorders such as diabetic retinopathy and benign
 CC hyperproliferative diseases such as haemangiomas. The polynucleotides can
 CC be used as hybridisation probes for cDNA and genomic DNA or as primers
 CC for a nucleic acid amplification (PCR) reaction, to isolate full-length
 CC cDNAs and genomic clones encoding polypeptides of this invention and to
 CC isolate cDNA and genomic clones of other genes which have a high sequence
 CC similarity to the SNK coding sequence. The differences between cDNA and
 CC genomic sequences can be observed and therefore mutations detected. Any
 CC mutations may then be attributed to likely causative agents of disease.
 CC The nucleotide sequences are also useful for chromosome identification.
 XX
 SQ Sequence 685 AA;
 Query Match 94.9%; Score 55; DB 20; Length 685;
 Best Local Similarity 90.9%; Pred. No. 0.11;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPFFTS 11
 LB 273 MLLGRPPFFET 283
 RESULT 6
 AAK68412
 ID AAK68412 standard; Protein; 685 AA;
 AC AAK68412;
 XX
 XX 14 APR 1993 (first entry);
 XX
 XX Disease associated protein kinase (APK-1).
 KW DAPK-1: disease associated protein kinase; human; diagnosis;
 KW therapy; adult respiratory distress syndrome; allergy; asthma;
 KW atelectasis; bronchitis; emphysema; hyperosinophilia;
 KW myocardial inflammation; pericardial inflammation; anasthma;
 KW rheumatoid arthritis; Addison's disease; AIDS; atherosclerosis;
 KW atopic dermatitis; dermatomyositis; diabetes mellitus;
 KW glomerulonephritis; gout; Grave's disease; lupus erythematosus;
 KW multiple sclerosis; myasthenia gravis; osteoarthritis;
 KW osteoporosis; pancreatitis; polycystic kidney disease;
 KW polyoma; scleroderma; Sjogren's syndrome;
 KW autoimmune thyroiditis; cancer; infection; trauma;
 KW cell proliferation.
 XX
 XX Homo sapiens
 CS
 XX
 XX Key Location/Qualifier
 XX Binding site 89..96
 XX /note="potential ATP binding site"
 XX Peptide 506..511
 XX /note="presumed regulatory sequence common to
 XX polo family protein kinases"
 XX
 XX W05593052-A2;
 XX
 XX 13 DEC 1998;
 XX
 XX 19 JUN 1998; 99WO-US12812;
 XX
 XX 19 JUN 1997; 97US-0878989;
 XX
 XX LINCY : INCYTE PHARM INC.
 XX
 XX Bradman G, Corley NC, Golt SK, Goshes EE, Hildman JD,
 XX La P, Shan P;
 XX
 XX W01, 1400-060952/07;
 XX N-1038; AAK68412
 XX

PT New disease associated protein kinases - used to stimulate cell
 PT proliferation and to treat the immune response and cancer
 XX
 PS Claim 1: Page 54-56; 93pp; English.
 XX
 CC This is the amino acid sequence of human disease associated protein
 CC kinase DAPK-1, as deduced from a consensus sequence (see AAK68412)
 CC of overlapping cDNA clones from libraries which are immortalised
 CC or cancerous and show inflammatory or immune responses. DAPK-1
 CC shows 53% homology to human proliferation-related protein kinase
 CC PRK 101 (48263). The invention provides DAPK-1 to DAPK-7
 CC polypeptides (see AAK68412-38) and cDNA clones encoding them (see
 CC AAK68411-36 and AAK68412), as well as expression vectors, host cells,
 CC agonists, antagonists and antibodies. The invention further
 CC provides uses of such products in the diagnosis, prevention and
 CC treatment of diseases associated with cell proliferation,
 CC especially cancer or an immune response (claimed). Conditions
 CC that may be treated include adult respiratory distress syndrome,
 CC allergies, asthma, atherosclerosis, bronchitis, emphysema,
 CC hyperosinophilia, myocardial or pericardial inflammation,
 CC rheumatoid arthritis, Addison's disease, AIDS, anaemia,
 CC atherosclerosis, various diseases of the digestive system, atopic
 CC dermatitis, dermatomyositis, diabetes mellitus, glomerulonephritis,
 CC gout, Grave's disease, lupus erythematosus, multiple sclerosis,
 CC myasthenia gravis, osteoarthritis, osteoporosis, pancreatitis,
 CC polycystic kidney disease, polymyositis, scleroderma, Sjogren's
 CC syndrome, autoimmune thyroiditis, complications of cancer,
 CC extracorporeal circulation, viral, bacterial, fungal, parasitic,
 CC protozoal and helminthic infections, and trauma (disclosed).
 XX
 SQ Sequence 685 AA;
 Query Match 94.9%; Score 55; DB 20; Length 685;
 Best Local Similarity 90.9%; Pred. No. 0.11;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPFFTS 11
 LB 273 MLLGRPPFFET 283
 RESULT 7
 ABP61474
 ID ABP61474 standard; Protein; 685 AA;
 AC ABP61474;
 XX
 XX 30-SEP-2002 (first entry)
 XX
 XX Human NF-kB activating protein SEQ ID NO 101.
 XX
 XX Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
 KW immunomodulator; cytostatic; antineoplastic; osteopathic; neurotropic;
 KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
 KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.
 XX
 XX Homo sapiens.
 OS
 XX
 XX W0200253737-A1.
 XX
 XX 11-JUL-2002.
 XX
 XX 25-DEC-2001; 2001WO-CPI1389.
 XX
 XX 28-DEC-2000; 2000JP-0422288.
 XX 26-MAR-2001; 2001JP-0098912.
 XX 24-AUG-2001; 2001JP-0254018.
 XX
 XX (ASAH) ASAHI KASEI KOGYO KK.
 PA
 XX
 XX Matsuda A, Honda G, Kikaratsu S, Nagano Y;
 XX
 XX WPI; 2002 583617/62.
 DR

DE N PSDB; ABQ91962.
XX
PT NF approximates activating gene and expressed protein, applicable in
PT diagnosis and screening inhibitors or promoters to control excessive
PT activation or inhibition for treating e.g. inflammations, autoimmune
PT diseases and cancer.
XX
XX
XX Claim 1; Page 445-453; 841pp; Japanese
XX
XX The invention relates to a purified protein 11, comprising one of 10
XX fully defined sequences (ABP1424-ABP6513) or a protein based on any of
XX the sequences with some amino acids deleted, substituted or added and
XX with a NF-KB nuclear factor kappa B activating effect. The protein and
XX encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening
XX inhibitors or promoters to control excessive activation or inhibition
XX and for treating e.g. inflammations, autoimmune diseases, cancers,
XX infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
XX disorders.
XX
XX Sequence 685 AA;
XX
XX Query Match 94.8%; Score 55; DB 23; Length 485;
XX Best Local Similarity 90.9%; Pred. No. 0.12;
XX Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY : MLGRRPPPTTS 1;
XX |||:|||||;
XX Db 273 MLGRRPPPTTS 283
XX
XX RESULT 8
XX AAB35805
XX ID AAB35805 standard; Protein: 626 AA.
XX AC AAB35805;
XX XX
XX DT 23-FEB-2001 (first entry)
XX XX
XX DE Protein involved in cell cycle regulation SEQ ID 46.
XX
XX Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
XX cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
XX cotton; rice; barley; millet.
XX
XX Zea mays.
XX
XX PN WC200065040-A2.
XX XX
XX PD 02-NOV-2000.
XX
XX PF 13-APR-2000; 2000CW-US09975.
XX
XX PR 22-APR-1999; 99US-0138849.
XX
XX XX (PION-) PIONEER HI-BRED INT. INC.
XX
XX Helentjaris TG, Habben JE, Sun Y;
XX WPI; 2000-687333/67.
XX DR N-PSDB; AAC83112.
XX

PS Claim 11; SEQ ID No 3124; 2922pp; English.
XX
XX The invention relates to 2175 novel human ovarian antigens (ABP4154-
XX ABA3228) and to cDNAs encoding them (ABQ54331-ABQ56305), and also
XX encompasses polypeptides 90% identical and polynucleotides 95% identical
XX to the sequences of the invention. The invention additionally relates to
XX recombinant vectors and host cells comprising human ovarian antigen
XX polynucleotides, antibodies against human ovarian antigens, and the use
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX treating, prognosing or preventing various ovary and/or breast-related
XX disorders. Such conditions include ovarian cancer and breast cancer, and
XX metastatic tumours of ovarian or breast origin, reproductive system
XX disorders (e.g., infertility, disorders of pregnancy, anovulation,
XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
XX vaginitis), immune disorders (e.g., congenital and acquired
XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
XX blood-related disorders (e.g., anaemia), cardiovascular disorders,
XX respiratory disorders, neurological disorders, gastrointestinal disorders
XX and urinary system disorders. Ovarian antigen polypeptides and
XX polynucleotides may also be used in screening for compounds which
XX modulate ovarian antigen expression or activity. The polynucleotides may
XX further be used for gene therapy, chromosome mapping, in the
XX identification of individuals and in forensic analysis, and the
XX polypeptides may be used as food additives or to prepare antibodies
XX useful in disease diagnosis, drug targeting and phenotyping. The present
XX sequence represents a human ovarian antigen of the invention.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 753 AA;
XX
XX Query Match 94.8%; Score 55; DB 23; Length 753;
XX Best Local Similarity 90.9%; Pred. No. 0.12;
XX Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY : MLGRRPPPTTS 1;
XX |||:|||||;
XX Db 341 MLGRRPPPTTS 351
XX
XX RESULT 9
XX AAB35805
XX ID AAB35805 standard; Protein: 626 AA.
XX AC AAB35805;
XX XX
XX DT 23-FEB-2001 (first entry)
XX XX
XX DE Protein involved in cell cycle regulation SEQ ID 46.
XX
XX Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean;
XX cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa;
XX cotton; rice; barley; millet.
XX
XX Zea mays.
XX
XX PN WC200065040-A2.
XX XX
XX PD 02-NOV-2000.
XX
XX PF 13-APR-2000; 2000CW-US09975.
XX
XX PR 22-APR-1999; 99US-0138849.
XX
XX XX (PION-) PIONEER HI-BRED INT. INC.
XX
XX Helentjaris TG, Habben JE, Sun Y;
XX WPI; 2000-687333/67.
XX DR N-PSDB; AAC83112.
XX

XX Nucleic acids useful for producing transgenic plants, preferably maize,
 PT with increased cell cycle gene activity, preferably activity of cyclin
 PT and/or cyclin-dependent kinase.
 XX
 XX
 PS Claim 15: Page 117-118; 122pp; English.
 XX
 CC Polynucleotide sequences AAC83111. AAC83111 encode proteins AAB35794 -
 CC AAB35806 which are involved in regulating the cell cycle. The protein and
 CC RNA sequences have been isolated from Zea mays (corn), and the invention
 CC also includes oligonucleotides AAC83114 - AAC83119 which are related to
 CC the cell cycle polynucleotides. The cell cycle polynucleotide sequences
 CC are useful for producing transgenic plants such as maize, soybean,
 CC sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley and
 CC millet with increased levels of cell cycle gene activity, such as
 CC activity of cyclin and cyclin-dependent kinases. The DNA sequences are
 CC also useful as probes for detecting deficiencies in the level of rRNA in
 CC screening for desired transgenic plants, for detecting mutations in the
 CC gene, for monitoring upregulation of expression or changes in enzyme
 CC activity in screening assays of compounds, for detecting any number of
 CC allelic variants, orthologs or paralogues of the gene, and site-directed
 CC mutagenesis in eukaryotic cells. The DNA sequences are also useful for
 CC recombinant expression of the encoded polypeptides and as immunogens for
 CC preparing and screening antibodies. A transgenic plant comprising an
 CC expression cassette including a cell cycle regulatory gene is useful for
 CC assaying enzyme agonists and antagonists, and as immunogens or antigens
 CC to obtain antibodies. The antibodies are useful in assaying expression
 CC levels of cell cycle regulatory proteins, for identifying and isolating
 CC nucleic acids from expression libraries, for identifying homologues of
 CC polypeptides from other species, and for purification of the proteins.
 XX
 SQ Sequence 628 AA;

Query Match 89.7%; Score 52; DB 21; Length 626;
 Best Local Similarity 81.8%; Pred. No. 0.16;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLGPPFFETS 11
 |||||
 DQ 228 LAGPPFFETS 238

RESULT 1:
 AAW74162
 ID AAW74162 standard; peptide; 9 AA.

AC AAW74162;

UT 05 MAY 1999 first entry;

DE HJ loop Peptide J-45.

KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.

OS Synthetic.

FH Key Location/Qualifiers
 FT Modified site 1
 FT Modified site 9 /note= "acetylated"
 FT Modified site 9 /note= "amidated"

XX W09853050-A2.

PN 26 NOV-1998.

XX 20 MAY 1998; 98WC-US:0319.

XX 21-MAY-1997; 97US-0861338.

XX

PA (CHIL-) CHILDRENS MEDICAL CENT.

XX (YISS) YISSUM RES & DEV CO.

PI Ben-Sasson SA;

XX WP1; 1999-070142/06.

DR
 XX New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders

XX Claim 14; Fig 4; 70pp; English.

CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.

XX Sequence 9 AA;

Query Match 84.5%; Score 49; DB 20; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LGRPPFFETS 11

|||||
 DQ 1 LGRPPFFETS 9

RESULT 1:

AAW74159

ID AAW74159 standard; peptide; 9 AA.

AC AAW74159;

UT 05 MAY-1999 (first entry);

DE HJ loop peptide J-42.

KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.

OS Synthetic.

FH Key Location/Qualifiers
 FT Modified-site 1 /note= "acetylated"
 FT Modified-site 9 /note= "amidated"
 FT Modified-site 9 /note= "benzyl ester of Glu"

XX W09853050-A2.

XX 26-NOV-1998.

XX 20-MAY-1998; 98WC-US:0319.

XX

PR 21-MAY-1997; 97JUS-0861338.
 PA (CHILD) CHILDRENS MEDICAL CENT.
 PA VISS J VISSUM RES & DEV CC.
 XX
 XX Ben Sasson SA;
 XX
 XX WPI: 1999 070142/26.
 XX
 XX New peptides for modulating serine/threonine kinase activity
 PT comprise a sequence corresponding to the HJ loop of a
 PT serine/threonine kinase, used for treating, e.g., cancers,
 PT inflammatory disorders or autoimmune disorders
 XX
 XX Claim 14; Fig 4; Popp; English.
 XX
 XX This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 84.5%; Score 49; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPPE 9
 DB 1 MLLGRPPPE 9
 ID AAU98315 standard; Peptide; 9 AA.
 XX
 XX AAU98315;
 AC
 DT 13-AUG-2002 (first entry)
 DE Polo kinase serine-threonine kinase HJ loop peptide J-42.
 XX
 XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
 KW modulating STK activity; polo kinase; J-42.
 XX
 XX Unidentified.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminal acetyl"
 FT
 FT Misc-difference 7
 FT Modified-site 9 /note= "Benzyl ester of Glutamic acid"
 FT /note= "C-terminal amide"
 XX
 XX US2002049301 A1.
 XX
 XX 25-APR-2002.

PD 25-APR-2002.
 XX
 PF 13-DEC-2000; 2000JUS 0716076.
 XX
 PR 21-MAY-1997; 97JUS-0861338.
 XX
 XX (CHILD) CHILDRENS MEDICAL CENT.
 PA Ben-Sasson SA;
 PI
 XX WPI: 2002-462787/49.
 DR
 XX New peptide from the HJ loop of serine-threonine kinase, useful for
 PT treating e.g. cancer and for producing diagnostic antibodies -
 XX
 XX Disclosure; Fig 4; 4lpp; English.
 PS
 XX The present invention relates to new peptides derived from the HJ loop
 CC of a serine/threonine kinase (STK). The peptides of the invention are
 CC used to modulate STK activity, especially for treating cancer, diabetes,
 CC obesity or a wide variety of central nervous system, inflammatory,
 CC autoimmune or cardiovascular disorders, also haemorrhagic shock, and for
 CC regulating lipid metabolism. The peptides are also used to generate
 CC antibodies that bind specifically to the parent STK, used e.g. for
 CC identifying STK-expressing cells and to study intracellular distribution
 CC of STK, and to identify or quantify ligands that bind to the HJ loop.
 CC The present amino acid sequence represents the polo kinase
 CC serine-threonine kinase HJ loop peptide J-42. This sequence is one of
 CC the short peptides of the invention that selectively modulate the
 CC activity of STK.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 84.5%; Score 49; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPPE 9
 DB 1 MLLGRPPPE 9
 ID AAU98318 standard; Peptide; 9 AA.
 XX
 XX AAU98318;
 AC
 DT 13-AUG-2002 (first entry)
 XX
 DE Polo kinase serine-threonine kinase HJ loop peptide J-45.
 XX
 XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 KW central nervous system disorder; inflammatory disorder;
 KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 KW antiinflammatory; immunosuppressive; cardiac; haemostatic;
 KW modulating STK activity; polo kinase; J-45.
 XX
 XX Unidentified.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminal acetyl"
 FT
 FT Misc-difference 7
 FT Modified-site 9 /note= "Benzyl ester of Glutamic acid"
 FT /note= "C-terminal amide"
 XX
 XX US2002049301 A1.
 XX
 XX 25-APR-2002.

XX 13 DEC-2000; 2000US-0736076.
 XX 21-MAY-1997; 97US-0861338.
 XX CHILDREN'S MEDICAL CENT.
 XX REC SASSON SA;
 XX WPI: 2002-462757/49.
 XX New peptide from the HJ loop of serine/threonine kinase, useful for
 XX treating e.g. cancer and for producing diagnostic antibodies -
 XX Disclosure; Fig 4; 41pp; English.
 XX The present invention relates to new peptides derived from the HJ loop
 XX of a serine/threonine kinase (STK). The peptides of the invention are
 XX used to modulate STK activity, especially for treating cancer, diabetes,
 XX obesity or a wide variety of central nervous system, inflammatory,
 XX autoimmune or cardiovascular disorders. Also haemorrhagic shock, and for
 XX regulating lipid metabolism. The peptides are also used to generate
 XX antibodies that bind specifically to the parent STK, used e.g. for
 XX identifying STK-expressing cells and to study intracellular distribution
 XX of STK, and to identify or quantify ligands that bind to the HJ loop.
 XX The present amino acid sequence represents the polo kinase
 XX serine/threonine kinase HJ loop peptide 3-45. This sequence is one of
 XX the short peptides of the invention that selectively modulate the
 XX activity of STK.
 XX Sequence 9 AA;
 XX
 XX Query Match: 84.5%; Score 49; DB 23; Length 9;
 XX Best Local Similarity 100.0%; Pred. No. 0.019;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQSPFFETS 11
 DB [|||||]
 : LQSPFFETS 9
 RESULT 14
 AAU7423
 ID AAU7423 standard; Peptide: 10 AA
 AC AAU7423;
 XX 65-MAY-1999 (first entry)
 XX HJ loop peptide K038H101.
 XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 XX haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 XX inflammatory disorder; central nervous system disease; septic shock;
 XX Parkinson's disease; hypertension.
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "myristylated"
 FT Modified-site 10 /note= "amidated"
 FT Modified-site 10 /note= "amidated"
 PK W09831055-A2
 XX 26 NOV-1998.
 XX 20-MAY-1998; 99WO-US10319
 XX 21-MAY-1997; 97US-0861338.
 XX CHILDREN'S MEDICAL CENT.

PA (YISS : YISSUM RES & DEV CO.
 XX Ber Sasson SA;
 XX WPI: 1999-070142/56.
 XX New peptides for modulating serine/threonine kinase activity -
 XX comprise a sequence corresponding to the HJ loop of a
 XX serine/threonine kinase, useful for treating, e.g. cancers,
 XX inflammatory disorders or autoimmune disorders
 XX Disclosure; Fig 6; 75pp; English.
 XX This sequence represents a peptide of the invention, and is a derivative
 XX of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 XX used for the treatment of disorders caused by overactivity or
 XX underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 XX shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 XX arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 XX hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 XX psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 XX of organ transplant rejection, multiple sclerosis, inflammatory bowel
 XX disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 XX disease, stroke and trauma), septic shock, Parkinson's disease or
 XX hypertension. The peptides can also be used to produce antibodies which
 XX can be used to identify cells expressing the STK and to study the
 XX intracellular distribution of the STK. In addition, the peptides can be
 XX used to identify and quantitate ligands which bind the HJ loop of the STK
 XX from which the peptide was derived.
 XX Sequence 10 AA;
 XX
 XX Query Match: 84.5%; Score 49; DB 23; Length 10;
 XX Best Local Similarity 100.0%; Pred. No. 0.019;
 XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGGRPFEE 9
 DB [|||||]
 2 MLGGRPFEE 10
 RESULT 15
 AAU98357
 ID AAU98357 standard; Peptide: 10 AA.
 AC AAU98357;
 XX 13-AUG-2002 (first entry)
 XX Polo kinase SNK serine-threonine kinase HJ loop peptide K038H101.
 XX HJ loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
 XX central nervous system disorder; inflammatory disorder;
 XX autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
 XX lipid metabolism; cytostatic; antidiabetic; anorectic; neurological;
 XX antiinflammatory; immunosuppressive; cardiac; haemostatic;
 XX modulating STK activity; polo kinase; SNK; K038H101.
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal myristyl"
 FT Modified-site 10 /note= "Benzy! Ester of Glutamic Acid, C-terminal amide"
 PK US2002049301-A1
 XX 25-APR-2002.
 XX 13 DEC-2000; 2000US-0736076.
 XX CHILDREN'S MEDICAL CENT.

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PR      21-MAY-1997;       97US-0861338.
XX
XX      (CHILD) : CHILDRENS MEDICAL CENT.
XX
XX      Ben-Sasson SA;
XX
XX      WPI: 2002-442787/43.
XX
XX      New peptide from the HJ loop of serine/threonine kinase, useful for
PT      treating e.g. cancer and for producing diagnostic antibodies
XX
XX      Enclosure; Fig #1: 4pp; English.
XX
XX      The present invention relates to new peptides derived from the HJ loop
CC      of a serine/threonine kinase (STK). The peptides of the invention are
CC      used to modulate STK activity, especially for treating cancer, diabetes,
CC      obesity or a wide variety of central nervous system inflammatory, and for
CC      treatment of cardiovascular disorders. Also haemorrhagic shock, and for
CC      regulating lipid metabolism. The peptides are also used to generate
CC      antibodies that bind specifically to the parent STK, used e.g. for
CC      identifying STK-expressing cells and to study intracellular distribution
CC      of STK, and to identify or quantify ligands that bind to the HJ loop.
CC      The present amino acid sequence represents the polo kinase SKX
CC      serine-threonine kinase HJ loop peptide KQSHN10. This sequence is one
CC      of the short peptides of the invention that selectively modulate the
CC      activity of STK.
XX
XX      Sequence   10 AA;
SQ
Query Match          84.5%; Score 49; DB 23; Length 10;
Seq-Ident Similarity 100.0%; Pred. No. C019;
Matches    9; Conservative    0; Mismatches    0; Gaps    0;
CY      1 NLGGRPFEE 9
UH      11 . . . . .
        2 NLGGRPFEE 10
RESULT 10
AAW74173
1U AAW74173 standard; peptide: 20 AA.
XX
XX AAW74173;
XX AC AC
XX AC AC
XX DT DT
XX DE DE
XX HW loop peptide: PQLD
XX HW loop; serine/threonine kinase; cellular haemorrhagic shock; therapy;
KW haemorrhagic shock; cardiovascular diseases; immunosuppressive disorder;
KW inflammatory disorder; central nervous system disease; septic shock;
KW Parkinson's disease; hypertension.
XX
XX CS Synthetic.
XX XX
XX XX WQWRAICDS-A2
XX XX
XX PO 16 NOV 1998.
XX
XX 20-MAY-1998; 96WO-US10319.
XX
XX 21-MAY-1997; 97US-0861338.
XX
XX (CHILD) : CHILDRENS MEDICAL CENT.
PA (YISS) : YISSUM RES & DEV CO.
XX
XX Ben-Sasson SA;
XX
XX WPI: 1999-070142/06.
XX
XX New peptides for modulating serine/threonine kinase activity
PT comprise a sequence corresponding to the HJ loop of a
PT serine/threonine kinase, used for treating, e.g., cancers.

```

inflammatory disorders or autoimmune disorders

Claim 41; Fig 3b; WOPP: English.

This sequence represents a peptide of the invention, and is a derivative of the HC loop of a serine/threonine kinase (STK). The peptides can be used for the treatment of disorders caused by overactivity or underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis, arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and hypertension), immunosuppressive and inflammatory disorders (e.g. asthma, psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression of organ transplant rejection, multiple sclerosis, inflammatory bowel disease and AIDS), central nervous system diseases (e.g. Alzheimer's disease, stroke and trauma), septic shock, Parkinson's disease or hypotension. The peptides can also be used to produce antibodies which can be used to identify cells expressing the STK and to study the intracellular distribution of the STK. In addition, the peptides can be used to identify and quantitate ligands which bind the HC loop of the STK from which the peptide was derived.

Sequence 20 AA;

Query Match 84.5%; Score 49; DB 20; Length 20;
Best Local Similarity 72.7%; Pred.No. 0.039;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLVGPPPTETS 11
|||
DB 3 LVGPPPTETS 13

RESULT 17
AAU983C6
ID AAU983C6 standard; Rep:ide; 20 NA.
XX AC AAU983C6;
XX DT 13-AUG-2002 (first entry)
XX DE Peptide sequence of HC loop of serine-threonine kinase polo kinase.
XX KW HC loop; serine/threonine kinase; STK; cancer; diabetes; obesity;
KW central nervous system disorder; inflammatory disorder;
KW autoimmune disorder; cardiovascular disorder; haemorrhagic shock;
KW lipid metabolism; cytostatic; antidiabetic; anorectic; neurologic;cal;
KW anti-inflammatory; immunosuppressive; cardiant; haerostatic;
XX modulating STK activity; polo kinase.
XX OS Unidentified.
XX OS US2002049301-A1.
PN XX 25-APR-2002.
PD PF 13-DEC-2000; 2000US-0736076.
PR XX 21-MAY-1997; 97US-0861338.
XX (CHILD-) CHILDRENS MEDICAL CENT.
PA Ben-Sasson SA;
XX WPI; 2002-462787/49.
XX New peptide from the HC loop of serine-threonine kinase, useful for treating e.g. cancer and for producing diagnostic antibodies -
XX Claim 33; Fig 3; 4ipp: English.
PS The present invention relates to new peptides derived from the HC loop of a serine/threonine kinase (STK). The peptides of the invention are CC used to modulate STK activity, especially for treating cancer, diabetes,

FT Misc-difference 355 /label= Unknown
 FT Misc-difference 356 /label= Unknown
 FT Misc-difference 357 /label= Unknown
 FT Misc-difference 358 /label= Unknown
 FT Misc-difference 359 /label= Unknown
 FT Misc-difference 360 /label= Unknown
 FT Misc-difference 361 /label= Unknown
 FT Misc-difference 362 /label= Unknown
 FT Misc-difference 363 /label= Unknown
 FT Misc-difference 364 /label= Unknown
 FT Misc-difference 365 /label= Unknown
 FT Region 410..439
 FT /label= Polo box
 FT /note= "Core polo-box consensus sequence"
 XX W02001:904C1-A2.
 XX 20-10 V 2001.
 XX 21-MAY-2001; 2001WO-US16923.
 XX 23-MAY-2000; 2000US-206588P.
 XX HARVARD COLLEGE.
 XX US DEPT HEALTH & HUMAN SERVICES.
 XX US NAT INST OF HEALTH.
 P Lee KS, Song S, Erikson R;
 XX WPI: 2002-106210/14.
 XX
 PT Identifying polo-like kinase modulators by contacting eukaryotic cells
 PT expressing polo-box peptides with test compounds and evaluating changes
 PT in dominant negative cytokinesis-defective growth patterns
 XX Example 1: Fig 5; 57pp; English.
 XX The invention describes a novel method of detecting compounds with
 XX polo-like kinase (PLK) modulating activity. This comprises contacting
 XX eukaryotic cells expressing polo-box or polo-box related peptides,
 XX binding peptides comprising 25 contiguous residues from a polo-like
 XX kinase C-terminal region, with a test compound. Ecopic expression of a
 XX polo-box in a eukaryotic cell causes a severe cytotoxic defect in the
 XX cell. These eukaryotic cells can also be tested with the test compound
 XX used in the method of the invention. The polo-box related peptides and
 XX polo-like kinase activity modulatory compounds can be used to inhibit or
 XX enhance cellular proliferation and subsequently for treating
 XX hyperproliferative disorders including neoplasia, solid tumours,
 XX carcinomas, sarcomas and cancers e.g. small cell carcinoma,
 XX adenocarcinoma, Mullerian tumours and squamous cell carcinoma. This
 XX is the amino acid sequence of a mammalian polo-like kinase (Plk),
 XX uncontrolled expression of the Plk family is implicated in the
 XX development of human cancers, discussed in the method of the invention.
 XX Sequence 531 AA:
 SQ
 Query Match 84.5%; Score 49; DB 23; Length 511;
 Best Local Similarity 72.7%; Pred. No. 1.1;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGKPPFETS 11

Db 204 LLVGKPPFETS 214
 RESULT 20
 AAR74620
 ID AAR74620 standard; Protein; 603 AA.
 AC AAR74620;
 XX
 XX 25-MAR-2003 (updated);
 DT 26-OCT-1995 (first entry);
 XX
 DE Human lung tumour Polo-like kinase.
 XX
 XX Polo-like kinase; PLK, serine threonine kinase; human; lung tumour;
 KW autoimmune disease; lymphocyte activity.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Binding-site 60..86
 FT /label= ATP-binding_motif
 FT Region 174..177
 FT /note= "motif that is highly conserved in protein
 FT kinases"
 FT Region 194..196
 FT /note= "motif that is highly conserved in protein
 FT kinases"
 XX
 XX DE4329177-A1.
 XX 02-MAR-1995.
 XX 30-AUG-1993; 93DE 4329177.
 XX 30-AUG-1993; 93DE-4329177.
 XX (CHEM-) CHEMOTHERAPEUTISCHES FORSCHUNG.
 XX
 XX Holtrich U, Rubsamen-Waigmann H, Strebhardt K;
 PI Rubsamen-Waigmann H;
 XX WPI: 1995-099454/14.
 DR N-PSDB; AA088155.
 XX
 FT A polo-like serine threonine kinase-protein - isolated from
 FT proliferating human tissue, useful in the determin of lymphocyte
 FT activity, eg in autoimmune diseases
 XX
 XX Claim 1: Page 8-10, 11pp; German.
 XX
 CC A human lung tumour-derived cDNA (AAQ88155) was found to have high
 CC homology with sequences from members of the serine/threonine kinase
 CC family. Due to the strong homology with the Drosophila polo gene,
 CC the protein encoded by the new cDNA (AAR74620) was designated a polo-
 CC like kinase (PLK). PLK mRNA is expressed in proliferating cells such
 CC as placenta, colon and tumours of the lung, oesophagus, gut and
 CC intestine. Resting lymphocytes do not express the PLK gene but after
 CC stimulation with phytohemagglutinin, PLK is expressed and can be
 CC used as an indicator of lymphocyte stimulation.
 CC Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 603 AA:
 SQ
 Query Match 84.5%; Score 49; DB 16; Length 603;
 Best Local Similarity 72.7%; Pred. No. 1.3;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGKPPFETS 11
 Db 244 LLVGKPPFETS 254

RESULT 21

AAU79306 standard; Peptide: 603 AA.

XX AC AAU79306;

XX DT 02-JUL-2002 (first entry)

XX DE Mouse polo-like kinase (Pik).

XX KW Polo box; Pbl; cytosolic; fungicide; protozoicide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Pik.

XX OS Mus musculus.

XX FN US6458738-B1.

XX PU 19-MAR-2002.

XX PA 13-MAY-1999; 99US-0311311.

XX PR 13-MAY-1998; 98US-085296P.

XX PA (HARD) HARVARD COLLEGE.

XX PI Erikson RL, Lee KS;

XX DR WPI: 2002-314756/35.

XX PT Administering polo kinase inhibitors for the treatment of cancers and
 fungal infections

XX PS Example 1; Column: 59-64; 47pp; English.

XX CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), and protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Pik), a
 CC protein from which mitotic protein polo kinase inhibitory peptides are
 CC derived.

XX SQ Sequence 603 AA;

Query Match 84.5%; Score 49; DB 23; Length 603;
 Best Local Similarity 72.7%; Pred. No. 1.3;

Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPPTS 11

Db 244 LVGKPPPTS 254

RESULT 22

AAU79306 standard; Peptide: 603 AA.

XX AC AAU79306;

XX DT 02-JUL-2002 (first entry)

XX DE Mouse polo-like kinase (Pik) T2ICE mutant.

XX

DE Mouse polo-like kinase (Pik) T2:0D mutant.

XX KW Polo box; Pbl; cytosolic; fungicide; protozoicide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Pik; mutant; mutain.

XX OS Mus musculus.

XX OS Synthetic.

XX PH Key Location/Qualifiers

XX FT Misc-difference 210 /note= "wild type Thr substituted by Asp"

XX PN US6358738-B1.

XX ZC 19-MAR-2002.

XX XX 13-MAY-1999; 99US-0311311.

XX XX 13-MAY-1998; 98US-085296P.

XX XX (HARD) HARVARD COLLEGE.

XX XX Erikson RL, Lee KS;

XX XX WPI: 2002-314756/35.

XX XX Administering polo kinase inhibitors for the treatment of cancers and
 fungal infections

XX PS Example 1; Page 47pp; English.

XX CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Pik).

XX CC mutant, used to determine the residues required for kinase activity.

XX CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79306 using information
 CC given in the invention.

XX SQ Sequence 603 AA;

Query Match 84.5%; Score 49; DB 23; Length 603;
 Best Local Similarity 72.7%; Pred. No. 1.3;

Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPPTS 11

Db 244 LVGKPPPTS 254

KW Polo box; Pbl; cytostatic; fungicide; protozoacide; antihelminthic;
 KW antipodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retinal cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
 XX
 XX Mus musculus.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc: difference 210 /note= "Wild type Thr substituted by Glu"
 FT
 XX
 XX US6358738-B1.
 XX 19-MAR-2002.
 XX 13-MAY-1999; 99US-0311311.
 XX 13-MAY-1998; 98US-085296P.
 XX (HARD) HARVARD COLLEGE.
 XX Erikson RL, Lee KS;
 XX WPI; 2002 3:4756/35.
 XX Administering polo kinase inhibitors for the treatment of cancers and
 fungal infections .
 XX
 XX Example 1; Page 4; 47pp; English.
 XX The invention describes a method of inhibiting growth of an isolated
 population of cells by inhibiting a cell polo kinase by administering a
 polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 carboxy terminal domain of the polo kinase which excludes the polo
 kinase catalytic domain. The method is used for the treatment of cancer
 (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 cervix, the epithelium, the brain, the retina, the prostate, and the
 throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
 mutant, used to determine the residues required for kinase activity.
 XX Note: This sequence does not appear in the specification but has been
 created from the wild type sequence shown in AAU79306 using information
 given in the invention.
 XX
 SQ Sequence 603 AA;
 Query Match 84.5%; Score 49; DB 23; Length 603;
 Best Local Similarity 72.7%; Pred. No. 1.3;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLVGKPPFETS 1;
 Db 244 LLVGKPPFETS 254
 RESULT 24
 AAU79310
 ID AAU79310 standard; Peptide; 603 AA.
 XX
 XX AAU79310;
 XX 02-JUL-2002 (first entry)
 XX Mouse polo like kinase (Plk) T21V mutant.
 KW Polo box; Pbl; cytostatic; fungicide; protozoacide; antihelminthic;
 KW antipodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;

KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retinal cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutain.
 XX
 XX Mus musculus.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc: difference 210 /note= "Wild type Thr substituted by Val"
 FT
 XX
 XX US6358738-B1.
 XX 19-MAR-2002.
 XX 13-MAY-1999; 99US-0311311.
 XX 13-MAY-1998; 98US-085296P.
 XX (HARD) HARVARD COLLEGE.
 XX Erikson RL, Lee KS;
 XX WPI; 2002 3:4756/35.
 XX Administering polo kinase inhibitors for the treatment of cancers and
 fungal infections .
 XX
 XX Example 1; Page 4; 47pp; English.
 XX The invention describes a method of inhibiting growth of an isolated
 population of cells by inhibiting a cell polo kinase by administering a
 polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 carboxy terminal domain of the polo kinase which excludes the polo
 kinase catalytic domain. The method is used for the treatment of cancer
 (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 cervix, the epithelium, the brain, the retina, the prostate, and the
 throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 XX This is the amino acid sequence of a mouse polo-like kinase (Plk)
 mutant, used to determine the residues required for kinase activity.
 XX Note: This sequence does not appear in the specification but has been
 created from the wild type sequence shown in AAU79306 using information
 given in the invention.
 XX
 SQ Sequence 603 AA;
 Query Match 84.5%; Score 49; DB 23; Length 603;
 Best Local Similarity 72.7%; Pred. No. 1.3;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLVGKPPFETS 1;
 Db 244 LLVGKPPFETS 254
 RESULT 25
 AAU79311
 ID AAU79311 standard; Peptide; 603 AA.
 XX
 XX AAU79311;
 XX 02-JUL-2002 (first entry)
 XX Mouse polo-like kinase (Plk) E206V mutant.
 KW Polo box; Pbl; cytostatic; fungicide; protozoacide; antihelminthic;
 KW antipodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;

XX Mus musculus.
 CS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 236 /note= "Wild type Asp substituted by Val"
 FT Misc-difference 210 /note= "Wild type Thr substituted by Val"

XX US6358738-B1.
 XX 19-MAR-2002.
 XX 13-MAY-1999; 98US-0311311.
 XX 13-MAY-1998; 98US-085296P.
 XX (HARD) HARVARD COLLEGE.
 XX Erikson RL, Lee KS;
 XX WPI; 2002-314756/35.

XX Administering polo kinase inhibitors for the treatment of cancers and
 FT fungal infections
 XX
 XX Example 1; Page -; 47pp; English.

CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC thymus), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79315 using information
 CC given in the invention.

XX Sequence 603 AA.

Query Match 84.5%; Score 49; DB 23; Length 603;
 Best Local Similarity 72.7%; Pred. No. 1.3;
 Matches 8; Conservation 3; Mismatches 0; Gaps 0;

QY 1 MLGRRPPETS 11
 1111111111
 Db 244 LNVGRPPETS 254

RESULT 29

AAU79315
 ID AAU79315 standard; Peptide; 603 AA.

XX
 AC AAU79315;

XX 02-JUL-2002 (first entry)
 XX
 DE Mouse polo-like kinase (Plk) D194R mutant.

XX Polo box, PB1; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutatin.

XX Mus musculus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 194 /note= "Wild type Asp substituted by Asn"

XX US6358738-B1.
 XX 19-MAR-2002.
 XX 13-MAY-1999; 98US-0311311.
 XX 13-MAY-1998; 98US-085296P.
 XX (HARD) HARVARD COLLEGE.
 XX Erikson RL, Lee KS;
 XX WPI; 2002-314756/35.

XX Administering polo kinase inhibitors for the treatment of cancers and
 FT fungal infections
 XX
 XX Example 1; Page -; 47pp; English.

CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC thymus), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79315 using information
 CC given in the invention.

XX Sequence 603 AA.

Query Match 84.5%; Score 49; DB 23; Length 603;
 Best Local Similarity 72.7%; Pred. No. 1.3;
 Matches 8; Conservation 3; Mismatches 0; Gaps 0;

QY 1 MLGRRPPETS 11
 1111111111
 Db 244 LNVGRPPETS 254

RESULT 29
 AAU79315

ID AAU79315 standard; Peptide; 603 AA.

XX
 AC AAU79315;

XX 02-JUL-2002 (first entry)
 XX
 DE Mouse polo-like kinase (Plk) D194R mutant.

XX Polo box, PB1; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW throat cancer; fungal infection; Candida; Lichen; Trichophyton;
 KW Epidermophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; mutatin.

XX Mus musculus.

OS Synthesis.

XX Key Location/Qualifiers

PH Misc-difference 194

FT /note: "Wild type Asp substituted by Asg"

XX US6358738-B1:

XX 19-MAR-2002.

XX 13-MAY-1999; 99US-0311311.

XX 13-MAY-1998; 98US-085236P.

XX (HARD) HARVARD COLLEGE.

XX Erikson RJ, Lee KS;

XX WPI; 2002-3:4756/35.

XX Administering polo kinase inhibitors for the treatment of cancers and

PT fungal infections -

XX Example 1; Page 47pp; English.

XX The invention describes a method of inhibiting growth of an isolated

XX population of cells by inhibiting a cell polo kinase by administering a

XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a

XX carboxy terminal domain of the polo kinase which excludes the polo

XX kinase catalytic domain. The method is used for the treatment of cancer

XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the

XX cervix, the epithelium, the brain, the retina, the prostate, and the

XX tract), infection by fungi (e.g. Candida, Lichen, Trichophyton,

XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.

XX This is the amino acid sequence of a mouse polo-like kinase (Plk)

XX mutant, used to determine the residues required for kinase activity.

XX Note: This sequence does not appear in the specification but has been

XX created from the wild type sequence shown in AAU79306 using information

XX given in the invention.

XX Sequence 603 AA;

XX

Query Match: 84.5%; Score 49; DB 23; Length 603;

Best Local Similarity 72.2%; Pred. No. 1.3;

Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPPETS 11

DB 244 LLVGRPPPPETS 254

RESULT 31

AAU79317

ID AAU79317 standard; Peptide; 603 AA.

XX AAU79317;

XX 02 JUL 2002 (first entry)

XX Mouse polo like kinase (Plk) K25M mutant.

XX Polo box; PBI; cytostatic; fungicide; protozoacide; antihelminthic;

XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;

XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;

XX cancer of the uterus; ovarian cancer; cervical cancer;

XX epithelial cancer; brain cancer; retina cancer; prostate cancer;

XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;

XX Epidermophyton; Microsporium; protozoan infection; helminthes infection;

XX arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.

XX Mus musculus.

OS Synthetic.

XX Key Location/Qualifiers

PH Misc-difference 415

FT

PH Key Location/Qualifiers

FT Misc-difference 28

XX /note: "Wild type Lys substituted by Met"

XX US6358738-B1:

XX 19-MAR-2002.

XX 13-MAY-1999; 99US-0311311.

XX 13-MAY-1998; 98US-085236P.

XX (HARD) HARVARD COLLEGE.

XX Erikson RJ, Lee KS;

XX WPI; 2002-3:4756/35.

XX Administering polo kinase inhibitors for the treatment of cancers and

PT fungal infections -

XX Example 2; Page 47pp; English.

XX The invention describes a method of inhibiting growth of an isolated

XX population of cells by inhibiting a cell polo kinase by administering a

XX polo kinase inhibitor. The inhibitor comprises a sequence derived from a

XX carboxy terminal domain of the polo kinase which excludes the polo

XX kinase catalytic domain. The method is used for the treatment of cancer

XX (e.g. cancer of the lung, the breast, the uterus, the ovaries, the

XX cervix, the epithelium, the brain, the retina, the prostate, and the

XX tract), infection by fungi (e.g. Candida, Lichen, Trichophyton,

XX Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.

XX This is the amino acid sequence of a mouse polo-like kinase (Plk)

XX mutant, used to determine the residues required for kinase activity.

XX Note: This sequence does not appear in the specification but has been

XX created from the wild type sequence shown in AAU79306 using information

XX given in the invention.

XX Sequence 603 AA;

XX

Query Match: 84.5%; Score 49; DB 23; Length 603;

Best Local Similarity 72.2%; Pred. No. 1.3;

Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPPPETS 11

DB 244 LLVGRPPPPETS 254

RESULT 31

AAU79317

ID AAU79317 standard; Peptide; 603 AA.

XX AAU79317;

XX 02 JUL 2002 (first entry)

XX Mouse polo like kinase (Plk) V415A mutant.

XX Polo box; PBI; cytostatic; fungicide; protozoacide; antihelminthic;

XX arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;

XX polo kinase catalytic domain; cancer; lung cancer; breast cancer;

XX cancer of the uterus; ovarian cancer; cervical cancer;

XX epithelial cancer; brain cancer; retina cancer; prostate cancer;

XX throat cancer; fungal infection; Candida; Lichen; Trichophyton;

XX Epidermophyton; Microsporium; protozoan infection; helminthes infection;

XX arthropod infection; mouse; polo-like kinase; Plk; mutant; muten.

XX Mus musculus.

OS Synthetic.

XX Key Location/Qualifiers

PH Misc-difference 415

FT

/note= "Wild type Val substituted by Ala"

FT XX US6358738-B1.
 PD 19-MAR-2002.
 XX PF 13-MAY-1999; 99US-0311311.
 AA PR 13-MAY-1998; 98US-085296P.
 XX PA (HARD) HARVARD COLLEGE.
 XX PI Erikson RL, Lee KS.
 XX DR WPI; 2002-314756/35.
 XX PT Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections -
 XX PS Example 7; Page : 47pp; English.
 XX CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79319 using information
 CC given in the invention.
 XX SQ Sequence 603 AA.
 XX
 Query Match 84.5%; Score 49; DB 23; Length 603;
 Best Local Similarity 72.7%; Pred. No. 1.3;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGRRPFETS 11
 344 LLVGRPFETS 254
 RESULT 12
 AAU79319
 ID AAU79319 standard; Peptide: 603 AA
 XX AC AAU79319;
 XX DT 02-JUL-2002 (first entry)
 XX DE Mouse polo-like kinase (Plk) L427A mutant.
 XX KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW trichophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; murein.
 XX OS Mus musculus.
 XX CS Synthetic.
 XX PH Key Location/Qualifiers
 FT Misc difference 427 /note= "Wild type Lys substituted by Ala"
 XX PN US6358738-B1.
 XX

PN US6358738-B1.
 XX 19-MAR-2002.
 XX PF 13-MAY-1999; 99US-0311311.
 XX PR 13-MAY-1998; 98US-085296P.
 XX PA (HARD) HARVARD COLLEGE.
 XX PI Erikson RL, Lee KS.
 XX DR WPI; 2002-314756/35.
 XX PT Administering polo kinase inhibitors for the treatment of cancers and
 PT fungal infections -
 XX PS Example 7; Page : 47pp; English.
 XX CC The invention describes a method of inhibiting growth of an isolated
 CC population of cells by inhibiting a cell polo kinase by administering a
 CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
 CC carboxy terminal domain of the polo kinase which excludes the polo
 CC kinase catalytic domain. The method is used for the treatment of cancer
 CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
 CC cervix, the epithelium, the brain, the retina, the prostate, and the
 CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
 CC Epidermophyton, and Microsporium), protozoans, helminthes, and arthropods.
 CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
 CC mutant, used to determine the residues required for kinase activity.
 CC Note: This sequence does not appear in the specification but has been
 CC created from the wild type sequence shown in AAU79319 using information
 CC given in the invention.
 XX SQ Sequence 603 AA.
 XX
 Query Match 84.5%; Score 49; DB 23; Length 603;
 Best Local Similarity 72.7%; Pred. No. 1.3;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGRRPFETS 11
 244 LLVGRPFETS 254
 RESULT 33
 AAU79319
 ID AAU79319 standard; Peptide: 603 AA.
 XX AC AAU79319;
 XX DT 02-JUL-2002 (first entry)
 XX DE Mouse polo-like kinase (Plk) N437I mutant.
 XX KW Polo box; PB1; cytostatic; fungicide; protozoacide; antihelminthic;
 KW arthropodicide; mitotic protein polo kinase; polo kinase inhibitor;
 KW polo kinase catalytic domain; cancer; lung cancer; breast cancer;
 KW cancer of the uterus; ovarian cancer; cervical cancer;
 KW epithelial cancer; brain cancer; retina cancer; prostate cancer;
 KW trichophyton; Microsporium; protozoan infection; helminthes infection;
 KW arthropod infection; mouse; polo-like kinase; Plk; mutant; murein.
 XX OS Mus musculus.
 XX CS Synthetic.
 XX PH Key Location/Qualifiers
 FT Misc difference 437 /note= "Wild type Asn substituted by Ile"
 XX PN US6358738-B1.
 XX

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PD 15-MAR-2002.
XX
XX
PF 13-MAY-1999; 99US-0311311.
XX
XX
PR 13-MAY-1998; 98US 065296P.
XX
XX
PA (HARD) HARVARD COLLEGE.
XX
XX
PI Erikson RL, Lee KS;
XX
XX
DR WPI; 2002-314756/35.
XX
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections.
XX
XX
PS Example 7; Page 7; 47pp; English.
XX
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporum), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
XX
SQ Sequence 603 AA;

Query Match 84.5%; Score 49; DB 23; Length 603;
Best Local Similarity 72.7%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLLGRPPFFETS 11
   |||||
DB 244 LLVGKPPFFETS 254

RESULT 35
ABR48196
ID ABR48196 standard; Peptide; 603 AA.
XX
XX
AC ABR48196;
XX
XX
DT 12 JUN-2003 (first entry)
XX
XX
DE Human bladder cancer associated protein sequence SEQ ID NO:110
XX
XX
KW Human; bladder cancer; cytostatic; gene therapy; vaccine.
XX
XX
OS Homo sapiens.
XX
XX
PN W0200303906-A2.
XX
XX
PD 16-JAN-2003.
XX
XX
PF 03-JUL-2002; 2002W0-US21338.
XX
XX
PR 03-JUL-2001; 2001US-302814P.
XX
XX
PR 03-AUG-2001; 2001US-313099P.
XX
XX
PR 08-NOV-2001; 2001US-343705P.
XX
XX
PR 13-NOV-2001; 2001US-352666P.
XX
XX
PR 12-APR-2002; 2002US-372246P.
XX
XX
PA (ECOB-) EOS BIOTECHNOLOGY INC.
XX
XX
PI Mack DH, Aziz N;
XX
XX

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PD 15-MAR-2002.
XX
XX
PF 13-MAY-1999; 99US-0311311.
XX
XX
PR 13-MAY-1998; 98US 065296P.
XX
XX
PA (HARD) HARVARD COLLEGE.
XX
XX
PI Erikson RL, Lee KS;
XX
XX
DR WPI; 2002-314756/35.
XX
XX
PT Administering polo kinase inhibitors for the treatment of cancers and
PT fungal infections.
XX
XX
PS Example 10; Page 7; 47pp; English.
XX
XX
CC The invention describes a method of inhibiting growth of an isolated
CC population of cells by inhibiting a cell polo kinase by administering a
CC polo kinase inhibitor. The inhibitor comprises a sequence derived from a
CC carboxy terminal domain of the polo kinase which excludes the polo
CC kinase catalytic domain. The method is used for the treatment of cancer
CC (e.g. cancer of the lung, the breast, the uterus, the ovaries, the
CC cervix, the epithelium, the brain, the retina, the prostate, and the
CC throat), infection by fungi (e.g. Candida, Lichen, Trichophyton,
CC Epidermophyton, and Microsporum), protozoans, helminthes, and arthropods.
CC This is the amino acid sequence of a mouse polo-like kinase (Plk)
CC mutant, used to determine the residues required for kinase activity.
CC Note: This sequence does not appear in the specification but has been
CC created from the wild type sequence shown in AAU79306 using information
CC given in the invention.
XX
XX
SQ Sequence 603 AA;

Query Match 84.5%; Score 49; DB 23; Length 603;
Best Local Similarity 72.7%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLLGRPPFFETS 11
   |||||
DB 244 LLVGKPPFFETS 254

RESULT 35
ABR48196
ID ABR48196 standard; Peptide; 603 AA.
XX
XX
AC ABR48196;
XX
XX
DT 12 JUN-2003 (first entry)
XX
XX
DE Human bladder cancer associated protein sequence SEQ ID NO:110
XX
XX
KW Human; bladder cancer; cytostatic; gene therapy; vaccine.
XX
XX
OS Homo sapiens.
XX
XX
PN W0200303906-A2.
XX
XX
PD 16-JAN-2003.
XX
XX
PF 03-JUL-2002; 2002W0-US21338.
XX
XX
PR 03-JUL-2001; 2001US-302814P.
XX
XX
PR 03-AUG-2001; 2001US-313099P.
XX
XX
PR 08-NOV-2001; 2001US-343705P.
XX
XX
PR 13-NOV-2001; 2001US-352666P.
XX
XX
PR 12-APR-2002; 2002US-372246P.
XX
XX
PA (ECOB-) EOS BIOTECHNOLOGY INC.
XX
XX
PI Mack DH, Aziz N;
XX
XX

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DR WHI 2003-201532/19.
 CR N PSHB; ACC51009.
 XX
 PT Detecting a bladder cancer-associated transcript in a cell from a
 PT patient, comprises contacting a biological sample from the patient with
 PT a bladder cancer-associated polynucleotide or antibody.
 XX
 PS Claim 10, Page 269, 307pp; English.
 XX
 CC The present invention describes a method for detecting a bladder cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with a polynucleotide
 CC that selectively hybridises to a sequence that is 90 % identical to a
 CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
 CC encode the human bladder cancer-associated proteins given in ABR48146 to
 CC ABR48421. Bladder cancer-associated sequences from the present invention
 CC have cytostatic activities, and can be used in antisense gene therapy and
 CC in vaccine production. The method can be used for detecting a bladder
 CC cancer associated transcript in a cell from a patient. The method is
 CC useful in diagnosing or treating bladder cancer and in screening for
 CC compounds that modulate bladder cancer, such as hormones or antibodies.
 CC The nucleic acid molecules from the present invention may be used in
 CC various screening and diagnostic methods, and for gene therapy, vaccine
 CC and/or antisense/inhibition applications.
 XX
 SQ Sequence 603 AA;
 Query Match 84.5%; Score 49; DB 24; Length 403;
 Best Local Similarity 72.7%; Pred. No. 1.3;
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPPET 1;
 DB 344 LLVGRPPPET 254
 !!:!!!:!!
 RESULT 1;
 ABR48146
 ID ABR48146 standard; Protein: 263 AA
 AC ABR48146;
 XX
 DT 25 MAR 2002 (first entry)
 DE Drosophila melanogaster polypeptide SEQ ID NO 14994;
 KW Drosophila developmental biology; cell signalling; transcription;
 KW transcription;
 XX
 CS Drosophila melanogaster.
 XX
 DN W200171542.A2.
 XX
 PF 25 SEP 2001.
 XX
 PF 24 MAR 2001; E001W0-USC9231.
 XX
 PR 23 MAR 2000; Z000US-191637P.
 PR 11 JUN 2000; Z000US-0614750.
 XX
 PA (FEK) FR CORP NY.
 PT Venturi JC, Adams M, Li PWD, Myers EW.
 XX
 CR WHI 2001-656860/75.
 CR N PSHB; ABR07170.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions
 XX
 PS Data source: SEQ ID NO 15993; 20pp + computer listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB161840-AB161675) and the encoded proteins
 CC (AB557737-AB572072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.
 XX
 SQ Sequence 769 AA;
 Query Match 82.8%; Score 48; DB 22; Length 769;
 Best Local Similarity 80.3%; Pred. No. 2.5;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLLGRPPPET 1;
 DB 206 LLVGRPPPET 215
 !!:!!!:!!
 RESULT 37
 AAW74161
 ID AAW74161 standard; peptide: 9 AA.
 XX
 AC AAW74161;
 XX
 DT 05 MAY 1999 (first entry)
 DE HC loop peptide J-43.1.
 XX
 KW HC loop, serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "acetylated"
 FT Modified-site 9 /note= "amidated"
 FT
 XX WC9853050.A2.
 XX 26-MAY-1998; 54WD US10119.
 XX 20-MAY-1998;
 XX 21-MAY-1997; 9JUS 086139.
 XX (CH1-) CHILDRENS MEDICAL CENT.
 XX (VISS) VISSUM RES & DEV CO.
 XX Ben-Sasson SA;
 XX WPI; 1999-070142/06.
 XX
 PT New peptides for modulating serine/threonine kinase activity -
 PT comprise a sequence corresponding to the HC loop of a
 PT serine/threonine kinase, used for treating, e.g. cancers,
 PT inflammatory disorders or autoimmune disorders
 XX
 PS Claim 14; Fig 4; 70pp; English.
 XX
 CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HC loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis).

CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension; immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate domains which bind to the HC loop of the STK
 CC from which the peptide was derived.

XX Sequence 9 AA;

Query Match 79.1%, Score 46; DB 23; Length 9;

Best Local Similarity 89.9%; Pred. No. 9.3e+05;

Mismatches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QV 1 MLLGRPPPE 9

|||

DE 1 MLLGRPPPE 9

RESULT 39

AAR92176

ID AAR92176 standard; Peptide: 9 AA.

XX AC AAR92176;

XX DT 25-MAY-1996 (first entry)

XX DE Sak serine-threonine kinase N-terminus.

XX KW Sak; serine-threonine kinase; STK; agonist; antagonist;

XX KW proliferative disease; cancer; tumour; antisense; transgenic animal;

XX KW therapy.

XX OS Mus musculus.

XX PN CA2150789-A.

XX PD 03-DEC-1995.

XX PF 01-JUN-1995; 95CA-2150789.

XX PR 02-JUN-1994; 94US-0252995.

XX PA (MOUN; MOUNT SINA; HOSPITAL CORP.

XX PI Dennis CW, Fode G, Heffernan M;

XX WP; 1996-129817714.

XX DR N-PSDB; NAT08710.

XX PT Nucleic acid encoding Sak serine-threonine kinase - useful for

XX PT identifying modulators potentially useful in treatment or prevention

XX PT of proliferative disease.

XX PS Claim 3; Page 46-48; 73pp; English.

XX CC 2 isoforms, sak a and sak-b, of a novel serine/threonine kinase

XX CC have an identical N-terminal sequence (AAR92176) that contains the

XX CC kinase domain and that shows significant homology to the polc

XX CC subfamily. The C-terminal sequences (each contg. 3 PEST regions)

XX CC of the 2 isoforms differ (see AAR92177 and AAR92214). Sak-a and Sak-b

XX CC are associated with mitotic and meiotic cell division, and may be

XX CC involved in cell proliferation. They can be obtd. in recombinant

XX CC form by expression of encoding sequences (see AAR08710-12) and used

XX CC to test for inhibitory or stimulatory cpds. that may be useful.

XX CC in the treatment/diagnosis of proliferative disorders, such as

XX CC cancer and viral (esp. HIV) infection.

XX SQ Sequence 416 AA;

Query Match 79.1%; Score 46; DB 17; Length 416;

Best Local Similarity 90.6%; Pred. No. 3.1;

CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension; immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate domains which bind to the HC loop of the STK
 CC from which the peptide was derived.

XX Sequence 9 AA;

Query Match 79.1%, Score 46; DB 23; Length 9;

Best Local Similarity 89.9%; Pred. No. 9.3e+05;

Mismatches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QV 1 MLLGRPPPE 9

|||

DE 1 MLLGRPPPE 9

RESULT 39

AAR92176

ID AAR92176 standard; Peptide: 9 AA.

XX AC AAR92176;

XX DT 25-MAY-1996 (first entry)

XX DE Sak serine-threonine kinase N-terminus.

XX KW Sak; serine-threonine kinase; STK; agonist; antagonist;

XX KW proliferative disease; cancer; tumour; antisense; transgenic animal;

XX KW therapy.

XX OS Mus musculus.

XX PN CA2150789-A.

XX PD 03-DEC-1995.

XX PF 01-JUN-1995; 95CA-2150789.

XX PR 02-JUN-1994; 94US-0252995.

XX PA (MOUN; MOUNT SINA; HOSPITAL CORP.

XX PI Dennis CW, Fode G, Heffernan M;

XX WP; 1996-129817714.

XX DR N-PSDB; NAT08710.

XX PT Nucleic acid encoding Sak serine-threonine kinase - useful for

XX PT identifying modulators potentially useful in treatment or prevention

XX PT of proliferative disease.

XX PS Claim 3; Page 46-48; 73pp; English.

XX CC 2 isoforms, sak a and sak-b, of a novel serine/threonine kinase

XX CC have an identical N-terminal sequence (AAR92176) that contains the

XX CC kinase domain and that shows significant homology to the polc

XX CC subfamily. The C-terminal sequences (each contg. 3 PEST regions)

XX CC of the 2 isoforms differ (see AAR92177 and AAR92214). Sak-a and Sak-b

XX CC are associated with mitotic and meiotic cell division, and may be

XX CC involved in cell proliferation. They can be obtd. in recombinant

XX CC form by expression of encoding sequences (see AAR08710-12) and used

XX CC to test for inhibitory or stimulatory cpds. that may be useful.

XX CC in the treatment/diagnosis of proliferative disorders, such as

XX CC cancer and viral (esp. HIV) infection.

XX SQ Sequence 416 AA;

Search completed: November 14, 2003, 14:35:32
Job time : 41 secs

Season completed: November 14, 2003, 14:03:32
Job time : 41 secs

Qy	: WLLGGPPPEET 1C
QC	LCAGGAGGPPPTTT 1C
	294 WLLGGPPPEET 2:1

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3	1	1	0
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5	1	1	0
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7	1	1	0
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CM protein - protein search, using sw mode.

Run on: November 14, 2003, 14:24:43, Search time 22 seconds
Without alignments:
25135 Matches: 0 cell updates/sec

Titles: US-09-736-076-19
Perfect scores: 58
Sequences: 1 MLAGPPPPETS 11

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-filtering: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Issued Patents AA*
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2: /cgn2_6/ptodata/1/aa/5B-COM5-pep1*
3: /cgn2_6/ptodata/1/aa/5A-COM5-pep1*
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	58	1000	11	Sequence 19, Appl
2	55	948	272	Sequence 12, Appl
3	55	948	272	Sequence 12, Appl
4	55	948	685	Sequence 1, Appl
5	55	948	685	Sequence 1, Appl
6	55	948	685	Sequence 2, Appl
7	55	948	685	Sequence 1, Appl
8	49	845	9	Sequence 15, Appl
9	49	845	9	Sequence 15, Appl
10	49	845	20	Sequence 6, Appl
11	49	845	272	Sequence 14, Appl
12	49	845	272	Sequence 14, Appl
13	49	845	603	Sequence 2, Appl
14	49	845	603	Sequence 2, Appl
15	46	793	9	Sequence 17, Appl
16	46	793	273	Sequence 10, Appl
17	46	793	273	Sequence 10, Appl
18	46	793	416	Sequence 2, Appl
19	46	793	416	Sequence 2, Appl
20	46	793	464	Sequence 6, Appl
21	46	793	925	Sequence 4, Appl
22	46	793	925	Sequence 4, Appl
23	46	793	925	Sequence 11, Appl
24	46	793	271	Sequence 11, Appl
25	46	793	271	Sequence 11, Appl
26	46	793	8	Sequence 16, Appl
27	46	793	607	Sequence 15, Appl

28	41	70.7	607	3	US-09-272-796-15	Sequence 15, Appl
29	40	69.0	344	2	US-08-755-728-3	Sequence 3, Appl
30	40	69.0	344	2	US-08-774-655-3	Sequence 3, Appl
31	40	69.0	344	3	US-09-283-011-3	Sequence 1, Appl
32	40	69.0	347	2	US-09-216-000-1	Sequence 1, Appl
33	39	67.2	264	2	US-07-857-224B-17	Sequence 17, Appl
34	39	67.2	303	4	US-09-739-455-12	Sequence 12, Appl
35	39	67.2	303	4	US-09-739-455-22	Sequence 22, Appl
36	39	67.2	403	2	US-08-755-728-4	Sequence 4, Appl
37	39	67.2	403	2	US-08-974-655-4	Sequence 4, Appl
38	39	67.2	403	3	US-09-283-011-4	Sequence 4, Appl
39	38	65.5	259	4	US-09-252-991A-28679	Sequence 28679, A
40	38	65.5	275	1	US-08-252-995D-13	Sequence 13, Appl
41	38	65.5	275	2	US-08-834-108-13	Sequence 13, Appl
42	38	65.5	767	4	US-09-772-647-4	Sequence 4, Appl
43	37	63.8	182	3	US-08-861-338-3	Sequence 3, Appl
44	37	63.8	182	4	US-09-134-001C-3742	Sequence 3742, Ap
45	37	63.8	220	1	US-08-233-146-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-861-338-19
Sequence 19, Application US/08861338
Patent No. 6174993
GENERAL INFORMATION:
APPLICANT: Reg-sasson, Shmuel A.
TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIt Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861.338
FILING DATE: 21-MAY-1997
CLASSIFICATION: 5.14
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CMCC-590
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "N-Acetyl Methionine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: /note= "Glutamic Acid Benzyl Ester"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11

OTHER INFORMATION: /note= "Serine-NH2"
US-08-661-338-19

Query Match 100.0% Score 58; EP 3; Length 11;
Best local Similarity 100.0%; Pred. No. 9,001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : MLGRRPFFTS 11
DB : MLGRRPFFTS 11

RESULT 3

US-08-661-338-19
Sequence 12, Application: US/08/661-338-19
Patent No. 5450501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661-338-19
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydko, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 364-7311
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-661-338-19

Query Match 94.8% Score 55; EP 3; Length 11;
Best local Similarity 90.9%; Pred. No. 9,001;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : MLGRRPFFTS 11
DB : MLGRRPFFTS 209

RESULT 3

US-08-661-338-19
Sequence 12, Application: US/08/661-338-19
Patent No. 5926693
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol

TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661-338-19
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydko, Linda M
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 364-7311
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-661-338-19

Query Match 94.8% Score 55; DB 2; Length 272;
Best local Similarity 90.9%; Pred. No. 9,001;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : MLGRRPFFTS 11
DB : MLGRRPFFTS 209

RESULT 4

US-08-661-338-19
Sequence 12, Application: US/08/661-338-19
Patent No. 5885403
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,969
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0321 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 685 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: HUVENOEJ1
 CLONE: 39043
 US-09-736-076-19

Query Match: 94.9% Score 55; DB 2; Length 685;
 Best Local Similarity 90.9% Pred No. 0.027;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFETS 11
 1 |||||
 DQ 273 MLLGRPPFET 283

RESULT 5
 US-09-736-076-19
 Sequence 1, Application US/09136282
 Patent No. 6063629
 GENERAL INFORMATION:
 APPLICANT: ANDERSON, KAREN
 APPLICANT: JACKSON, JEFFREY
 APPLICANT: HANSEBURY, MICHAEL
 APPLICANT: NERURKAR, SANDHYA
 APPLICANT: KOSHYAK, ANV
 APPLICANT: BOLZAK, MARK
 TITLE OF INVENTION: HUMAN SERUM INTERLEUKIN KINASE GENE
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ralston & Pratt 14
 STREET: P.O. Box 980
 CITY: Valley Forge
 STATE: PA
 COUNTRY: USA
 ZIP: 19482
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/136,282
 FILING DATE: 20-AUG-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/056,112
 FILING DATE: 20-AUG-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Prestia, Paul F.
 REGISTRATION NUMBER: 231,041
 REFERENCE/DOCKET NUMBER: GH 70241
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0700

TELEX: 846169
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 685 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-136-282 2

Query Match: 94.9% Score 55; DB 3; Length 685;
 Best Local Similarity 90.9% Pred No. 0.027;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPFETS 11
 1 |||||
 DQ 273 MLLGRPPFET 283

RESULT 6
 US-09-272-796-1
 Sequence 1, Application US/09272796
 Patent No. 6207148
 GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Corley, Neil C.
 APPLICANT: Guegler, Karl G.
 APPLICANT: Lai, Preeti
 APPLICANT: Goli, Surya K.
 APPLICANT: Shah, Parvi
 TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/272,796
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/878,959
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0321 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 685 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: HUVENOEJ1
 CLONE: 39043
 US-09-272-796-1

Query Match: 94.9% Score 55; DB 3; Length 685;

```

Best Local Similarity 90.9%; Pred. No. 0.027; 0; Indels 0; Gaps 0;
Matches 10; Conservative 1; Mismatches 0;

QY : MLGPPPPETS 11
ED : 273 MLGPPPPETT 293

RESULT 1
US 09 503 744 2
: Sequence 2; Application US/09505744
: Patent No. 6245544
: GENERAL INFORMATION:
: APPLICANT: Karen M. Anderson
: APPLICANT: Yolk W. Bonzyk
: APPLICANT: Michael J. Hansbury
: APPLICANT: Jeffrey R. Jackson
: APPLICANT: Sandhya S. Neruikar
: APPLICANT: Avy K. Reshak
: TITLE OF INVENTION: HUMAN SERUM INDUCIBLE KINASE (HSIK)
: FILE REFERENCE: GH-70231-C
: CURRENT APPLICATION NUMBER: US/09/503,744
: EARLIER FILING DATE: 2000-02-16
: EARLIER APPLICATION NUMBER: 09/136,092
: EARLIER FILING DATE: 1998-08-20
: EARLIER APPLICATION NUMBER: 60/054,112
: EARLIER FILING DATE: 1997-08-20
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: FastSeq for Windows Version 1.2
: SEQ ID NO 1
: LENGTH: 855
: TYPE: PRT
: ORGANISM: Homo sapiens
US 09 503 744 2

Query Match 94.9%; Score 49; DR 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : MLGPPPPET 9
Db : 1 MLGPPPPET 9

RESULT 9
US 08 861 338 18
: Sequence 18; Application US/08861338
: Patent No. 6174993
: GENERAL INFORMATION:
: APPLICANT: Ben-Sasson, Shmuel A.
: TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
: STREET: Two Militia Drive
: CITY: Lexington
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/861,338
: FILING DATE: 21-MAY-1997
: CLASSIFICATION: 5:4
: ATTORNEY/AGENT INFORMATION:
: NAME: Brook, David E.
: REGISTRATION NUMBER: 22,592
: REFERENCE/DOCKET NUMBER: CMCC-590
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (781) 861-6240
: TELEFAX: (781) 861-9540
: INFORMATION FOR SEQ ID NO: 18:
: LENGTH: 9 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: not relevant
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Modified site
: LOCATION: 1
: OTHER INFORMATION: (note= "N-Acetyl Leucine")

US-08-861-338-15
Query Match 84.5%; Score 49; DR 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : MLGPPPPET 9
Db : 1 MLGPPPPET 9

RESULT 9
US 08 861 338 18
: Sequence 18; Application US/08861338
: Patent No. 6174993
: GENERAL INFORMATION:
: APPLICANT: Ben-Sasson, Shmuel A.
: TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
: STREET: Two Militia Drive
: CITY: Lexington
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/861,338
: FILING DATE: 21-MAY-1997
: CLASSIFICATION: 5:4
: ATTORNEY/AGENT INFORMATION:
: NAME: Brook, David E.
: REGISTRATION NUMBER: 22,592
: REFERENCE/DOCKET NUMBER: CMCC-590
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (781) 861-6240
: TELEFAX: (781) 861-9540
: INFORMATION FOR SEQ ID NO: 18:
: LENGTH: 9 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: not relevant
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Modified site
: LOCATION: 1
: OTHER INFORMATION: (note= "N-Acetyl Leucine")

```

```

FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: /note= "Glutamic Acid Penny; Ester"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: /note= "Serine NH2"
US-09-841-338-18

```

```

Query Match      84.5%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2,5e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 3 LGRPPPTS 11
DB 3 LGRPPPTS 9

```

```

RESULT 10
US-08-661-338-6
Sequence 6; Application US/0886139
Patent No. 6,749,933
GENERAL INFORMATION:
APPLICANT: Ben-Sasson, Samuel A.
TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brock, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,338
FILING DATE: 21 MAY 1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brock, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CMPC 697
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 861-6040
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-661-338-6

```

```

Query Match      84.5%; Score 49; DB 3; Length 20;
Best Local Similarity 72.7%; Pred. No. 2.6e-05;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MLLGRPPPTS 11
DB 3 LLVGKPPPTS 13

```

```

RESULT 11
US-09-250-995D-14
Sequence 14; Application US/09250995D
Patent No. 5450501

```

```

GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02 JUN 1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M
REGISTRATION/DOCKET NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3,253-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: XUS tuscusculus
US-08-252-995D-14

```

```

Query Match      84.5%; Score 49; DB 1; Length 272;
Best Local Similarity 72.7%; Pred. No. 0.13;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MLLGRPPPTS 11
DB 199 LLVGKPPPTS 209

```

```

RESULT 12
US-08-834-108-14
Sequence 14; Application US/08834108
Patent No. 5976893
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108

```

```

; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M.
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 364-1398
; INFORMATION FOR SEQ ID NO: 14
; SEQUENCE CHARACTERISTICS:
; LENGTH: 272 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-09-736-108-14

Query Match 84.5%; Score 49; DB 2; Length 272;
Best Local Similarity 72.7%; Pred. No. 0.31;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGKPPPTTS 11
      |||
DB 193 LLVGKPPPTTS 209

RESULT 13
US-09-198-122-2
; Sequence 26, Application US/09198122
; Patent No. 6140180
; GENERAL INFORMATION:
; APPLICANT: Streibardt, Klaus; Rufmann-Waltmann, Heide;
; ARDAGHI, Heide; Uwe
; TITLE OF INVENTION: CLONING OF A MEMBER OF THE SERINE
; TITLE OF INVENTION: THREONINE KINASE FAMILY
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESS: STROH HORN WEAVER & WONDOS
; STREET: 660 White Plains Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-5144
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: Not Powermate 88.40
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09-198-122
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08-601-014
; FILING DATE: 23-FEB-1996
; APPLICATION NUMBER: PCT/EP94/02703
; FILING DATE: 30-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4329177
; FILING DATE: 30-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurt G. Briscoe
; REGISTRATION NUMBER: 33,141
; REFERENCE/DOCKET NUMBER: Bayer 9520 RSH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 332-1700
; TELEFAX: (914) 332-1844
; TELEX:
; INFORMATION FOR SEQ ID NO: 23

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein;
US-09-198-122-2

Query Match 84.5%; Score 49; DB 3; Length 603;
Best Local Similarity 72.7%; Pred. No. 0.31;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGKPPPTTS 11
      |||
DB 244 LLVGKPPPTTS 254

RESULT 14
US-09-311-311C-26
; Sequence 26, Application US/09311311C
; Patent No. 6358738
; GENERAL INFORMATION:
; APPLICANT: Erikson, et al.
; TITLE OF INVENTION: POLY BOX THERAPEUTIC COMPOSITIONS,
; TITLE OF INVENTION: METHODS, AND USES THEREFOR
; FILE REFERENCE: 1874/117
; CURRENT APPLICATION NUMBER: US/09/311,311C
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,296
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 603
; TYPE: PPT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: 11...1603;
; OTHER INFORMATION: plx protein
US-09-311-311C-26

Query Match 84.5%; Score 49; DB 4; Length 603;
Best Local Similarity 72.7%; Pred. No. 0.31;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGKPPPTTS 11
      |||
DB 244 LLVGKPPPTTS 254

RESULT 15
US-08-961-338-17
; Sequence 17, Application US/08961338
; Patent No. 6174993
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,338

```


;; FILING DATE: 21-MAY-1997
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMC-593
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6242
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "N-Acetyl Methionine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Gamma Benzyl Ester of
; OTHER INFORMATION: Glutamine Acid-NH2"
US 09-251-336-17

Query Match 79.3%; Score 46; DB 1; Length 9;
Best Local Similarity 70.0%; Pred. No. 2,592;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

QY 1 MLGRRPPT 9
DB 1 MLGRRPPT 9

RESULT 14
US-08-251-995D-10
; Sequence 10, Application US/28252995D
; Patent No. 5655501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.0
; CURRENT APPLICATION DATA:
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kardydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153 96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid

;; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-252-995D-10

Query Match 79.3%; Score 46; DB 1; Length 273;
Best Local Similarity 70.0%; Pred. No. 0,48;
Matches 7; Conservative 3; Mismatches 0; Gaps 0;

QY 1 MLGRRPPT 10
DB 200 LLIGRRPPT 209

RESULT 17
US-08-934-108-10
; Sequence 10, Application US/08934-08
; Patent No. 5976893
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 05/08/934,108
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kardydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-934-108-10

Query Match 79.3%; Score 46; DB 2; Length 273;
Best Local Similarity 70.0%; Pred. No. 0,48;
Matches 7; Conservative 3; Mismatches 0; Gaps 0;

QY 1 MLGRRPPT 10
DB 200 LLIGRRPPT 209

RESULT 18
US-08-252-995D-2
; Sequence 2, Application US/08252995D
; Patent No. 5655501

GENERAL INFORMATION:
 APPLICANT: Dennis, James W
 APPLICANT: Heffernan, Mike
 APPLICANT: Fode, Carol
 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERESKIN & PARR
 STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/252,995D
 FILING DATE: 02 JUN 1994
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Kurdydyk, Linda M
 REGISTRATION NUMBER: 34,971
 REFERENCE/DOCKET NUMBER: 3153-96
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 416 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08 252-995D-2

Query Match 79.3% Score 46; DB 1; Length 416;
 Best Local Similarity 70.0%; Pred. No. 0.75;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPEF 10
 DB 204 LLGRRPPEF 213

RESULT 13
 US-08-514-106-2
 Sequence 2, Application US/08-411-5
 Patent No. 56-0501
 GENERAL INFORMATION:
 APPLICANT: Dennis, James W
 APPLICANT: Heffernan, Mike
 APPLICANT: Fode, Carol
 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERESKIN & PARR
 STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08 834-138-2
 FILING DATE:
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:

NAME: Kurdydyk, Linda M
 REGISTRATION NUMBER: 34,971
 REFERENCE/DOCKET NUMBER: 3153-210
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 416 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08 834-138-2

Query Match 79.3% Score 46; DB 2; Length 416;
 Best Local Similarity 70.0%; Pred. No. 0.75;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPEF 10
 DB 204 LLGRRPPEF 213

RESULT 20
 US-08-252-995D-6
 Sequence 6, Application US/08252995D
 Patent No. 56-0501
 GENERAL INFORMATION:
 APPLICANT: Dennis, James W
 APPLICANT: Heffernan, Mike
 APPLICANT: Fode, Carol
 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERESKIN & PARR
 STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/252,995D
 FILING DATE: 02 JUN 1994
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Kurdydyk, Linda M
 REGISTRATION NUMBER: 34,971
 REFERENCE/DOCKET NUMBER: 3153-96
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 464 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-252-995D-6

Query Match 79.3% Score 46; DB 1; Length 464;
 Best Local Similarity 70.0%; Pred. No. 0.84;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPPEF 10
 DB 204 LLGRRPPEF 213

RESULT 21
 US-08-834-108-6
 1 Sequence 6, Application US/08834108
 2 Patent No. 5976693
 3 GENERAL INFORMATION:
 4 APPLICANT: Dennis, James W
 5 APPLICANT: Heffernan, Mike
 6 APPLICANT: Fode, Carol
 7 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 8 NUMBER OF SEQUENCES: 14
 9 CORRESPONDENCE ADDRESS:
 10 ADDRESSEE: BERESKIN & PARR
 11 STREET: 40 King Street West
 12 CITY: Toronto
 13 STATE: Ontario
 14 COUNTRY: Canada
 15 ZIP: M5H 3Y2
 16 COMPUTER READABLE FORM:
 17 MEDIUM TYPE: Floppy disk
 18 COMPUTER: IBM PC compatible
 19 OPERATING SYSTEM: PC-DOS/MS-DOS
 20 SOFTWARE: Patent in Release #1.0, Version #1.0
 21 CURRENT APPLICATION DATA:
 22 APPLICATION NUMBER: US/88/834,108
 23 FILING DATE:
 24 CLASSIFICATION: 536
 25 ATTORNEY/AGENT INFORMATION:
 26 NAME: Kurdydyk, Linda M
 27 REGISTRATION NUMBER: 34,971
 28 REFERENCE/DOCKET NUMBER: 3153-210
 29 TELECOMMUNICATION INFORMATION:
 30 TELEPHONE: (416) 364-7311
 31 TELEFAX: (416) 364-7319
 32 INFORMATION FOR SEQ ID NO: 6
 33 LENGTH: 464 amino acids
 34 TYPE: amino acid
 35 TOPOLOGY: linear
 36 MOLECULE TYPE: protein
 37 US-08-834-108-6
 38
 39 Query Match 79.3%; Score 46; DB 2; Length 464;
 40 Best Local Similarity 70.0%; Pred. No. 1.7;
 41 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

42 1 MLGRRPPPT 10
 43 284 LLIGRRPPT 213

RESULT 22
 US-08-834-108-4
 1 Sequence 4, Application US/08834108
 2 Patent No. 5976693
 3 GENERAL INFORMATION:
 4 APPLICANT: Dennis, James W
 5 APPLICANT: Heffernan, Mike
 6 APPLICANT: Fode, Carol
 7 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 8 NUMBER OF SEQUENCES: 14
 9 CORRESPONDENCE ADDRESS:
 10 ADDRESSEE: BERESKIN & PARR
 11 STREET: 40 King Street West
 12 CITY: Toronto
 13 STATE: Ontario
 14 COUNTRY: Canada
 15 ZIP: M5H 3Y2
 16 COMPUTER READABLE FORM:
 17 MEDIUM TYPE: Floppy disk
 18 COMPUTER: IBM PC compatible
 19 OPERATING SYSTEM: PC-DOS/MS-DOS
 20 SOFTWARE: Patent in Release #1.0, Version #1.0
 21 CURRENT APPLICATION DATA:
 22 APPLICATION NUMBER: US/88/834,108
 23 FILING DATE:
 24 CLASSIFICATION: 536
 25 ATTORNEY/AGENT INFORMATION:
 26 NAME: Kurdydyk, Linda M
 27 REGISTRATION NUMBER: 34,971
 28 REFERENCE/DOCKET NUMBER: 3153-210
 29 TELECOMMUNICATION INFORMATION:
 30 TELEPHONE: (416) 364-7311
 31 TELEFAX: (416) 364-7319
 32 INFORMATION FOR SEQ ID NO: 4
 33 LENGTH: 925 amino acids
 34 TYPE: amino acid
 35 TOPOLOGY: linear
 36 MOLECULE TYPE: protein
 37 US-08-834-108-4

38 Query Match 79.3%; Score 46; DB 2; Length 925;
 39 Best Local Similarity 70.0%; Pred. No. 1.7;
 40 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

41 1 MLGRRPPPT 10

1 APPLICATION NUMBER: US/08/252,995D
 2 FILING DATE: 02-JUN-1994
 3 CLASSIFICATION: 536
 4 ATTORNEY/AGENT INFORMATION:
 5 NAME: Kurdydyk, Linda M
 6 REGISTRATION NUMBER: 34,971
 7 REFERENCE/DOCKET NUMBER: 3153-210
 8 TELECOMMUNICATION INFORMATION:
 9 TELEPHONE: (416) 364-7311
 10 TELEFAX: (416) 364-7319
 11 INFORMATION FOR SEQ ID NO: 4
 12 SEQUENCE CHARACTERISTICS:
 13 LENGTH: 925 amino acids
 14 TYPE: amino acid
 15 TOPOLOGY: linear
 16 MOLECULE TYPE: protein
 17 US-08-252-995D-4

18 Query Match 79.3%; Score 46; DB 1; Length 925;
 19 Best Local Similarity 70.0%; Pred. No. 1.7;
 20 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

21 1 MLGRRPPPT 10
 22 284 LLIGRRPPT 213

RESULT 23
 US-08-834-108-4
 1 Sequence 4, Application US/08834108
 2 Patent No. 5976693
 3 GENERAL INFORMATION:
 4 APPLICANT: Dennis, James W
 5 APPLICANT: Heffernan, Mike
 6 APPLICANT: Fode, Carol
 7 TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
 8 NUMBER OF SEQUENCES: 14
 9 CORRESPONDENCE ADDRESS:
 10 ADDRESSEE: BERESKIN & PARR
 11 STREET: 40 King Street West
 12 CITY: Toronto
 13 STATE: Ontario
 14 COUNTRY: Canada
 15 ZIP: M5H 3Y2
 16 COMPUTER READABLE FORM:
 17 MEDIUM TYPE: Floppy disk
 18 COMPUTER: IBM PC compatible
 19 OPERATING SYSTEM: PC-DOS/MS-DOS
 20 SOFTWARE: Patent in Release #1.0, Version #1.30
 21 CURRENT APPLICATION DATA:
 22 APPLICATION NUMBER: US/88/834,108
 23 FILING DATE:
 24 CLASSIFICATION: 536
 25 ATTORNEY/AGENT INFORMATION:
 26 NAME: Kurdydyk, Linda M
 27 REGISTRATION NUMBER: 34,971
 28 REFERENCE/DOCKET NUMBER: 3153-210
 29 TELECOMMUNICATION INFORMATION:
 30 TELEPHONE: (416) 364-7311
 31 TELEFAX: (416) 364-7319
 32 INFORMATION FOR SEQ ID NO: 4
 33 SEQUENCE CHARACTERISTICS:
 34 LENGTH: 925 amino acids
 35 TYPE: amino acid
 36 TOPOLOGY: linear
 37 MOLECULE TYPE: protein
 38 US-08-834-108-4

39 Query Match 79.3%; Score 46; DB 2; Length 925;
 40 Best Local Similarity 70.0%; Pred. No. 1.7;
 41 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

42 1 MLGRRPPPT 10

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US      204  LLLGGPPEET 213
      11: 11: 11:
      204  LLLGGPPEET 213

RESULT 24
US-08-961-338-11
: Sequence 11, Application US/08934109
: Patent No. 6174993
: GENERAL INFORMATION:
: APPLICANT: Dennis, James W
: APPLICANT: Heffernan, Mike
: APPLICANT: Fode, Carol
: TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: PERESKIN & PARR
: STREET: 40 King Street West
: CITY: Toronto
: STATE: Ontario
: COUNTRY: Canada
: ZIP: M5H 3Y2
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent in Release #1.0, Version #1.3
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/252,993D
: FILING DATE: 02 JUN-1994
: CLASSIFICATION: 516
: ATTORNEY/AGENT INFORMATION:
: NAME: Kurydyk, Linda M
: REGISTRATION NUMBER: 34,971
: REFERENCE/DOCKET NUMBER: 3153-94
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (416) 364-7311
: TELEFAX: (416) 361-1398
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 271 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: Drosophila melanogaster
: US-08-934-109-11

Query Match 75.9% Score 44; DB 2; Length 271;
Best Local Similarity 70.0%; Pred No. 1.1;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGGPPEET 10
      11: 11: 11:
      199  LLLGGPPEET 207

Db 199  LLLGGPPEET 207

RESULT 26
US-08-961-338-16
: Sequence 16, Application US/08934109
: Patent No. 6174993
: GENERAL INFORMATION:
: APPLICANT: Ben-Sasson, Samuel A
: TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
: STREET: Two Millia Drive
: CITY: Lexington
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02173
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent in Release #1.0, Version #1.3
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/861,338
: FILING DATE: 21-MAY-1997
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Brook, David E.
: REGISTRATION NUMBER: 22,592
: REFERENCE/DOCKET NUMBER: CMCC-590
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (781) 861-6240
: TELEFAX: (781) 861-9540
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid

```

1 STRANDEDNESS: not relevant
 2 TOPOLOGY: not relevant
 3 MOLECULE TYPE: peptide
 4 FEATURE:
 5 NAME/KEY: Modified-site
 6 LOCATION: 1
 7 OTHER INFORMATION: /note= "N Acetyl Methionine"
 8 FEATURE:
 9 NAME/KEY: Modified-site
 10 LOCATION: 6
 11 OTHER INFORMATION: /note= "Phenylalanine NH2"
 12 US-08-878-989-15

Query Match 70.7% Score 41; DB 3; Length 607;
 Best Local Similarity 63.6%; Pred. No. 9.5;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLLGRPPFF 8
 |||||
 Db 1 MLLGRPPF 8

RESULT 27
 US-08-878-989-15
 Sequence 15, Application US/06827985
 Patent No. 5885803

GENERAL INFORMATION:
 APPLICANT: Bardman, Olga
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Corley, Neil C.
 APPLICANT: Guegler, Karl G.
 APPLICANT: Lal, Preeti
 APPLICANT: Goli, Surya K.
 APPLICANT: Shah, Purvi
 TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08-878-989
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0321 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:

INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 607 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1827450

US-08-878-989-15

Query Match 70.7% Score 41; DB 2; Length 607;
 Best Local Similarity 63.6%; Pred. No. 9.5;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLLGRPPFF 11
 |||||
 Db 214 LLCSPFFETA 224

RESULT 28

US-09-272-796-15
 Sequence 15, Application US/03272796
 Patent No. 6207148
 GENERAL INFORMATION:
 APPLICANT: Bardman, Olga
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Corley, Neil C.
 APPLICANT: Guegler, Karl G.
 APPLICANT: Lal, Preeti
 APPLICANT: Goli, Surya K.
 APPLICANT: Shah, Purvi
 TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/272.796
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/878,989
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0321 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:

INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 607 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1827450
 US-09-272-796-15

Query Match 70.7% Score 41; DB 3; Length 607;
 Best Local Similarity 63.6%; Pred. No. 9.5;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLLGRPPFF 11
 |||||
 Db 214 LLCSPFFETA 224

```

RESULT 22
US-09-755-728-3
Sequence 3, Application US/08755728
Patent No. 5972676
GENERAL INFORMATION:
APPLICANT: PLOWMAN, Gregory
APPLICANT: MOSSIE, Kevin
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08755728
FILING DATE: August 14, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/755,728
FILING DATE: November 25, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYDROTHERICAL: NO
ANTI-SENSE: NO
US-09-755-728-3
Query Match: 69.08; Score 40; DB 1; Length 344;
Best Loca: Similarity 54.51; Pred. No. 8;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MLCRRPFFETS 11
DB 266 LLYVGNPFESA 276

RESULT 10
US-09-755-728-3
Sequence 3, Application US/08755728
Patent No. 5972676
GENERAL INFORMATION:
APPLICANT: PLOWMAN, Gregory
APPLICANT: MOSSIE, Kevin
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible

```

```

STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08755728
FILING DATE: August 14, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/755,728
FILING DATE: November 25, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYDROTHERICAL: NO
ANTI-SENSE: NO
US-08-974-655-3
Query Match: 69.08; Score 40; DB 2; Length 344;
Best Loca: Similarity 54.51; Pred. No. 8;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MLCRRPFFETS 11
DB 266 LLYVGNPFESA 276

RESULT 1:
US-09-283-011-3
Sequence 3, Application US/09283011
Patent No. 6207401
GENERAL INFORMATION:
APPLICANT: PLOWMAN, Gregory
APPLICANT: MOSSIE, Kevin
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible

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1 OPERATING SYSTEM: IBM P.C. DOS 5.0
2 SOFTWARE: FASTSEQ for Windows 2.0
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/09/283,011
5 FILING DATE:
6 CLASSIFICATION:
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: 09/011,135
9 FILING DATE: January 22, 1998
10 APPLICATION NUMBER: 05/755,728
11 FILING DATE: No. 62074C1e-Per 25, 1994
12 APPLICATION NUMBER: 63/231,943
13 FILING DATE: August 14, 1996
14 APPLICATION NUMBER: 63/268,562
15 FILING DATE: December 18, 1995
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Warburg, Richard J.
18 REGISTRATION NUMBER: 32,127
19 REFERENCE/DOCKET NUMBER: 231/28-
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: 213, 463,1600
22 TELEFAX: 213, 955-0440
23 TELEX: 67 3510
24 INFORMATION FOR SEQ ID NO: 1:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 344 amino acids
27 TYPE: amino acid
28 STRANDEDNESS: single
29 TOPOLOGY: linear
30 MOLECULE TYPE: protein
31 HYTHETICAL: NO
32 ANTI SENSE: NO
33 US 09-283 011-3
34
35 Query Match 69.0% Score 40, DB 1, Length 344,
36 Best Local Similarity 54.5% Pred. No. 8,
37 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
38
39 QY 1 MLGRRPPTS 11
40 DB 266 LVGNPFESA 276
41
42 RESULT 13
43 US-09-283 011-3
44 Sequence 1, Application US/0901135
45 Patent No. 5962232
46 GENERAL INFORMATION:
47 APPLICANT: H. Liman, GmbH & Co.
48 APPLICANT: B. J. Preet
49 APPLICANT: Bachmann, G. & Co.
50 APPLICANT: Akablon, GmbH & Co.
51 APPLICANT: Shah, Purvi
52 APPLICANT: Corley, Neil C.
53 APPLICANT: Guebler, Karl G.
54 TITLE OF INVENTION: PROTEIN KINASE MOLECULES
55 NUMBER OF SEQUENCES: 12
56 CORRESPONDENCE ADDRESS:
57 ADDRESSEE: Incyte Pharmaceuticals, Inc.
58 STREET: 114 Porter Drive
59 CITY: Palo Alto
60 STATE: CA
61 COUNTRY: USA
62 ZIP: 94304
63 COMPUTER READABLE FORM:
64 MEDIUM TYPE: Diskette
65 COMPUTER: IBM Compatible
66 OPERATING SYSTEM: DOS
67 SOFTWARE: FASTSEQ for Windows Version 2.0
68 CURRENT APPLICATION DATA:
69 APPLICATION NUMBER: US/09 283,011
70 FILING DATE: HEREWITH
71 CLASSIFICATION:

```

```

1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER:
3 FILING DATE:
4 ATTORNEY/AGENT INFORMATION:
5 NAME: Billings, Lucy J.
6 REGISTRATION NUMBER: 36,749
7 REFERENCE/DOCKET NUMBER: PF-0465 US
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: 650-855-0555
10 TELEFAX: 650-845-4166
11 TELEX:
12 INFORMATION FOR SEQ ID NO: 1:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 347 amino acids
15 TYPE: amino acid
16 STRANDEDNESS: single
17 TOPOLOGY: linear
18 IMMEDIATE SOURCE:
19 LIBRARY: HMCINOT01
20 CLONE: 2340
21 US-09-316-000-1
22
23 Query Match 59.0% Score 40, DB 2, Length 347,
24 Best Local Similarity 54.5% Pred. No. 8,
25 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
26
27 QY 1 MLGRRPPTS 11
28 DB 269 LVGNPFESA 279
29
30 RESULT 33
31 US-07-857-224B-17
32 Sequence 17, Application US/07857224B
33 Patent No. 5958784
34 GENERAL INFORMATION:
35 APPLICANT: Benner, Steven A.
36 TITLE OF INVENTION: Predicting Folded Structures of Proteins
37 NUMBER OF SEQUENCES: 114
38 CORRESPONDENCE ADDRESS:
39 ADDRESSEE: Steven A. Benner
40 STREET: Hadlaubstrasse 15;
41 CITY: Zurich
42 STATE: none
43 COUNTRY: Switzerland
44 ZIP: (note: this is an international post code) CH-8092
45 COMPUTER READABLE FORM:
46 MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
47 COMPUTER: Apple Macintosh
48 OPERATING SYSTEM: Macintosh 7.0
49 SOFTWARE: MicroSoft Word
50 CURRENT APPLICATION DATA:
51 APPLICATION NUMBER: US/07/857,224B
52 FILING DATE: 03/25/92
53 CLASSIFICATION: 436
54 PRIOR APPLICATION DATA: none
55 TELECOMMUNICATION INFORMATION:
56 TELEPHONE: (international) 41 1 632 2830
57 TELEFAX: (international) 41 1 262 2437
58 TELEX: none
59 INFORMATION FOR SEQ ID NO: 17:
60 SEQUENCE CHARACTERISTICS:
61 LENGTH: 264
62 TYPE: amino acid
63 TOPOLOGY: linear
64 MOLECULE TYPE:
65 DESCRIPTION: protein
66 ORIGINAL SOURCE:
67 ORGANISM: Drosophila melanogaster
68 FEATURE: Protein kinase; Table 3 Column 19
69 PUBLICATION INFORMATION:
70 AUTHORS
71 AUTHORS: Banks, G. R.

```

```

1  AUTHORS: Quinn, A. W.
2  AUTHORS: Hunter, T.
3  TITLE: The protein kinase family
4  JOURNAL: Science
5  VOLUME: 241
6  PAGES: 42-52
7  DATE: 1989
8  US 09 736-076-19
9
10 Query Match 67.2%, Score 19; DB 4; Length 403;
11 Best Local Similarity 66.7%; Pred. No. 11;
12 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
13
14 QY 1 MLCORPPE 9
15 111111
16 135 MLCORPPE 215
17
18 RESULT 14
19 US-09-736-455-12
20 : Sequence 12, Application US/0971945
21 : Patent No. 6413756
22 : GENERAL INFORMATION:
23 : APPLICANT: YAN, Chunhua et al
24 : TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES
25 : TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
26 : TITLE OF INVENTION: THEREOF
27 : FILE REFERENCE: C0000653
28 : CURRENT APPLICATION NUMBER: US/09/736-455
29 : CURRENT FILING DATE: 2000-12-19
30 : NUMBER OF SEQ ID NOS: 23
31 : SOFTWARE: FASTSEQ for Windows Version 4.0
32 : SEQ ID NO: 12
33 : LENGTH: 403
34 : TYPE: PRT
35 : ORGANISM: tetrahymena mexicana
36 US-09-736-455-12
37
38 Query Match 67.2%, Score 19; DB 4; Length 403;
39 Best Local Similarity 66.7%; Pred. No. 11;
40 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
41
42 QY 1 MLCORPPE 9
43 111111
44 207 MLCORPPE 215
45
46 RESULT 15
47 US-09-736-455-22
48 : Sequence 22, Application US/0971945
49 : Patent No. 6413756
50 : GENERAL INFORMATION:
51 : APPLICANT: YAN, Chunhua et al
52 : TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES
53 : TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
54 : TITLE OF INVENTION: THEREOF
55 : FILE REFERENCE: C0000653
56 : CURRENT APPLICATION NUMBER: US/09/736-455
57 : CURRENT FILING DATE: 2000-12-19
58 : NUMBER OF SEQ ID NOS: 23
59 : SOFTWARE: FASTSEQ for Windows Version 4.0
60 : SEQ ID NO: 22
61 : LENGTH: 303
62 : TYPE: PRT
63 : ORGANISM: Leishmania mexicana
64 US-09-736-455-22
65
66 Query Match 67.2%, Score 19; DB 4; Length 403;
67 Best Local Similarity 66.7%; Pred. No. 11;
68 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
69
70 QY 1 MLCORPPE 9
71 111111
72
73
74
75
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100 DB 207 MLCORPPE 215
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102 RESULT 16
103 US-08-755-728-4
104 : Sequence 4, Application US/06755728
105 : Patent No. 5962112
106 : GENERAL INFORMATION:
107 : APPLICANT: PLOWMAN, Gregory
108 : APPLICANT: MOSSIE, Kevin
109 : TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
110 : TITLE OF INVENTION: AND/OR AUR 2 RELATED DISORDERS
111 : NUMBER OF SEQUENCES: 29
112 : CORRESPONDENCE ADDRESS:
113 : ADDRESSEE: LYON & LYON
114 : STREET: 633 West Fifth Street
115 : CITY: Los Angeles
116 : STATE: California
117 : COUNTRY: U.S.A.
118 : ZIP: 90071-2066
119 : COMPUTER READABLE FORM:
120 : MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
121 : MEDIUM TYPE: Storage
122 : COMPUTER: IBM compatible
123 : OPERATING SYSTEM: IBM P.C. DOS 5.0
124 : SOFTWARE: FASTSEQ for Windows 2.0
125 : CURRENT APPLICATION DATA:
126 : APPLICATION NUMBER: US/08/755,728
127 : FILING DATE: August 14, 1996
128 : CLASSIFICATION: 510
129 : PRIOR APPLICATION DATA:
130 : APPLICATION NUMBER: 60/008,659
131 : FILING DATE: December 19, 1995
132 : APPLICATION NUMBER: 60/023,943
133 : FILING DATE: August 14, 1996
134 : ATTORNEY/AGENT INFORMATION:
135 : NAME: WARBURG, Richard J.
136 : REGISTRATION NUMBER: 32,327
137 : REFERENCE/OCCKET NUMBER: 223/113
138 : TELECOMMUNICATION INFORMATION:
139 : TELEPHONE: (213) 489-1600
140 : TELEFAX: (213) 955 0442
141 : TELEX: 67-3510
142 : INFORMATION FOR SEQ ID NO: 4:
143 : SEQUENCE CHARACTERISTICS:
144 : LENGTH: 403 amino acids
145 : TYPE: amino acid
146 : STRANDEDNESS: single
147 : TOPOLOGY: linear
148 : MOLECULE TYPE: protein
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161 RESULT 17
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163 : Sequence 4, Application US/08974655
164 : Patent No. 5972576
165 : GENERAL INFORMATION:
166 : APPLICANT: PLOWMAN, Gregory
167 : APPLICANT: MOSSIE, Kevin
168 : TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
169 : TITLE OF INVENTION: AND/OR AUR 2 RELATED DISORDERS
170

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1 NUMBER OF SEQUENCES: 29
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: Lyon & Lyon
4 STREET: 633 West Fifth Street
5 CITY: Los Angeles
6 STATE: California
7 COUNTRY: U.S.A.
8 ZIF: 90071-2066
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
11 MEDIUM TYPE: storage
12 COMPUTER: IBM Compatible
13 OPERATING SYSTEM: IBM P.C. DOS 5.0
14 SOFTWARE: FastSeq for Windows 2.0
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/474,654
17 FILING DATE:
18 CLASSIFICATION: 435
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 08/755,728
21 FILING DATE: January 25, 1996
22 APPLICATION NUMBER: 60/008,809
23 FILING DATE: December 18, 1995
24 APPLICATION NUMBER: 60/023,943
25 FILING DATE: August 14, 1996
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Warburg, Richard J.
28 REGISTRATION NUMBER: 32,327
29 REFERENCE/DOCKET NUMBER: 223/113
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (213) 489-1600
32 TELEFAX: (213) 955-0440
33 INFORMATION FOR SEQ ID NO: 4:
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35 LENGTH: 403 amino acids
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52 RESULT 48
53 US-09-283-011-4
54 Sequence 4, Application US/09283011
55 Patent No. 6207401
56 GENERAL INFORMATION:
57 APPLICANT: Plowman, Gregory
58 APPLICANT: Mossie, Kevin
59 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AIDS
60 TITLE OF INVENTION: AND/OR AIDS-2 RELATED DISORDERS
61 NUMBER OF SEQUENCES: 39
62 CORRESPONDENCE ADDRESS:
63 ADDRESSEE: Lyon & Lyon
64 STREET: 633 West Fifth Street
65 CITY: Los Angeles
66 STATE: California
67 COUNTRY: U.S.A.
68 ZIF: 90071-2066
69 COMPUTER READABLE FORM:

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1 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
2 MEDIUM TYPE: storage
3 COMPUTER: IBM Compatible
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10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: 09/012,135
12 FILING DATE: January 22, 1998
13 APPLICATION NUMBER: 08/755,728
14 FILING DATE: No. 6207401, December 25, 1996
15 APPLICATION NUMBER: 60/023,943
16 FILING DATE: August 14, 1996
17 APPLICATION NUMBER: 60/008,809
18 FILING DATE: December 18, 1995
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Warburg, Richard J.
21 REGISTRATION NUMBER: 32,327
22 REFERENCE/DOCKET NUMBER: 231/282
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: (213) 489-1600
25 TELEFAX: (213) 955-0440
26 INFORMATION FOR SEQ ID NO: 4:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 403 amino acids
29 TYPE: amino acid
30 STRANDEDNESS: single
31 TOPOLOGY: linear
32 MOLECULE TYPE: protein
33 HYPOTHEtical: NO
34 ANTI-SENSE: NO
35 US-09-283-011-4
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38 Best Local Similarity 60.0%; Pred. No. 14;
39 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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42 1:|||||
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45 RESULT 39
46 US-09-252-991A-28679
47 Sequence 28679, Application US/09252991A
48 Patent No. 6551795
49 GENERAL INFORMATION:
50 APPLICANT: Maisel, Robertfield et al
51 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
52 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
53 FILE REFERENCE: 137196,136
54 CURRENT APPLICATION NUMBER: US/09/252,991A
55 CURRENT FILING DATE: 1999-02-18
56 PRIOR APPLICATION NUMBER: US 60/074,788
57 PRIOR FILING DATE: 1998-02-18
58 PRIOR APPLICATION NUMBER: US 60/094,190
59 PRIOR FILING DATE: 1998-07-27
60 NUMBER OF SEQ ID NOS: 33142
61 SEQ ID NO 28679
62 LENGTH: 259
63 TYPE: PRT
64 ORGANISM: Pseudomonas aeruginosa
65 US-09-252-991A-28679
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DB          152 MCGRPP 158

RESULT 40
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Sequence 13, Application US/08252995D
Patent No. 5655501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRESKIN & PARR
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 1Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.1.6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/252,914D
FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Kudryak, Linda M
REGISTRATION NUMBER: 34,471
REFERENCE/DOCKET NUMBER: 0153 97
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-364-7311
TELEFAX: 416-361-1398
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
US-09-252 995D 13

Query Match          65.8% Score 100.00 10.00 10.00
Best local similarity 65.8% P001 0.00
Matches 3: Conservative 41 Mismatches 1 Subst 64 Gaps 33

07          1 MCGRPP 9
13          152 MCGRPP 208

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CPU time 1:22 secs

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GenCore version 5.1.6
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Q: protein - protein search, using sw model

Run on: November 14, 2003, 14:36:48 ; Search time 29 seconds

William Allen
69-247 William St.
Dallas, Texas

File: US-09-736-076-19

85-2966

11 STEELED IN 1

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2	55	94.8	400	15	US-10-26-076	5	Sequence 5, Appl
3	53	94.8	469	15	US-09-059-076	14	Sequence 14, Appl
4	53	94.8	685	10	US-09-011-01A	29	Sequence 29, Appl
5	53	94.8	685	10	US-09-011-01A	29	Sequence 250, Appl
6	55	94.8	685	10	US-09-011-01A	29	Sequence 251, Appl
7	55	94.8	685	12	US-09-024-098	1	Sequence 101, Appl
8	55	94.8	685	12	US-09-024-098	1	Sequence 1, Appl
9	55	94.8	685	12	US-09-042-21A	1	Sequence 101, Appl
10	49	84.5	9	9	US-09-076-076	15	Sequence 15, Appl
11	49	84.5	9	9	US-09-076-076	14	Sequence 18, Appl
12	49	84.5	10	9	US-09-076-076	17	Sequence 57, Appl
13	49	84.5	20	9	US-09-076-076	5	Sequence 6, Appl
14	49	84.5	129	10	US-09-025-100	128	Sequence 1268, Appl
15	49	84.5	367	15	US-10-026-021	6	Sequence 6, Appl

16	49	84.5	516	10	US-09-771-16:A-123	Sequence 123, Appl
17	49	84.5	603	10	US-09-771-16:A-214	Sequence 214, Appl
18	49	84.5	603	10	US-09-771-16:A-186	Sequence 186, Appl
19	46	79.3	9	3	US-09-736-076-17	Sequence 17, Appl
20	46	79.3	379	5	US-10-026-021-3	Sequence 3, Appl
21	46	79.3	970	15	US-10-026-021-2	Sequence 2, Appl
22	41	70.7	8	9	US-09-736-076-16	Sequence 16, Appl
23	41	70.7	373	15	US-10-026-021-4	Sequence 4, Appl
24	41	70.7	607	12	US-09-769-970-15	Sequence 15, Appl
25	41	70.7	607	12	US-10-024-041-16	Sequence 16, Appl
26	41	70.7	607	15	US-10-108-580-2	Sequence 2, Appl
27	40	69.0	344	3	US-09-012-135A-3	Sequence 3, Appl
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29	40	69.0	344	15	US-10-171-311-214	Sequence 214, Appl
30	40	69.0	347	10	US-09-974-298-136	Sequence 136, Appl
31	40	69.0	528	12	US-10-032-585-7571	Sequence 7571, Ap
32	39	67.2	303	12	US-10-153-919-12	Sequence 12, Appl
33	39	67.2	303	12	US-10-153-919-22	Sequence 22, Appl
34	39	67.2	403	9	US-09-312-135A-4	Sequence 4, Appl
35	39	67.2	403	15	US-10-026-021-7	Sequence 7, Appl
36	39	67.2	403	15	US-10-059-585-33	Sequence 33, Appl
37	39	67.2	403	15	US-10-209-324-2	Sequence 2, Appl
38	38	65.5	8	9	US-09-736-076-58	Sequence 58, Appl
39	38	65.5	256	12	US-09-898-837A-32	Sequence 32, Appl
40	38	65.5	348	12	US-1C-291-253A-16	Sequence 16, Appl
41	38	65.5	737	10	US-09-771-16:A-195	Sequence 195, App
42	38	65.5	737	15	US-1C-228-931-4	Sequence 4, Appl
43	37	63.8	23	9	US-09-736-076-3	Sequence 3, Appl
44	37	63.8	347	10	US-09-801-876B-8	Sequence 8, Appl
45	37	63.8	347	15	US-1C-254-969-8	Sequence 8, Appl

ALIGNMENTS

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2  US-09-736-C76 19
3  Sequence 19, Application US/09736076
4  Patent No. US2002054910A.
5  GENERAL INFORMATION:
6  APPLICANT: Ben Sasson Shmuel A.
7  TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
8  TITLE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
9  FILE REFERENCE: 1242.1215-C39
10 CURRENT APPLICATION NUMBER: US/09/736, 076
11 CURRENT FILING DATE: 2000-12-13
12 PRIOR APPLICATION NUMBER: US 08/861,338
13 PRIOR FILING DATE: 1997-05-21
14 NUMBER OF SEQ. NOS: 68
15 SOFTWARE: FastSeq for Windows Version 4.0

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Query Match      100.0%; Score 58; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 11; Conservative 0; Mismatches 0; Idels

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QY 1 MLLGRPPETS 11

1 VLLGRPPETS 11

RESULTS

```
US-10-059-021-5
; Sequence 5, Application US/10026021
; Publication No. US20030027756A;
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi;
; APPLICANT: Gekins, Yordhu;
; APPLICANT: Rigel Pharmaceuticals, Inc.;
; TITLE OF INVENTION: SAK, Modulation of cellular proliferation for;
; TITLE OF INVENTION: Treatment of Cancer;
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10026021
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/101,412
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: DOMAIN
; LOCATION: (21..400)
; OTHER INFORMATION: Human SMK mitotic kinase Kinase domain
US-10-059-021-5
Query Match          94.8%   Score 55; DB 15; Length 400;
Best Local Similarity 90.9%   Pred. No. 0.15;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGRPPFFTS 11
      1 |||||
      57 MLLGRPPFFTS 283

TS      283 MLLGRPPFFTS 283

RESULT 1
US-10-059-021-5
; Sequence 14, Application US/10026021
; Publication No. US20030027756A;
; GENERAL INFORMATION:
; APPLICANT: Grg, Toshio
; APPLICANT: Issaga, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Hayashi, Koji
; APPLICANT: Otsuka, Kacuo
; APPLICANT: Yaeguchi, Sun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Saito, Tomoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nara, Keiichi
; APPLICANT: Furukashi, Shin Ichi
; APPLICANT: Senoo, Chika
; APPLICANT: Nara, Jiro-ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 06502-09803
; CURRENT APPLICATION NUMBER: US/10026021
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP00/60000
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/189,142
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: US 60/159,530
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: JP 2000-118074
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183000
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248004
; NUMBER OF SEQ ID NOS: 64
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-595-14
Query Match          94.8%   Score 55; DB 15; Length 469;
Best Local Similarity 90.9%   Pred. No. 0.17;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGRPPFFTS 11
      1 |||||
      57 MLLGRPPFFTS 283

DB      57 MLLGRPPFFTS 283

RESULT 4
US-09-771-161A-249
; Sequence 249, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 249
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-249
Query Match          94.8%   Score 55; DB 10; Length 685;
Best Local Similarity 90.9%   Pred. No. 0.25;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLLGRPPFFTS 11
      1 |||||
      273 MLLGRPPFFTS 283;

DB      273 MLLGRPPFFTS 283;

RESULT 5
US-09-771-161A-250
; Sequence 250, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 250
; LENGTH: 685
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-250
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Query Match 94.8% Score 55; DB 10; Length 685;
Best Local Similarity 90.9%; Pred. No. 0.25;
Matches 10; Conservative 1; Mismatches 0; Indels 0;

QY 1 MLGRRPPEFTS 11
DB 273 MLGRRPPEFT 283

RESULT 4

US-09-736-076-19.rapb
1 Sequence 283; Application US/2007/1161A
2 Patent No. US2008011811A;
3 GENERAL INFORMATION:
4 APPLICANT: LEVINE, et al.
5 TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
6 FILE REFERENCE: 802620-2075-1
7 CURRENT APPLICATION NUMBER: US/29/771,161A
8 PRIOR FILING DATE: 2001-01-26
9 PRIOR APPLICATION NUMBER: 09/724,676
10 PRIOR FILING DATE: 2000-11-28
11 PRIOR APPLICATION NUMBER: 136776
12 PRIOR FILING DATE: 2000-06-15
13 PRIOR APPLICATION NUMBER: 135619
14 PRIOR FILING DATE: 2000-04-12
15 NUMBER OF SEQ ID NOS: 273
16 SOFTWARE: Patcom in version 2.0
17 SEQ ID NO 25:
18 LENGTH: 685
19 TYPE: PRT
20 ORGANISM: Homo sapiens
21 US-09-736-076-19.rapb

Query Match 94.8% Score 55; DB 10; Length 685;
Best Local Similarity 90.9%; Pred. No. 0.25;
Matches 10; Conservative 1; Mismatches 0; Indels 0;

QY 1 MLGRRPPEFTS 11
DB 273 MLGRRPPEFT 283

RESULT 5

US-10-024-298A-10;
1 Sequence 101; Application US/100-4208A
2 Publication No. US20030143540A1
3 GENERAL INFORMATION:
4 APPLICANT: ASARI KASEI; KASUSHIKI KATSUMA
5 APPLICANT: AKIO MATSUDA
6 APPLICANT: GISHI, HONDA
7 APPLICANT: SHIRI, MURAYASU
8 APPLICANT: YUKIKO NAGANO
9 TITLE OF INVENTION: NF-K B Activating Agents
10 FILE REFERENCE: 1254-0191P
11 CURRENT APPLICATION NUMBER: US/10/724,298A
12 CURRENT FILING DATE: 2003-04-08
13 PRIOR APPLICATION NUMBER: 60/314,385
14 PRIOR FILING DATE: 2001-08-24
15 PRIOR APPLICATION NUMBER: 60/276,641
16 PRIOR FILING DATE: 2001-03-26
17 PRIOR APPLICATION NUMBER: 60/258,315
18 PRIOR FILING DATE: 2000-12-28
19 PRIOR APPLICATION NUMBER: JP254018/2001
20 PRIOR FILING DATE: 2001-08-24
21 PRIOR APPLICATION NUMBER: JP0089912/2001
22 PRIOR FILING DATE: 2001-03-26
23 PRIOR APPLICATION NUMBER: JP402388/2000
24 PRIOR FILING DATE: 2000-12-28
25 NUMBER OF SEQ ID NOS: 182
26 SOFTWARE: Patent in Ver. 2.0
27 SEQ ID NO 101
28 LENGTH: 685
29 TYPE: PRT

1 ORGANISM: Homo sapiens
US-10-024-298A-10;

Query Match 94.8% Score 55; DB 12; Length 685;
Best Local Similarity 90.9%; Pred. No. 0.25;
Matches 10; Conservative 1; Mismatches 0; Indels 0;

QY 1 MLGRRPPEFTS 11
DB 273 MLGRRPPEFT 283

RESULT 8

US-09-769-970-1
1 Sequence 1; Application US/09/769970
2 Publication No. US20031170219A;
3 GENERAL INFORMATION:
4 APPLICANT: Bandman, Olga
5 Hillman, Jennifer L.
6 Corley, Neil C.
7 Guegler, Karl G.
8 Lai, Preeti
9 Goli, Surva K.
10 Shah, Purvi
11 TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
12 KINASES
13 NUMBER OF SEQUENCES: 21
14 CORRESPONDENCE ADDRESS:
15 ADDRESSEE: Incyte Pharmaceuticals, Inc.
16 STREET: 3174 Porter Drive
17 CITY: Palo Alto
18 STATE: CA
19 COUNTRY: USA
20 ZIP: 94304
21 COMPUTER READABLE FORM:
22 MEDIUM TYPE: Diskette
23 COMPUTER: IBM Compatible
24 OPERATING SYSTEM: DOS
25 SOFTWARE: FastSeq for Windows Version 2.0
26 CURRENT APPLICATION DATA:
27 APPLICATION NUMBER: US/09/769,970
28 FILING DATE: 24-Jan-2001
29 CLASSIFICATION: <Unknown>
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: 09/272,796
32 FILING DATE: <Unknown>
33 ATTORNEY/AGENT INFORMATION:
34 NAME: Billings, Lucy J.
35 REGISTRATION NUMBER: 36,749
36 REFERENCE/LOCKET NUMBER: PF-0321 US
37 TELECOMMUNICATION INFORMATION:
38 TELEPHONE: 415 855-0555
39 TELEFAX: 415-845-4166
40 TELEX: <Unknown>
41 INFORMATION FOR SEQ ID NO: 1:
42 SEQUENCE CHARACTERISTICS:
43 LENGTH: 685 amino acids
44 TYPE: amino acid
45 STRANDEDNESS: single
46 TOPOLOGY: linear
47 IMMEDIATE SOURCE:
48 LIBRARY: HUVENB01
49 CLONE: 39243
50 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-769-970-1

Query Match 94.8% Score 55; DB 12; Length 685;
Best Local Similarity 90.9%; Pred. No. 0.25;
Matches 10; Conservative 1; Mismatches 0; Indels 0;

QY 1 MLGRRPPEFTS 11
DB 273 MLGRRPPEFT 283

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RESULT 3
US 10 042 211A-101
1 Sequence 101, Application US/10042211A
2 Publication No. US2003017079A1
3 GENERAL INFORMATION:
4 APPLICANT: MATSUDA, AKIO et al.
5 TITLE OF INVENTION: NEKP Activating Device
6 FILE REFERENCE: 1054-0192F
7 CURRENT APPLICATION NUMBER: US/10042211A
8 PRIORITY FILING DATE: 2002-01-11
9 PRIOR APPLICATION NUMBER: JP 2000-402484
10 PRIOR FILING DATE: 2000-12-28
11 PRIOR APPLICATION NUMBER: JP 2001-089411
12 PRIOR FILING DATE: 2001-03-26
13 PRIOR APPLICATION NUMBER: JP 2001-254014
14 PRIOR FILING DATE: 2001-06-24
15 PRIOR APPLICATION NUMBER: US 6024584.1.5
16 PRIOR FILING DATE: 2000-12-28
17 PRIOR APPLICATION NUMBER: US 602494.4.40
18 PRIOR FILING DATE: 2001-03-26
19 PRIOR APPLICATION NUMBER: US 602314.1.40
20 PRIOR FILING DATE: 2001-06-24
21 NUMBER OF SEQ ID NOS: 162
22 SOFTWARE: Patent In Ver. 2.0
23 SEQ ID NO 101
24 TYPE: FRT
25 LENGTH: 685
26 ORGANISM: Homo sapiens
27 US 10 042 211A-101
28 Query Match: 34.98; Score 15; DB 12; Length 685;
29 Best Local Similarity 90.98; Pred. No. 0.25;
30 Matches 16; Conservative 1; Mismatches 0; Gaps 0;
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QY 1 MLLGRPPETS 9
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DB 2 MLLGRPPETS 13

RESULT 13
US-09-736-076-6
; Sequence 6, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE OF INVENTION: MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015 OC9
; CURRENT APPLICATION NUMBER: US/09/736-076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,138
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURES:
; OTHER INFORMATION: PCLO
US-09-736-076-6

Query Match 84.5%; Score 49; DB 9; Length 20;
Best Local Similarity 72.7%; Pred. No. 3.082;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPETS 11
   |||||
DB 3 LLVGKPPETS 13

RESULT 14
US-09-925-300-1268
; Sequence 1268, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P4101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05400
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/144,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1268
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: SITE
; LOCATION: 13
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; LOCATION: 159;
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: 1307;
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: 1308;
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE

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; LOCATION: 1314;
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: 1317;
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: 1323;
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: 1327;
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: 1329;
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: 1329;
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1268

Query Match 84.5%; Score 49; DB 10; Length 329;
Best Local Similarity 72.7%; Pred. No. 1.3;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPETS 11
   |||||
DB 260 LLVGKPPETS 270

RESULT 15
US-10-026-021-6
; Sequence 6, Application US/10026021
; Publication No. US20030027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Demo, Susan
; APPLICANT: Jenkins, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-5012-005
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: DOMAIN
; LOCATION: 11..1367;
; OTHER INFORMATION: human p1A; mitotic kinase kinase domain
US 10-026-021-6

Query Match 84.5%; Score 49; DB 15; Length 367;
Best Local Similarity 72.7%; Pred. No. 1.4;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLGRPPETS 11
   |||||
DB 244 LLVGKPPETS 254

RESULT 16
US-09-771-16-A-123
; Sequence 123, Application US/0977116A
; Patent No. US20020113811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1

```

```

; CURRENT APPLICATION NUMBER: US/09/771,161A
; FILE REFERENCE: MRI-035
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136774
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patent version 3.0
; SEQ ID NO 123
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-771,161A-123

```

```

Query Match      84.5%; Score 49; DB 10; Length 516;
Best Local Similarity 72.7%; Pred. No. 21;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLGKPPPE 11
      1111111111
DB      157 LLVGKPPPE 167

```

```

RESULT 17
US-09-771,161A-214
; Sequence 214, Application US/09771,161A
; Patent No. US002010181A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2305.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patent version 3.0
; SEQ ID NO 214
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-771,161A-214

```

```

Query Match      84.6%; Score 49; DB 10; Length 603;
Best Local Similarity 72.7%; Pred. No. 21;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLGKPPPE 11
      1111111111
DB      244 LLVGKPPPE 254

```

```

RESULT 18
US-10-171,311-126
; Sequence 186, Application US/10171,311
; Publication No. US2003087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Menabad, John
; APPLICANT: Kamatkar, Shubhandi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Mantula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY

```

```

; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 62/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-171-311-186

```

```

Query Match      84.5%; Score 49; DB 15; Length 603;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLGKPPPE 11
      1111111111
DB      244 LLVGKPPPE 254

```

```

RESULT 19
US-09-736-076-17
; Sequence 17, Application US/09736076
; Patent No. US2002004931A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; MODULATE THE ACTIVITY OF SERINE/THREONINE KINASES
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: ACETYLATION
; NAME/KEY: ACETYLATION
; LOCATION: 11...16
; OTHER INFORMATION: Position 9 is benzylester
; NAME/KEY: AMIDATION
; LOCATION: 10...19
; OTHER INFORMATION: 143.1
; US-09-736-076-17

```

```

Query Match      79.3%; Score 46; DB 9; Length 9;
Best Local Similarity 88.9%; Pred. No. 5.9e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MLGKPPPE 9
      1111111111
DB      1 MLGKPPPE 9

```

```

RESULT 20
US-10-026-021-3
; Sequence 3, Application US/10026021
; Publication No. US20030027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Dero, Susan
; APPLICANT: Gekking, Yonchu
; APPLICANT: Rigel Pharmaceuticals, Inc.

```



```

; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(379)
; OTHER INFORMATION: SAK serine/threonine kinase kinase domain
US-10-026-021-3

```

```

Query Match          79.3%; Score 46; DB 15; Length 379;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MLLGRPPPT 10
   |||||
DB 204 MLLGRPPPT 213

```

```

RESULT 21
US-10-026-021-2
; Sequence 2, Application US/10026021
; Publication No. US2003027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Detsu, Susan
; APPLICANT: Jenkins, Yochu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(373)
; OTHER INFORMATION: human SAK serine/threonine kinase
US-10-026-021-2

```

```

Query Match          79.3%; Score 46; DB 15; Length 379;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MLLGRPPPT 10
   |||||
DB 204 MLLGRPPPT 213

```

```

RESULT 22
US-09-736-076-16
; Sequence 16, Application US/09736076
; Patent No. US2002049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; MODULATE THE ACTIVITY OF SERINE THREONINE KINASES
; FILE REFERENCE: 1242,1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076

```

```

; CURRENT FILING DATE: 2003-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(8)
; NAME/KEY: AMIDATION
; LOCATION: (3)...(8)
; OTHER INFORMATION: J43
US-09-736-076-16

```

```

Query Match          70.7%; Score 41; DB 9; Length 8;
Best Local Similarity 87.5%; Pred. No. 5;9+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MLLGRPPF 8
   |||||
DB 1 MLLGRPPF 8

```

```

RESULT 23
US-10-026-021-4
; Sequence 4, Application US/10026021
; Publication No. US2003027756A1
; GENERAL INFORMATION:
; APPLICANT: Hitoshi, Yasumichi
; APPLICANT: Detsu, Susan
; APPLICANT: Jenkins, Yochu
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: SAK: Modulation of Cellular Proliferation for
; TITLE OF INVENTION: Treatment of Cancer
; FILE REFERENCE: 021044-001210US
; CURRENT APPLICATION NUMBER: US/10/026,021
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/309,632
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(373)
; OTHER INFORMATION: human FNK mitotic kinase kinase domain
US-10-026-021-4

```

```

Query Match          70.7%; Score 41; DB 15; Length 373;
Best Local Similarity 63.6%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 MLLGRPPFETS 11
   |||||
DB 253 MLLGRPPFETA 263

```

```

RESULT 24
US-09-769-970-15
; Sequence 15, Application US/09769970
; Publication No. US20030170219A1
; GENERAL INFORMATION:
; APPLICANT: Bardman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: La, Preeti

```



```

; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. US20020081578A1enter 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J
; REGISTRATION NUMBER: 32,127
; REFERENCE/DOCKET NUMBER: 231/262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; FAX: 62-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYDROPHOBIC: NO
; ART1-SENSE: NO
; ART2-SENSE: NO
US 09-012-136A-3

Query Match: 69.0%; Score 40; DB 9; Length 344;
Best Local Similarity 54.5%; Pred. No. 47;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

CY : MLGPPFFETS 11
DB : ||| |||
266 LLVGNPPESA 276

RESULT 29
US-10-059-584-34
; Sequence 34, Application US/1005942
; Publication No. US200308276A1
; GENERAL INFORMATION:
; APPLICANT: Oae, Toshio
; APPLICANT: Isogai, Takao
; APPLICANT: Nishikawa, Tetsuo
; APPLICANT: Rayashi, Koji
; APPLICANT: Otsuka, Kaoru
; APPLICANT: Yamamoto, Jun-ichi
; APPLICANT: Ishii, Shizuko
; APPLICANT: Shojiyama, Tokoyasu
; APPLICANT: Wakamatsu, Ai
; APPLICANT: Nagai, Atsushi
; APPLICANT: Otsuka, Tetsuo
; APPLICANT: Funahashi, Shin-ichi
; APPLICANT: Senoo, Chiaki
; APPLICANT: Naga, Jun-ichi
; TITLE OF INVENTION: NOVEL GENES ENCODING KINASE
; TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
; FILE REFERENCE: 68501-09800
; CURRENT APPLICATION NUMBER: US/1005942
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/JP96/05062
; PRIOR FILING DATE: 2002-07-28
; PRIOR APPLICATION NUMBER: US 60/153,320
; PRIOR FILING DATE: 2003-02-17
; PRIOR APPLICATION NUMBER: US 60/153,350
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: JP 2000-118774
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183087
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 11-248044
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 34

```

```

; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-585-34

Query Match: 69.0%; Score 40; DB 15; Length 344;
Best Local Similarity 54.5%; Pred. No. 47;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

CY : MLGPPFFETS 11
DB : ||| |||
266 LLVGNPPESA 276

RESULT 29
US-10-171-311-214
; Sequence 214, Application US/10171311
; Publication No. US200308276A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhang
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sepastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10171311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/135,934
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 214
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-214

Query Match: 69.0%; Score 40; DB 15; Length 344;
Best Local Similarity 54.5%; Pred. No. 47;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

CY : MLGPPFFETS 11
DB : ||| |||
266 LLVGNPPESA 276

RESULT 30
US-09-974-298-136
; Sequence 136, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hwei-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO: 136
; LENGTH: 347
; TYPE: PRT

```


APPLICATION NUMBER: 60/268 809
FILING DATE: December 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Wartburg, Richard C.
REGISTRATION NUMBER: 32,327
REFERENCES/DOCKET NUMBER: 231/282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1650
TELEFAX: (213) 955-0440
TELEFAX: 67-3510

Query Match 67.2%; Score 19; DB 9; Length 43;
Best Local Similarity 60.0%; Pred. No. 52;
Matches 6; Conservative 3; Mismatches 1; Indels

```

1  RESULT 35
2  US-10 626-021-7
3  Sequence 7, Application US/1002602;
4  Publication NO. US200302756A1
5  GENERAL INFORMATION:
6  APPLICANT: Hitoshi, Yasumichi;
7  APPLICANT: Hiro, Susan
8  APPLICANT: Jenkins, Yorche
9  APPLICANT: Rygel Pharmaceuticals, S. Inc
10 TITLE OF INVENTION: SAK: Modulation of Cell
11 FILE OF INVENTION: Treatment of Cancer;
12 FILE REFERENCE: 021044-0012130US
13 CURRENT APPLICATION NUMBER: US/10/226,921
14 CURRENT FILING DATE: 2002-06-25
15 PRIOR APPLICATION NUMBER: US 603309.612
16 FILING DATE: 2001-08-01
17 NUMBER OF SEQ ID NOS: 8
18 SOFTWARE: PatentIn Ver. 2.1
19 SEQ ID NO 7
20 LENGTH: 403
21 TYPE: PRT
22 ORGANISM: Homo sapiens
23 FEATURE:
24 OTHER INFORMATION: Human ARK mitotic kinase
25 US-10 626-021-7

```

Query Match	67.2%	Score 19	EP 15	Length 403
Best Local Similarity	60.0%	Pos. No. 32		
Matches	6	Conservative	37	Mismatches 24
				Indels 0
				Gaps 0

RESULT is
US 10-059 585-33
Sequence 33, Application US/10059585
Publication No. US2003008276A;
GENERAL INFORMATION:
APPLICANT: Ota, Toshio
APPLICANT: Isogai, Takao
APPLICANT: Nishikawa, Tetsuo

1	APPLICANT:	Havashi, Ko-1
2	APPLICANT:	Otsuka, Kaoru
3	APPLICANT:	Yamamoto, Jun-ichi
4	APPLICANT:	Ishii, Shizuko
5	APPLICANT:	Sugiyama, Tomoyasu
6	APPLICANT:	Wakamatsu, A.
7	APPLICANT:	Nagai, Keiichi
8	APPLICANT:	Otsuki, Tatsuzi
9	APPLICANT:	Funahashi, Shin-ichi
10	APPLICANT:	Senoo, Chikaki
11	APPLICANT:	Nezu, Jun-ichi

Query Match: 67.2%; Score 39; DB 15; Length 403;
Best Local Similarity 60.0%; Pred. No. 82;
Matches 6; Conservative 3; Mismatches 1; Indels

```

RESULT 37
US 6-209,324-2
Sequence 2, Application US/102209324
Publication No. US2536189910A1
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF CALIFORNIA SAN FRANCISCO
APPLICANT: TOLLAND, Amanda E.
APPLICANT: BALMAIN, Arian
TITLE OF INVENTION: STK15 (STK6) GENE POLYMORPHISMS
FILE REFERENCE: JCSF112C-2
CURRENT APPLICATION NUMBER: US/102209,324
CURRENT FILING DATE: 2002-07-29
PRIORITY FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: US 60/334,146
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: US 60/308,911
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ IDS NOS: 34
SOFTWARE: Patent version 3.1

```

```

Query Match      67.2%; Score 39; DB 18; Length 403;
Best Local Similarity 60.0%; Pred. No. 82;
Matches 6; Conservative 3; Mismatches 1; Indels 2; Gaps 0;

QY 3 MLGRPFPE 1;
DB 323 LVGRPFPEAN 312

RESULT 38
US-09-736-076-58
Sequence 56, Application US/09/36094
Patent No. US2002084930A1
GENERAL INFORMATION:
APPLICANT: Ben Sasson Shmuel A.
TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
FILE REFERENCE: 1942.1035-039
CURRENT APPLICATION NUMBER: US/09/736-076
CURRENT FILING DATE: 2003-12-13
PRIOR APPLICATION NUMBER: US/09/861,114
PRIOR FILING DATE: 1997-05-21
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 58
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
NAME/KEY: MYRISTATE
LOCATION: (1)...(60)
NAME/KEY: ANIMATION
LOCATION: (1)...(18)
OTHER INFORMATION: SNK
US-09-736-076-59

Query Match      65.5%; Score 38; DB 18; Length 403;
Best Local Similarity 100.0%; Pred. No. 5; Seq ID 7;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY 1 MLGRPF 7
DB 1 MLGRPF 9

RESULT 39
US-09-898-817A-12
Sequence 12, Application US/09/898817A
Patent No. US2003007697A1
GENERAL INFORMATION:
APPLICANT: Quinn, Kerry E.
APPLICANT: Spytka, Kimberly A.
APPLICANT: Majumder, Kumud
APPLICANT: Vermet, Corine
APPLICANT: Herrmann, John L.
APPLICANT: Burgess, Catherine
APPLICANT: Fernandes, Ema
APPLICANT: Tappier Jr., Raymond
APPLICANT: Fastelli, Luca
APPLICANT: Gerlach, Valerie L.
APPLICANT: MacDougall, John P.
TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
FILE REFERENCE: 15966-598 CIP
CURRENT APPLICATION NUMBER: US/09/898,817A
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: U.S.S.N. 60/165,986
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,839
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: U.S.S.N. 60/195,637
PRIOR FILING DATE: 2000-04-07

```

```

1 PRIOR APPLICATION NUMBER: U.S.S.N. 60/197,080
2 PRIOR FILING DATE: 2000-04-13
3 PRIOR APPLICATION NUMBER: U.S.S.N. 60/232,677
4 PRIOR FILING DATE: 2000-09-15
5 PRIOR APPLICATION NUMBER: U.S.S.N. 60/181,347
6 PRIOR FILING DATE: 2000-02-09
7 PRIOR APPLICATION NUMBER: U.S.S.N. 60/194,195
8 PRIOR FILING DATE: 2000-04-03
9 PRIOR APPLICATION NUMBER: U.S.S.N. 60/215,906
10 PRIOR FILING DATE: 2000-07-03
11 PRIOR APPLICATION NUMBER: U.S.S.N. 03/775,427
12 PRIOR FILING DATE: 2000-11-16
13 NUMBER OF SEQ ID NOS: 53
14 SOFTWARE: PatentLITE Version 2.1;
15 SEQ ID NO 32
16 LENGTH: 256
17 TYPE: PRT
18 ORGANISM: Saccharomyces cerevisiae
19 US-09-898-817A-32

Query Match      65.5%; Score 38; DB 11; Length 256;
Best Local Similarity 55.6%; Pred. No. 78;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRPFPE 9
DB 193 LLGRPFQ 201

RESULT 40
US-10-291-253A-16
Sequence 16, Application US/10/291253A
Patent No. US20030150017A1
GENERAL INFORMATION:
APPLICANT: Botella, Jose
APPLICANT: Graham, Michael
APPLICANT: Fairbairn, David
TITLE OF INVENTION: A Method for Facilitating Pathogen Resistance
FILE REFERENCE: noma0040
CURRENT APPLICATION NUMBER: US/10/291,253A
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: PR8706
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: PR8802
PRIOR FILING DATE: 2001-11-12
PRIOR APPLICATION NUMBER: US60/341404
PRIOR FILING DATE: 2001-12-14
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentLITE Version 3.1
SEQ ID NO 16
LENGTH: 348
TYPE: PRT
ORGANISM: Meloidogyne incognita
US-10-291-253A-16

Query Match      65.5%; Score 38; DB 12; Length 348;
Best Local Similarity 66.7%; Pred. No. 11e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRPFPE 9
DB 210 MMGRPFPE 218

Search completed: November 14, 2003, 14:42:09
Job time : 29 secs

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GenCore version 5.1.6
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N protein - protein search, using sw model

Run on: November 14, 2003, 14:34:18 / Search time 21 seconds
(without alignments)
50,374 Million cell updates/sec

Title: US-09-736-076-19

Perfect score: 58

Sequence: 1 MLGRPFETS 11

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 28332 seqs, 9616582 residues

Total number of hits satisfying chosen parameters: 18136

Minimum DP seq length: 0

Maximum DP seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR76**

2: PIR1**

3: PIR2**

4: PIR3**

5: PIR4**

SUMMARIES

Used No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Length	PIR ID	Description
1	55	94.9	682	2 A4493	serum-inducible kinase
2	49	84.5	603	2 S1410	serine/threonine kinase
3	49	84.5	603	2 A47945	protein kinase EC
4	49	84.5	603	2 A47945	protein kinase EC
5	46	79.3	465	2 P55744	protein kinase EC
6	46	79.3	925	2 A55434	protein kinase EC
7	45	77.6	521	2 A46611	protein kinase EC
8	44	76.4	576	2 S12311	protein kinase EC
9	41	74.1	383	2 A42344	protein kinase EC
10	41	74.1	407	2 A42344	protein kinase EC
11	41	74.1	631	2 A42344	protein kinase EC
12	39	67.2	451	2 P71526	hypothetical prote
13	39	67.2	403	2 JC5974	autolysate-related kin
14	39	67.2	547	2 A44931	R06137.1: Protein -
15	39	67.2	556	2 S12044	nuclear factor kappa
16	39	67.2	639	2 A42344	protein kinase C1
17	39	67.2	648	2 A41344	calcium-like kinase 1
18	38	65.5	256	2 A41344	glutamine-binding
19	38	65.5	256	2 P72411	iron(II) ABC tran
20	38	65.5	305	2 A42344	serine/threonine kinase
21	38	65.5	329	2 P87732	protein B307.4 (1
22	38	65.5	547	2 P72056	hypothetical prote
23	38	65.5	634	1 S12302	protein kinase C1
24	38	65.5	656	2 P72056	hypothetical prote
25	38	65.5	683	2 P72056	hypothetical prote
26	38	65.5	705	2 A48144	protein kinase C1
27	38	65.5	707	1 A52532	protein kinase C1
28	38	65.5	736	1 A48144	protein kinase C1
29	38	65.5	737	1 S28942	protein kinase C1

30 38 65.5 737 1 KINTCE protein kinase C (

31 38 65.5 737 1 KIMSCE protein kinase C (

32 38 65.5 766 2 S69657 hypothetical prote

33 37 63.8 220 1 B42725 nitrite hydratase

34 37 63.8 345 2 JC1665 protein kinase EC

35 37 63.8 379 2 T23688 hypothetical prote

36 37 63.8 380 2 S75564 pkn5 protein - Myx

37 37 63.8 615 2 T22223 hypothetical prote

38 37 63.8 672 1 KIHUCA protein kinase C (

39 37 63.8 672 1 KIRTC protein kinase C (

40 37 63.8 672 1 KIMSQA protein kinase C (

41 37 63.8 672 1 KIRBC protein kinase C (

42 37 63.8 672 1 KIRBC protein kinase C (

43 37 63.8 676 2 A37237 protein kinase C (

44 37 63.8 682 1 KIBOGC protein kinase C (

45 37 63.8 697 1 KIRTCG protein kinase C (

ALIGNMENTS

RESULT 1

A44493

serum-inducible kinase mouse

C:Species: Mus musculus (house mouse)

C>Date: 10-Jun-1993 #sequence_revision: 18-Nov-1994 #text_change: 10-Sep-1997

C:Accession: A44493

R:Simmons, D.L.; Neel, B.G.; Stevens, R.; Evett, G.; Erikson, R.L.

Mol. Cell. Biol. 12, 4:64-4:169, 1992

A:Title: Identification of an early-growth-response gene encoding a novel putative pr

A:Reference number: A44493, MIM:92375095, PMID:1508211

A:Accession: A44493

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-682 <SIM>

A:Experimental source: F-2 cells

A:Note: sequence extracted from NCBI backbone (NCBI:111721, NCBI:111721)

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

C:Keywords: Atp

F:77-331/Domain: protein kinase homology <Kin>

Query Match: 94.9% Score 557 DB 2 Length 682

Best Loca: Similarity 90.9% Pred. NO. 0.036

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 MLGRPFETS 11

Db 270 MLGRPFETS 280

RESULT 2

S1410

serine/threonine specific protein kinase PLK (EC 2.7.1.1) - human

C:Alternate names: polo-like protein kinase; protein kinase plk-1

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision: 06-Jan-1995 #text_change: 24-Sep-1999

C:Accession: S1410, J18121, S1413

R:Goldstein, R.W.; Schultz, S.; Bartek, J.; Ziemiecki, A.; Ried, T.; Nigg, E.A.

Submitted to the EMBL Data Library, June 1993

A:Description: Cloning and characterization of a novel human protein kinase plk-1 a p

through mitosis.

A:Reference number: S1410

A:Accession: S1410

A:Molecule type: mRNA

A:Residues: 1-603 <GO>

A:Cross-references: EMBL:X13458; NID:9112997; PIDN:CAA51837.1; PID:9112993

A:Experimental source: nasopharyngeal carcinoma

A:Holtrich, C.; Wolf, G.; Straubinger, A.; Karn, T.; Bohme, B.; Rubsamen-Waigmann, H.,

Proc. Natl. Acad. Sci. U.S.A. 91, 1736-1740, 1994

A:Title: Induction and down-regulation of PLK, a human serine/threonine kinase expres

A:Reference number: A53134, MIM:9473304, PMID:8127874

A:Accession: A53134

A>Status: preliminary; NCBI:111721 and sequence not shown.

```

A:Molecule type: mRNA
A:Residues: 1-140; P: 142-226; E: 228-603 <RES>
A:Cross-references: EMBL:X75932; NID:g460769; PID:CAA33536.1; PID:g460769
C:Experimental source: lung tumor
R:Brauninger, A.; Strehardt, K.; Ruebsaen-Walshmann, H.
Oncogene 11, 1993-1995
A:Title: Identification and functional characterization of the human and murine polo-like
kinase 1.
A:Reference number: S61543; MUID:9605964; PID:g47869
A:Accession: S61543
A:Molecule type: DNA
A:Residues: 1-122; T: 124-136 <RR>
A:Cross-references: EMBL:X92725; NID:g460769; PID:CAA33536.1; PID:g460769
A:Experimental source: placenta
A:Note: the authors translated the cloned A3P for residue 167 as Met
C:Gene: Plk
A:Gene: CDK-PLK
A:Cross-references: GDB:331603
A:Map position: 17cen-17p12
C:Superfamily: unassigned Ser/Thr or Tyr specific protein kinases; protein kinase homol
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
P:51-305/Domain: protein kinase homology <KIN>
Query Match 84.5%; Score 49; DB 2; Length 603;
Best Local Similarity 72.7%; Pred. No. 0.4;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGRRPPFETS 11
DB 244 LLVGKPPFETS 254
RESULT 5
A:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 19-Dec 1997
C:Accession: B55748
R:Code, C.; Metro, B.; Yousefi, S.; Hefferman, M.; Dennis, J.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 6388-6392, 1994
A:Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosoph
A:Reference number: A55748; MUID:94294387; PMID:8022793
A:Accession: B55748
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-465 <FOC>
A:Cross-references: GDB:129480
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: ATP; phosphotransferase
P:10-265/Domain: protein kinase homology <KIN>
F:18-26/Region: protein kinase ATP-binding motif
Query Match 79.3%; Score 46; DB 2; Length 465;
Best Local Similarity 70.3%; Pred. No. 1.1;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGRRPPFET 10
DB 204 LLGRRPPFET 213
RESULT 6
A:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 24-Sep 1999
C:Accession: A55748
R:Code, C.; Metro, B.; Yousefi, S.; Hefferman, M.; Dennis, J.W.
Proc. Natl. Acad. Sci. U.S.A. 91, 6388-6392, 1994
A:Title: Sak, a murine protein-serine/threonine kinase that is related to the Drosoph
A:Reference number: A55748; MUID:94294387; PMID:8022793
A:Accession: A55748
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-925 <FOC>
A:Cross-references: GDB:129479; NID:g487869; PID:AAC37648.1; PID:g487870
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: ATP; phosphotransferase
P:10-265/Domain: protein kinase homology <KIN>
F:18-26/Region: protein kinase ATP-binding motif
Query Match 79.3%; Score 46; DB 2; Length 925;
Best Local Similarity 70.3%; Pred. No. 2.3;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLGRRPPFET 10
DB 204 LLGRRPPFET 213
RESULT 7
A:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 24-Sep 1999
C:Accession: A54596
R:Blake, R.F.; Delnek, W.R.
Mol. Cell. Biol. 13, 7793-7801, 1993
A:Title: Cell cycle and terminal differentiation-related regulation of the mouse mRNA
A:Reference number: A54596; MUID:9429140; PMID:8071811
A:Accession: A54596
A>Status: preliminary; translated from GDB:EMR12087
A:Molecule type: mRNA
A:Residues: 1-603 <SPS>

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protein F5A8.2 (imported) - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10 May-2001 #sequence_revision 10-May-2001 #text_change 17 May-2002
C:Accession: D88540
R:Annotation: The C. elegans Sequencing Consortium.
Science 263, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MIM:976961; PMID:985916
A:Note: See websites genome.wustl.edu/geno/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg
A:Note: published errata appeared in Science 283, 25, 1999; Science 283, 2103, 1999; and
A:Accession: D86540
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-521 <RCG>
A:Cross-references: GB:chr_IV; PDB:AACT1986.1; PDB:1J34.48; GSP:US-ONC0022; GESP:F5A8
C:Genetics:
A:Gene: F5A8.2
A:Map position: 4
C:Superfamily: cAMP dependent protein kinase; cAMP receptor protein cyclic nucleotide-bi
Query Match 77.6%; Score 45; DB 2; Length 521;
Best Local Similarity 53.6%; Pred. No. 1.9;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY : YLGRPPFET 11
DB 401 LVGRPPFQAS 411

RESULT 1
S52242
protein kinase polo (EC 2.7.1.1) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 10 Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Sep-1999
C:Accession: S52127
R:Submitted to the EMBL Data Library, November 1991
A:Reference number: S52127
A:Accession: S52127
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-576 <SGN>
A:Cross-references: EMBL:X63361; NID:G8355; PDB:1CAA44.3.1; PDB:8355
C:Genetics:
A:Gene: Flybase:polo
A:Cross-references: Flybase:FBgn003124
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP; phosphotransferase
F:127-277/Domain: protein kinase homology <KIN>
Query Match 75.9%; Score 49; DB 2; Length 576;
Best Local Similarity 50.0%; Pred. No. 3.2;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY : YLGRPPFET 10
DB 216 LVGRPPFET 225

RESULT 2
S52242
protein kinase (EC 2.7.1.1) p66X:Eg22 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 18 Jun-1999
C:Accession: S52242
R:Roghi, C.; Le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A:Description: Eg2, selected by differential screening encodes a new Xenopus protein kin
A:Reference number: S52242
A:Accession: S52242
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-389 <RCG>

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A:Cross-references: EMBL:217206; NID:G609279; PDB:CAA78914.1; PDB:G609280
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase
F:119-371/Domain: protein kinase homology <KIN>
F:127-135/Region: protein kinase ATP-binding motif
Query Match 74.1%; Score 43; DB 2; Length 389;
Best Local Similarity 77.8%; Pred. No. 3.3;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY : 2 LVGRPPFET 10
DB 311 LVGRPPFET 319

RESULT 10
S52243
p46Eg265 protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 24-Sep-1999
C:Accession: S52243; S34642; I51695
R:Roghi, C.; Le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
submitted to the EMBL Data Library, October 1992
A:Description: Eg2, selected by differential screening encodes a new Xenopus protein
A:Reference number: S52242
A:Accession: S52243
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-407 <RCG>
A:Cross-references: EMBL:217207; NID:G609281; PDB:CAA78915.1; PDB:G609282
R:Bouvet, P.; Omilli, F.; Ariot-Bonnemains, Y.; Legagneux, V.; Roghi, C.; Basset, T.;
submitted to the EMBL Data Library, June 1993
A:Description: Targetted deadenylation of specific mRNAs in Xenopus embryos by a mech.
A:Reference number: S34642
A:Accession: S34642
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 328-407 <RCG>
A:Cross-references: EMBL:234453; NID:G394756; PDB:CAA80826.1; PDB:G394757
R:Bouvet, P.; Omilli, F.; Ariot-Bonnemains, Y.; Legagneux, V.; Roghi, C.; Basset, T.;
Mol. Cell. Biol. 14, 1891-1900, 1994
A:Title: The deadenylation conferred by the 3' untranslated region of a developmental
A:Reference number: I51695; MIM:5415861; PMID:8114721
A:Accession: I51695
A:Status: preliminary; translated from GB/EMBL/CDDBJ
A:Molecule type: mRNA
A:Residues: 328-407 <RCG>
A:Cross-references: EMBL:244453; NID:G394756; PDB:CAA80826.1; PDB:G394757
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: ATP; phosphotransferase; protein kinase
F:138-390/Domain: protein kinase homology <KIN>
F:146-154/Region: protein kinase ATP-binding motif
Query Match 74.1%; Score 43; DB 2; Length 407;
Best Local Similarity 77.8%; Pred. No. 3.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY : 2 LVGRPPFET 10
DB 330 LVGRPPFET 339

RESULT 11
A57286
probable serine/threonine protein kinase (EC 2.7.1.1) fnk - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 10-Sep-1997
C:Accession: A57286
R:Donohue, P.C.; Alberts, G.F.; Guo, Y.; Winkles, J.A.
J. Biol. Chem. 270, 10351-10357, 1995
A:Title: Identification by targeted differential display of an immediate early gene e
A:Reference number: A57286; MIM:395247749; PMID:7730342
A:Accession: A57286

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A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-631 <DN>
A.Cross-references: GB:U21392; GB:U22434
C.Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C.Keywords: ATP; phosphotransferase
F.125-319/Domain: protein kinase homology <KIN>

Query Match      70.7%; Score 41; DB 2; Length 631;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRPPFETS 11
DB 254 LLGQPPFETA 264

RESULT 12
JC2304
A.Title: Hypothetical protein CT338 - Chlamydia trachomatis serotype D, strain UW3/Cx1
C.Species: Chlamydia trachomatis
C.Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C.Accession: E71526
C.Stechnon: R. S.; Kaiman, S.; Lammel, C.G.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A.Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trad
A.Reference number: A71570; MUID:9900609; PMID:9794136
A.Accession: E71526
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-553 <APN>
A.Cross-references: GB:AC001307; GB:AC001273; NID:9456474; PIND:AC00933.1; PID:g332879
A.Experimental source: serotype D, strain UW3/Cx
C.Keywords:
A.Gene: CT338

Query Match      67.2%; Score 49; DB 2; Length 553;
Best Local Similarity 60.0%; Pred. No. 68;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGRPPFET 10
DB 11 LGPPFET 18

RESULT 13
JC5974
A.Title: Neuro-related kinase 1 (EC 2.7.1.1) - human
C.Species: Homo sapiens (man)
C.Date: 15-Feb-1999 #sequence_revision 15-Feb-1999 #text_change 11-Jan-2000
C.Accession: JC5974
C.Stechnon: M. Nakano, H. Kuroyama, H. Kuroyama, T. Yabuta, N. Gilbert, D.C. Jenk
Biochem Biophys Res Commun 244, 255-261, 1998
A.Title: RNA cloning, expression, subcellular localization, and chromosomal assignment
A.Reference number: JC5974; MUID:9818943; PMID:9845910
A.Accession: JC5974
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-403 <SR>
A.Cross-references: GB:AF008551
C.Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C.Keywords: phosphotransferase
F.125-319/Domain: protein kinase homology <KIN>

Query Match      67.2%; Score 39; DB 2; Length 403;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLGRPPFETS 11
DB 323 LVGRPPFEAN 332

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RESULT 14
S44841
A.Title: K06H7.1 protein - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C.Accession: S44841
C.Stechnon: R. Favello, A.D.
submitted to the EMBL Data Library, May 1993
A.Description: Sequence of the C. elegans cosmid K06H7.
A.Reference number: S44820
A.Accession: S44841
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-547 <FAV>
A.Cross-references: EMBL:U15314; NID:g299690; PIND:AAA28084.1; PID:g289691
C.Genetics:
A.Introns: 25/3; 36/3; 90/3; 149/3; 186/2; 229/3; 311/3
C.Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hor
C.Keywords: ATP; serine/threonine-specific protein kinase
F.125-518/Domain: protein kinase homology <KIN>

Query Match      67.2%; Score 39; DB 2; Length 547;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRPPFET 10
DB 457 LLGQPPFES 466

RESULT 15
JC2304
A.Title: nuclear factor-kappa B p65 chain - chicken
C.Species: Gallus gallus (chicken)
C.Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C.Accession: JC2304
C.Stechnon: R. Ikeda, T.; Horjo, K.; Hirota, Y.; Onodera, T.
Gene 133, 237-242, 1993
A.Title: Isolation of the chicken NF-kappaB p65 subunit-encoding cDNA and characteriz
A.Reference number: JC2304; MUID:94040817; PMID:7916720
A.Accession: JC2304
A.Molecule type: mRNA
A.Residues: 1-558 <IKS>
A.Cross-references: GB:D13721; NID:9455463; PIND:BA02874.1; PID:g460974
C.Comment: This protein contains the Rel homology domain in its amino-terminal 286 aa
C.Superfamily: rel transforming protein; rel homology
C.Keywords: DNA binding; phosphoprotein
F.125-319/Domain: rel homology <REL>
F.306-309/Region: nuclear location signal
F.128-/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match      67.2%; Score 39; DB 2; Length 558;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLGRPPFET 10
DB 428 LLGQPPFET 436

RESULT 16
A32545
A.Title: protein kinase C (EC 2.7.1.1) - fruit fly (Drosophila melanogaster)
C.Species: Drosophila melanogaster
C.Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1999
C.Accession: A32545
C.Stechnon: A. J. Rhee, L.; Yadgar, R.; Paro, R.; Ullrich, A.; Goeddel, D.V.
EMBO J. 6, 433-441, 1987
A.Title: Structure and nucleotide sequence of a Drosophila melanogaster protein kin
A.Reference number: A32545; MUID:87218499; PMID:3107983
A.Accession: A32545
A.Status: preliminary
A.Molecule type: mRNA

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A:Residues: 1-639 <RCS>
A:Cross-references: GB:X05076; NID:98152; PIDN:CAA28724.1; PID:98353; GB:X00042
C:Genetics:
A:Gene: FlyBase:FK053E
A:Cross-references: FlyBase:FBgn000309
C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein kinase C superfamily; ATP; phosphotransferase; serine/threonine-specific protein kinase
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F146-95/Domain: protein kinase C zinc binding repeat homology <K21>
F111-60/Domain: protein kinase C zinc-binding repeat homology <K22>
F161-273/Domain: protein kinase C C2 region homology <K25>
F139-539/Domain: protein kinase homology <K18>
F1347-355/Region: protein kinase ATP-binding motif

Query Match: 67.2%; Score 39; DB 2; Length 649;
Best Local Similarity: 66.7%; Pred. No. 30;
Matches: 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLGGRPPPE 9
| | | | |
DB 533 MLVQCHPPD 541

RESULT 17
T43337
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 01-Dec-2000
C:Accession: T43337; S4476;
R:Case: 3; Serafinas, C.; Ashcroft, N.; Kostinski, M.; Longo, D.; Ferris, D.K.; Golden, R.; Chase, B.; Serafinas, C.; Ashcroft, N.; Kostinski, M.; Longo, D.; Ferris, D.K.; Golden, R. submitted to the EMBL Data Library, July 1998
A:Description: The polo-like kinase PLK-1 is required for nuclear envelope breakdown and
A:Reference number: 222438
A:Accession: T43337
A:Status: preliminary; translated from GB/EVBL/D849
A:Molecule type: mRNA
A:Residues: 1-648 <CHA>
A:Cross-references: EMBL:AF085581; PIDN:AA034661.1
R:Favell, A.C.
A:Submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans subunit C1499
A:Reference number: S44617
A:Accession: S44761
A:Status: preliminary
A:Molecule type: DNA
A:Residues: MKTLLPAG-648 <PAV>
A:Cross-references: EMBL:J55186; NID:928964; PID:928964
C:Genetics:
A:Gene: PLK-1
A:Map position: 1
A:Introns: 391/3; 542/3; 578/3
C:Superfamily: unassigned Ser/Thr or Tyr kinases; protein kinase homology

Query Match: 67.2%; Score 39; DB 2; Length 649;
Best Local Similarity: 66.7%; Pred. No. 30;
Matches: 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLGGRPPPE 10
| | | | |
DB 228 LLPGQPPPE 237

RESULT 18
A81354
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C:Accession: A81354
R:Parkhill, J.; Wren, B.W.; Murgali, K.; Kestley, J.M.; Hutcher, C.; Basham, D.; Chillingworth, G.; Quail, M.; Rutherford, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrall, Nature 403, 665-668, 2000
A:Title: The genome sequence of the food borne pathogen Campylobacter jejuni reveals hyp
A:Reference number: A81250; MUID:20150917; PID:10694204
A:Accession: A81354

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-256 <PAR>
A:Cross-references: GB:AC139076; GB:AL111168; NID:96968128; PIDN:CAB73082.1; PID:9696
A:Experimental source: serotype O2, strain NCTC 11169
C:Genetics:
A:Gene: GlnH; Cj0817
C:Superfamily: lysine-arginine ornithine-binding protein

Query Match: 65.5%; Score 38; DB 2; Length 256;
Best Local Similarity: 72.7%; Pred. No. 19;
Matches: 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLGGRPPPE 11
| | | | |
DB 25 MEUGYPPPEVS 35

RESULT 19
F72421
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 08-Sep-2000
C:Accession: F72421
R:Neison, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.B.; Dodson, R.J.; Haft, D.H.; Hicl Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M. Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: F72421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-256 <ARN>
A:Cross-references: GB:AE000512; NID:94980558; PIDN:AAC35172.1; PID:94980
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0078
C:Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homolo

Query Match: 65.5%; Score 38; DB 2; Length 256;
Best Local Similarity: 80.0%; Pred. No. 18;
Matches: 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLGRRPPPE 11
| | | | |
DB 62 LLGRRPPPE 71

RESULT 20
T43221
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C:Accession: T43221
R:Schumacher, J.M.; Golden, A.; Donovan, P.J.
J. Cell Biol. 143, 1635-1646, 1998
A:Title: AIR-2: An aurora/Ipl1-related protein kinase associated with chromosomes and
A:Reference number: 222347; MUID:99869487; PMID:9852156
A:Accession: T43221
A:Status: preliminary; translated from GB/EMBL/COBJ
A:Molecule type: mRNA
A:Residues: 1-305 <SCH>
A:Cross-references: EMBL:AF071207; PIDN:AAC70945.1
C:Genetics:
A:Gene: AIR-2
A:Map position: 1
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: phosphotransferase

Query Match: 65.5%; Score 38; DB 2; Length 305;
Best Local Similarity: 75.0%; Pred. No. 2;
Matches: 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 25
 C3R254
 Serine/threonine-specific protein kinase p101 (EC 2.7.1.1) - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
 C:Accession: U38254; U45128
 R:Brown, R.; Churcher, C.M.; Barrell, B.G.; Rands, M.A.; Wood, V.; submitted to the EMBL Data Library, August 1995
 A:Reference number: 221781
 A:Accession: U38254
 A:Status: preliminary; translated from GP/EMBL/DBM1
 A:Molecule type: DNA
 A:Residues: 1-691 <PRO>
 A:Cross-references: EMBL:U38254; FID:CA450116; SFD:SPAC23011.16
 A:Experimental source: strain 9720; GenBank C23011
 R:Okuka, H.; Hatan, T.M.; Glover, D.M.
 Genes Dev. 9: 1055-1073, 1995
 A:Title: The conserved Schizosaccharomyces pombe kinase p101, required to form a bipolar spindle
 A:Reference number: 222921; MIM:19562899; FID:U44254
 A:Accession: U45128
 A:Status: preliminary; translated from GP/EMBL/DBM1
 A:Molecule type: DNA
 A:Residues: 1-693 <ORF>
 A:Cross-references: EMBL:U45128; FID:U45128; FID:U45128
 A:Experimental source: strain 972 derivative
 C:Genetics:
 A:Gene: p101; SPAC23011.16
 A:Map position: 1
 C:Function:
 A:Description: required to form a bipolar spindle and early in the regulatory cascade that
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 C:Keywords: phosphotransferase; protein kinase
 Query Match 65.5%; Score 36; DB 2; Length 693;
 Best Local Similarity 55.6%; Pred. No. 49;
 Matches 5; Conservative 4; Mismatches 0; Gaps 0;
 CQ 1 MLCGRPPF 9
 DE 239 LLIKKPPF 241
 RESULT 26
 A48-44
 Protein kinase C (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)
 A:Alternate names: protein kinase PKA; protein kinase PKA; protein kinase PKA
 C:Species: Saccharomyces cerevisiae
 C:Date: 30-Jun-1995 #sequence_revision 10-Jun-1995 #text_change 24-Sep-1999
 C:Accession: M48144; S53030; S27445
 R:Kitada, K.; Johnson, A.L.; Johnston, L.B.; Saitoh, A.
 Yea. Cell. Biol. 33: 4445-4459, 1993
 A:Title: A multiplicity suppressor gene of the dominant temperature-sensitive G1 cell cycle mutant
 A:Reference number: A48-44; MIM:300647; FID:U45128
 A:Accession: A48-44
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-705 <K1>
 A:Cross-references: EMBL:M48144; FID:U45128; FID:U45128
 R:Devlin, K.; Churcher, C.M.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53028
 A:Accession: S53030
 A:Molecule type: DNA
 A:Residues: 1-705 <DEV>
 A:Cross-references: EMBL:U48144; FID:U45128; FID:U45128
 C:Genetics:
 A:Gene: SGD; PKX2
 A:Cross-references: SGD:SC004603; MIPS:YVR010
 A:Map position: 119
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 C:Keywords: ATP; cell cycle control; phosphotransferase; protein kinase
 F:30-137; Domain: protein kinase homolog <K1>

Query Match 65.5%; Score 38; DB 2; Length 705;
 Best Local Similarity 55.6%; Pred. No. 51;
 Matches 5; Conservative 4; Mismatches 0; Gaps 0;
 CQ 1 MLCGRPPF 9
 DB 274 LLIKKPPF 281
 RESULT 27
 A53530
 protein kinase C (EC 2.7.1.1) epsilon-related - Caenorhabditis elegans
 A:Alternate names: protein kinase C PKC1B; neuronal
 C:Species: Caenorhabditis elegans
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jun-1999
 C:Accession: A53530
 R:Land, M.; Islas-Trejo, A.; Freedman, J.H.; Rubin, C.S.
 J. Biol. Chem. 269: 9234-9244, 1994
 A:Title: Structure and expression of a novel, neuronal protein kinase C (PKC1B) from
 1 signals.
 A:Reference number: A53530; MIM:19417945; PMID:8132661
 A:Accession: A53530
 A:Molecule type: mRNA
 A:Residues: 1-707 <LAN>
 A:Cross-references: GB:U00181; MIM:19417945; FID:U45128; FID:U45128
 C:Genetics:
 A:Gene: kin-13
 A:Map position: V
 A:Note: located near myo-3, col-1, and CPROT/2 genes
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
 A:Note: activity is calcium-independent, phospholipid-dependent, and activated by dia
 C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology;
 C:Keywords: Arp; duplication; phorbol ester binding; phospholipid binding; phosphotri
 F:157-162; Region: pseudophosphorylation motif
 F:171-220; Domain: protein kinase C zinc-binding repeat homology <K21>
 F:249-296; Domain: protein kinase C zinc-binding repeat homology <K22>
 F:376-638; Domain: protein kinase homolog <KIN>
 F:384-392; Region: protein kinase ATP-binding motif
 F:171-221; 204,220; Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:184-197; 209,212; Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:249-279; 282,298; Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:262-265; 287,290; Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:407-426; 502,504; Active site: Lys, Glu, Asp, Lys #status predicted
 Query Match 65.5%; Score 38; DB 1; Length 707;
 Best Local Similarity 66.7%; Pred. No. 51;
 Matches 6; Conservative 2; Mismatches 1; Gaps 0;
 CQ 1 MLCGRPPF 9
 DB 570 MXAGQPPF 576
 RESULT 28
 KIRBCE
 protein kinase C (EC 2.7.1.1) epsilon - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 21-Nov-1997
 C:Accession: A29880
 R:Ohno, S.; Akita, Y.; Konno, Y.; Inajoh, S.; Suzuki, K.
 Cell. 53: 731-741, 1988
 A:Title: A novel phorbol ester receptor/protein kinase, nPKC, distantly related to th
 A:Reference number: A29880; MIM:18223367; PMID:3370672
 A:Accession: A29880
 A:Molecule type: mRNA
 A:Residues: 1-736 <OHN>
 A:Cross-references: GB:M20014
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
 A:Note: activity is calcium-independent, phospholipid-dependent, and activated by dia
 C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology,

C:Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid binding; pseudophosphorylation motif

F:156-161/Region: pseudophosphorylation motif

F:170-225/Domain: protein kinase C zinc-binding repeat homology <K21>

F:243-292/Domain: protein kinase C zinc-binding repeat homology <K22>

F:425-467/Domain: protein kinase homology <KIN>

F:425-467/Domain: protein kinase homology <KIN>

F:413-421/Region: protein kinase ATP-binding motif

F:170-225/Domain: protein kinase C zinc-binding repeat homology <K21>

F:183-186/209,212/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F:243-273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F:256-259,281,284/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F:437-456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted

F:702-710/Binding site: phosphate (Thr) (covalent) by autophosphorylation; #status predicted

Query Match: 65.5% Score 48 DB 1 Length 336

Best Local Similarity: 66.7% Pred No: 54

Matches: 6; Conservative: 2; Mismatches: 1; Indels: 0; Gaps: 0

CY: 1 MLGRPFPE 9

DB: 600 NWASQPFPE 607

RESULT 3:

Protein kinase C (EC 2.7.11.3) epsilon human

C:Species: Homo sapiens (man)

C:Date: 11-Jan-1995 #sequence_revision: 11-Jun-1999

C:Accession: S28942

F:Rasta, P., Strickland, M.B., Holmes, W., Loomis, C.R., Hallas, L.M., Burris, D.J., Biochim. Biophys. Acta 1132, 154-165, 1992

A:Title: Sequence and expression of human protein kinase C epsilon.

A:Reference number: S28942; XJID:9306316; PMID:19460

A:Accession: S28942

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-717 <PAS>

C:Cross references: EMBL:X65293; NID:9206182; PID:9206182

C:Comment: This is a calcium-independent, phospholipid-dependent, serine- and threonine-kinase. This protein is a receptor for tumor-promoting phorbol ester analogs.

C:Keywords: ATP; PKC

A:Access references: GDB:128039; OMIM:104760

A:Map position: 1p11-q11

C:Function:

A:Description: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate. Activity is calcium-independent, phospholipid-dependent, and activated by diacylglycerol and protein kinase C delta. Protein kinase C zinc-binding repeat homology; duplication; phorbol ester binding; pseudophosphorylation motif

F:156-161/Region: pseudophosphorylation motif

F:170-225/Domain: protein kinase C zinc-binding repeat homology <K21>

F:243-292/Domain: protein kinase C zinc-binding repeat homology <K22>

F:425-467/Domain: protein kinase homology <KIN>

F:413-421/Region: protein kinase ATP-binding motif

F:170-225/Domain: protein kinase C zinc-binding repeat homology <K21>

F:183-186,209,212/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F:243-273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F:256-259,281,284/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F:437-456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted

F:702-710/Binding site: phosphate (Thr) (covalent) by autophosphorylation; #status predicted

Query Match: 65.5% Score 48 DB 1 Length 336

Best Local Similarity: 66.7% Pred No: 54

Matches: 6; Conservative: 2; Mismatches: 1; Indels: 0; Gaps: 0

CY: 1 MLGRPFPE 9

DB: 600 NWASQPFPE 608

RESULT 3:

Protein kinase C (EC 2.7.11.3) epsilon human

C:Species: Homo sapiens (man)

C:Date: 11-Jan-1995 #sequence_revision: 11-Jun-1999

C:Accession: S28942

F:Rasta, P., Strickland, M.B., Holmes, W., Loomis, C.R., Hallas, L.M., Burris, D.J., Biochim. Biophys. Acta 1132, 154-165, 1992

A:Title: Sequence and expression of human protein kinase C epsilon.

A:Reference number: S28942; XJID:9306316; PMID:19460

A:Accession: S28942

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-717 <PAS>

C:Cross references: EMBL:X65293; NID:9206182; PID:9206182

C:Comment: This is a calcium-independent, phospholipid-dependent, serine- and threonine-kinase. This protein is a receptor for tumor-promoting phorbol ester analogs.

C:Keywords: ATP; PKC

A:Access references: GDB:128039; OMIM:104760

A:Map position: 1p11-q11

C:Function:

A:Description: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate. Activity is calcium-independent, phospholipid-dependent, and activated by diacylglycerol and protein kinase C delta. Protein kinase C zinc-binding repeat homology; duplication; phorbol ester binding; pseudophosphorylation motif

F:156-161/Region: pseudophosphorylation motif

F:170-225/Domain: protein kinase C zinc-binding repeat homology <K21>

F:243-292/Domain: protein kinase C zinc-binding repeat homology <K22>

F:425-467/Domain: protein kinase homology <KIN>

F:413-421/Region: protein kinase ATP-binding motif

F:170-225/Domain: protein kinase C zinc-binding repeat homology <K21>

F:183-186,209,212/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F:243-273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F:256-259,281,284/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F:437-456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted

F:702-710/Binding site: phosphate (Thr) (covalent) by autophosphorylation; #status predicted

C:Accession: B28163; B26409; S20216

R:Ono, Y., Fujita, T., Ogita, K., Kikkawa, U., Igarashi, K., Nishizuka, Y., J. Biol. Chem. 263, 6921-6932, 1988

A:Title: The structure, expression, and properties of additional members of the protein kinase C family. A2717; MIM:181927; PMID:2834397

A:Reference number: A2717; MIM:181927; PMID:2834397

A:Accession: B28163

A:Molecule type: DNA

A:Residues: 1-737 <OHO>

C:Cross references: GDB:X:833; NID:9206182; PID:9206182

R:Housey, G.M., O'Brian, C.A., Johnson, M.D., Kirschmeier, P., Weinstein, I.B., Proc. Natl. Acad. Sci. U.S.A. 84, 1065-1069, 1987

A:Title: Isolation of cDNA clones encoding protein kinase C: evidence for a protein kinase C family. A2717; MIM:181927; PMID:2834397

A:Reference number: A2717; MIM:181927; PMID:2834397

A:Accession: B26409

A:Molecule type: mRNA

A:Residues: 397-447; GDB:128039; NID:9206182; PID:9206182

C:Cross references: GDB:128039; NID:9206182; PID:9206182

C:Comment: Protein kinase C epsilon and epsilon' appear to be encoded by the same gene.

C:Function:

A:Description: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate. Activity is calcium-independent, phospholipid-dependent, and activated by diacylglycerol and protein kinase C delta. Protein kinase C zinc-binding repeat homology; duplication; phorbol ester binding; pseudophosphorylation motif

F:156-161/Region: pseudophosphorylation motif

F:170-225/Domain: protein kinase C zinc-binding repeat homology <K21>

F:243-292/Domain: protein kinase C zinc-binding repeat homology <K22>

F:406-669/Domain: protein kinase homology <KIN>

F:414-422/Region: protein kinase ATP-binding motif

F:170-225/Domain: protein kinase C zinc-binding repeat homology <K21>

F:183-186,209,212/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F:243-273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F:256-259,281,284/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F:437-456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted

F:703-710/Binding site: phosphate (Thr) (covalent) by autophosphorylation; #status predicted

Query Match: 65.5% Score 38; DB 1; Length 737

Best Local Similarity: 66.7% Pred No: 53

Matches: 6; Conservative: 2; Mismatches: 1; Indels: 0; Gaps: 0

CY: 1 MLGRPFPE 9

DB: 600 NWASQPFPE 608

RESULT 3:

Protein kinase C (EC 2.7.11.3) epsilon mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1992 #sequence_revision: 30-Sep-1992 #text_change: 21-Nov-1997

C:Accession: S22773

R:Schaap, C., Parker, P.J., Bristol, A., Kriz, R., Knopf, J., FEBS Lett. 241, 351-357, 1989

A:Title: Unique substrate specificity and regulatory properties of PKC-epsilon: a rat protein kinase C delta. S22773; XJID:89137541; PMID:2917856

A:Reference number: S22773; XJID:89137541; PMID:2917856

A:Accession: S22773

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-737 <SCH>

C:Function:

A:Description: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate. Activity is calcium-independent, phospholipid-dependent, and activated by diacylglycerol and protein kinase C delta. Protein kinase C zinc-binding repeat homology; duplication; phorbol ester binding; pseudophosphorylation motif

F:156-161/Region: pseudophosphorylation motif

F:170-225/Domain: protein kinase C zinc-binding repeat homology <K21>

F:243-292/Domain: protein kinase C zinc-binding repeat homology <K22>

F:406-669/Domain: protein kinase homology <KIN>

F:414-422/Region: protein kinase ATP-binding motif

F:170-225/Domain: protein kinase C zinc-binding repeat homology <K21>

F:183-186,209,212/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F:243-273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

F:256-259,281,284/Binding site: zinc (His, Cys, Cys, Cys) #status predicted

P:437,456,532,534/Active site: Lys, Glu, Asp, Lys #status: predicted
 F:733,740/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status: predicted

Query Match 65.5%; Score 38; DB 1; Length 737;
 Best Local Similarity 66.7%; Pred. No. 53;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRPPPE 9
 : : : : :
 Db 600 VMAGQPPPE 608

RESULT 32
 S69657
 Hypothetical protein YDR490c - Yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C:Date: 22-Aug-1996 #sequence_revision 0; #text_change 19-Apr-2002
 C:Accession: S69657
 R:Dieterich, F.S.
 Submitted to the EMBL Data Library, August 1995
 A:Description: The sequence of S. cerevisiae cosmid 9410, 8015, 8165, and 9787.
 A:Reference number: S69554
 A:Accession: S69657
 A:Molecule type: DNA
 A:Residues: 1766 <CIE>
 A:Cross-references: EMBL:U33050; NID:Q927726; PDB:1AB64917.1; PDB:Q927745; MIPS:YDR490c
 C:Genetics:
 A:Gene: SGP:PKH;
 A:Cross references: SGP:S0002898
 A:Map position: 4K
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases, protein kinase homolog
 C:Keywords: ATP
 F:123-191/Domain: protein kinase homology <KIN>
 F:123-191/Region: protein kinase ATP-binding motif

Query Match 65.5%; Score 38; DB 2; Length 764;
 Best Local Similarity 54.5%; Pred. No. 56;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLGRPPPE 1
 : : : : :
 Db 330 MLGRPPPEKAA 340

RESULT 33
 S42725
 Nitrate hydratase (EC 4.2.1.84; beta chain - Pseudomonas chlororaphis (strain 923)
 C:Species: Pseudomonas chlororaphis
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 15-Jun-2000
 C:Accession: B42725
 R:Nishiyama, M.; Horinouchi, S.; Kobayashi, M.; Nishimura, T.; Yamada, H.; Heppu, T.
 J. Bacteriol. 173, 2465-2472, 1991
 A:Title: Cloning and characterization of genes responsible for metabolism of nitrate com
 A:Reference number: A42725; MCB:91.91222; PMID:2014569
 A:Accession: B42725
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-220 <NIS>
 A:Cross-references: GB:D90216; NID:Q921650; PDB:5AA-4C46.1; PDB:Q21653
 C:Superfamily: nitrate hydratase beta chain
 C:Keywords: carbon-oxygen lyase; hydrolase

Query Match 63.8%; Score 37; DB 1; Length 220;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LGRPPPE 9
 : : : : :
 Db 118 ITGRPPPE 125

RESULT 34
 JC4665

protein kinase (EC 2.7.1.37) - mouse
 N:Alternate names: serine/threonine protein kinase; STK-1 protein
 C:Species: Mus musculus (house mouse)
 C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 17-Mar-1999
 C:Accession: JC4665
 R:Niwa, H.; Abe, K.; Kunisada, T.; Yamamura, K.
 Gene 169, 197-201, 1996
 A:Title: Cell-cycle-dependent expression of the STK-1 gene encoding a novel murine pu
 A:Reference number: JC4665; MUID:96194801; PMID:8647446
 A:Accession: JC4665
 A:Molecule type: mRNA
 A:Residues: 1-345 <NIK>
 A:Cross-references: CDB:J21099
 A:Experimental source: embryonic stem cell
 A:Note: The authors translated the codon GCT for residue 328 as Thr
 C:Comment: This enzyme regulates a wide array of cellular responses to changing enviro
 C:Genetics:
 A:Gene: stk-1
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphotransferase; protein kinase
 F:80-332/Domain: protein kinase homology <KIN>
 F:88-96/Region: protein kinase ATP-binding motif
 F:111/Binding site: ATP (Lys) #status: predicted
 F:205/Active site: Asp #status: predicted

Query Match 63.8%; Score 37; DB 2; Length 345;
 Best Local Similarity 50.0%; Pred. No. 37;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRPPPE 10
 : : : : :
 Db 271 LMVGNPPPE 280

RESULT 35
 T23688
 Hypothetical protein M03C11.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
 C:Accession: T23688
 R:McMurray, A.
 Submitted to the EMBL Data Library, April 1995
 A:Reference number: Z197A3
 A:Accession: T23688
 A:Status: preliminary; translated from GB/EMBL/DDSU
 A:Molecule type: DNA
 A:Residues: 1-379 <WIL>
 A:Cross-references: EMBL:Z49128; PDB:CAA88953.1; GSPDB:GN0021; CESP:M73C11.1
 A:Experimental source: clone M03C11
 C:Genetics:
 A:Gene: CESP:M03C11.1
 A:Map position: 3
 A:Anticodon: 41/73; 67/3; 96/3; 127/2; 240/3; 298/2; 358/3
 C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 63.8%; Score 37; DB 2; Length 379;
 Best Local Similarity 72.7%; Pred. No. 41;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLGRPPPE 11
 : : : : :
 Db 223 MLGRTPPEFS 233

RESULT 36
 S73964
 pkn5 protein - Myxococcus xanthus
 N:Alternate names: serine protein kinase homolog
 C:Species: Myxococcus xanthus
 C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 08-Oct-1999
 C:Accession: S73964
 R:Zhang, W.; Inouye, M.; Inouye, S.
 Mol. Microbiol. 20, 435-447, 1996

A:Title: Reciprocal regulation of the differentiation of *Myxococcus xanthus* by PKs and
 A:Reference number: S70964; MUID:96310380; PMID:8731241
 A:Accession: S70964
 A:Status: Preliminary; nucleic acid sequence not shown, translation not shown
 A:Molecule type: DNA
 A:Residues: 1380 <ZHA>
 A:Cross references: EMBL:U40656; NID:3111924; PID:AA04049.1; PID:gill1925
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
 C:Genetics:
 A:Gene: pks5

Query Match 63.8%; Score 37; DB 2; Length 672;
 Best Local Similarity 66.7%; Pred. No. 74;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
 |||
 DB 314 MLGRRPPE 322

RESULT 37
 T29223
 Hypothetical protein F55G1.8 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31 Jan-2000
 C:Accession: T29223
 A:Status: Preliminary; translated from CB/EMBL/DBJ
 A:Molecule type: cDNA
 A:Residues: 1-615 <MUR>
 A:Cross references: EMBL:U58750; PID:AA04049.1; QSPIN:R00022; GSP:F55G1.8
 A:Experimental source: strain Bristol N2; clone F56.1
 C:Genetics:
 A:Gene: CESP-F55G1.8
 A:Map position: 4
 A:Intermap: 1037; 2017; 23873; 37271; 4137; 52573
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 63.8%; Score 37; DB 2; Length 672;
 Best Local Similarity 60.0%; Pred. No. 68;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLGRRPPE 10
 |||
 DB 324 MLGRRPPE 234

RESULT 38
 KIMUCA
 Protein Kinase C (EC 2.7.11.-) alpha domain
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11 Jun 1999
 C:Accession: S09496
 R:Finckenziever, G.; Marre, D.; Hug, H
 Nucleic Acids Res. 18, 2183, 1990
 A:Title: Sequence of human protein kinase C alpha
 A:Reference number: S09496; MUID:90245676; PMID:213040
 A:Accession: S09496
 A:Molecule type: mRNA
 A:Residues: 1-672 <FIN>
 A:Cross references: EMBL:X52479; NID:310449; PID:CAAP19.1; PID:g35493
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine- and threonine-sp
 i inositol phospholipids. This protein is a receptor for tumor-promoting phorbol esters,
 C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane may
 C:Comment: The zinc-stabilized regions bind diacylglycerol and phorbol esters.
 C:Genetics:
 A:Gene: PKC- α
 A:Cross references: GDB:126015; OMIM:176460
 A:Map position: 17q22-17q23.2

C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein k
 C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bin
 F:19-29/Region: phospholipid binding #status experimental
 F:22-27/Region: pseudophosphorylation motif
 F:37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:102-151/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:152-264/Domain: protein kinase C C2 region homology <K2>
 F:337-597/Domain: protein kinase homology <K1N>
 F:345-353/Region: protein kinase ATP-binding motif
 F:37-67/70-86/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:50-53/75/78/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:102-132/135/151/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:115/119/140/143/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:368/Active site: Lys #status predicted
 F:631/638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status f

Query Match 63.8%; Score 37; DB 1; Length 672;
 Best Local Similarity 66.7%; Pred. No. 74;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
 |||
 DB 531 MLGRRPPE 539

RESULT 39

KIRTC

Protein Kinase C (EC 2.7.11.-) alpha - rat
 N:Alternate names: protein kinase C type III
 C:Species: *Rattus norvegicus* (Norway rat)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
 C:Accession: S02248; S02620
 R:Kono, Y.; Fujii, T.; Igarashi, K.; Kikkawa, U.; Ogita, K.; Nishizuka, Y.
 Nucleic Acids Res. 16, 5199-5205, 1988
 A:Title: Nucleotide sequences of cDNAs for alpha and gamma subtypes of rat brain pr
 A:Reference number: S02129; MUID:89262515; PMID:3387228
 A:Accession: S02249
 A:Molecule type: mRNA
 A:Residues: 1-672 <ONO>
 A:Cross references: EMBL:X07286; NID:956913; PID:CAA10266.1; PID:956914
 C:Comment: This is a calcium-activated, phospholipid-dependent, serine and threonin
 i inositol phospholipids. This protein is a receptor for tumor-promoting phorbol est
 C:Comment: Binding to acidic phospholipids (phosphatidylserine) in the cell membrane
 C:Superfamily: protein kinase C alpha; protein kinase C C2 region homology; protein
 C:Keywords: ATP; autophosphorylation; calcium binding; duplication; phorbol ester bin
 F:19-29/Region: phospholipid binding #status experimental
 F:22-27/Region: pseudophosphorylation motif
 F:37-86/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:102-151/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:152-264/Domain: protein kinase C C2 region homology <K2>
 F:337-597/Domain: protein kinase homology <K1N>
 F:345-353/Region: protein kinase ATP-binding motif
 F:368/Active site: Lys #status predicted
 F:631/638/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status

Query Match 63.8%; Score 37; DB 1; Length 672;
 Best Local Similarity 66.7%; Pred. No. 74;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGRRPPE 9
 |||
 DB 531 MLGRRPPE 539

RESULT 40

KIMSCA

Protein Kinase C (EC 2.7.11.-) alpha - mouse
 C:Species: *Mus musculus* (house mouse)
 C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun 1999
 C:Accession: S07104; J00078
 R:Wegidish, T.; Mazurek, N.
 Nature 342, 807-811, 1989

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OM protein - protein search, using sw model

Run On: November 14, 2003, 14:34:37 : Search time 11 seconds
(without alignments)
47 027 Million coll updates/sec

Title: US-09-736-076-19
Project name: 52
Sequence: 1 XLOGAPPETS.1

Scoring table: BLOSUM62
Gap: 10.0, Gapext 0.5

Sequences: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41*

Note: K₀ is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	40	94.4	682	1	SNK_MOUSE
2	40	94.4	682	1	SNK_RAT
3	40	94.4	685	1	SNK_HUMAN
4	40	94.5	601	1	FLK1_HUMAN
5	40	94.5	601	1	FLK1_MOUSE
6	40	94.5	601	1	FLK1_RAT
7	40	94.5	601	1	FLK1_BOVINE
8	40	94.5	601	1	FLK1_PIG
9	40	94.5	601	1	FLK1_CHICK
10	40	94.5	601	1	FLK1_DUCK
11	40	94.5	601	1	FLK1_GALLUS
12	40	94.5	601	1	FLK1_CAELESTIS
13	40	94.5	601	1	FLK1_XENOPUS
14	40	94.5	601	1	FLK1_DROSOPHILA
15	40	94.5	601	1	FLK1_MUSCULUS
16	40	94.5	601	1	FLK1_RATTUS
17	40	94.5	601	1	FLK1_HOMO
18	40	94.5	601	1	FLK1_PAN
19	40	94.5	601	1	FLK1_PITHEC
20	40	94.5	601	1	FLK1_HOMO
21	40	94.5	601	1	FLK1_PAN
22	40	94.5	601	1	FLK1_PITHEC
23	40	94.5	601	1	FLK1_HOMO
24	40	94.5	601	1	FLK1_PAN
25	40	94.5	601	1	FLK1_PITHEC
26	40	94.5	601	1	FLK1_HOMO
27	40	94.5	601	1	FLK1_PAN
28	40	94.5	601	1	FLK1_PITHEC
29	40	94.5	601	1	FLK1_HOMO
30	40	94.5	601	1	FLK1_PAN
31	40	94.5	601	1	FLK1_PITHEC
32	40	94.5	601	1	FLK1_HOMO
33	40	94.5	601	1	FLK1_PAN
34	40	94.5	601	1	FLK1_PITHEC
35	40	94.5	601	1	FLK1_HOMO

34	37	63.8	220	1	NHAB_PSECL
35	37	63.8	343	1	STKC_MOUSE
36	37	63.8	343	1	STKC_MOUSE
37	37	63.8	380	1	PKNS_MYXA
38	37	63.8	615	1	PLK3_CAELE
39	37	63.8	649	1	KPC1_AP-CA
40	37	63.8	659	1	KPC1_LVTP
41	37	63.8	672	1	KPCA_BOVIN
42	37	63.8	672	1	KPCA_HUMAN
43	37	63.8	672	1	KPCA_MOUSE
44	37	63.8	672	1	KPCA_RABIT
45	37	63.8	672	1	KPCA_RAT

ALIGNMENTS

RESULT 1	SNK_MOUSE	STANDARD;	PRT;	682 AA.
AC	PS3351;			
DT	01-OCT-1996 (Ref. 34, Created)			
DT	01-OCT-1996 (Ref. 34, Last sequence update)			
DT	16-OCT-2001 (Ref. 40, Last annotation update)			
DE	Serine/threonine-protein kinase SNK (EC 2.7.1.1) (Serum inducible kinase).			
DE	kinase).			
GN	SNK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCB:TaxID=10090;			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=2375085; Pubmed=1508211;			
RT	Simmons D.L., Neel B.G., Stevens R., Evelt G., Erikson R.L.,			
RT	"Identification of an early-growth response gene encoding a novel			
RT	putative protein kinase."			
RL	Mol. Cell. Biol. 12:4164-4169 (1992).			
CC	FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL			
CC	TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS,			
CC	WOUND HEALING OR NEOPLASIA.			
CC	TISSUE SPECIFICITY: BRAIN, LUNG AND HEART.			
CC	INDUCTION: BY SERUM AND PHORBOL ESTER.			
CC	SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	CDC5/PCLO SUBFAMILY.			
CC	SIMILARITY: Contains 2 PCLO box domains.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
EMBL	M61613; NOT ANNOTATED_CDS.			
PIR	A44493; A44493; Snk			
MGD	XGI:1099790; Snk			
InterPro	IPR000599; PCLO box.			
InterPro	IPR000719; Prot_kinase.			
InterPro	IPR002292; Ser_thr_kinase.			
PIfam	PF00069; pkinase; 1			
PIfam	PF00659; PCLO box; 2			
ProDom	PD002001; Prot_kinase; 1			
SMART	SM02226; S_TKc; 1			
PROSITE	PS00378; PCLO BOX; 2			
PROSITE	PS00107; PROTEIN KINASE ATP; 1			
PROSITE	PS00011; PROTEIN KINASE DOM; 1			
PROSITE	PS00108; PROTEIN KINASE ST; 1			
Transferase	Serine/threonine-protein kinase; ATP-binding; Repeat			
DOMAIN	54 59			
DOMAIN	79 93			
NP_6120	95 93			

FT BINDING 108 108 ATP (BY SIMILARITY)
 FT AC SITE 202 202 BY SIMILARITY
 FT DOMAIN 507 570 PCLO BOX 1
 FT DOMAIN 603 674 PCLO BOX 2
 SQ SEQUENCE 682 AA; 77811 MW; 5860505BDE83D5F3 CRC64;
 Query Match 94.8%; Score 55; DB 1; Length 682;
 Best Local Similarity 90.9%; Pred. No. 0.011;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPFFETS 11
 DB 270 MLGRRPFFET 280

RESULT 3
 SNK_HUMAN STANDARD; PRT; 685 AA.
 ID SNK_HUMAN STANDARD; PRT; 685 AA.
 AC Q9NY33; C63679; Q96V77; Q9LE61;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Serine/threonine-protein kinase SNK (EC 2.7.1.1) (Serum inducible kinase).
 GN SNK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Guyang B., Dai W.,
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Anderson K.M., Nerurkar S.S., Hansbury M.J., Fornwald J., Scott G.,
 RA Bouayk M., Mui P., Imbruglia C.S., Carlson K., Marshall L.A.,
 RA Roshak A.K.;
 RT "Identification and characterization of human serum-inducible kinase (SNK), a novel member of the polo-kinase family of cell cycle regulators: potential implication for regulation of vascular smooth muscle proliferation."
 RT Submitted (CAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Krausberg R., Ringold S.A., Strouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan M., Moore T., Max S.I., Wang C., Hsieh F.,
 RA Diachenko L., Vatsisana K., Farer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares V.B., Rosaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein Y., Rubin T.S., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wexley K.C., Hale S., Garcia A.M., Gay L.C., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman A., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchran J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz C., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M., Skalska U., Smalley D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP SEQUENCE OF 110-408 FROM N.A.
 RA Fidler C., Boulton J., Wang Jabs E., Wainscoat J.S.;
 RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS, WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
 CC -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CC05/PCLO SUBFAMILY.

FT BINDING 108 108 ATP (BY SIMILARITY)
 FT AC SITE 202 202 BY SIMILARITY
 FT DOMAIN 507 570 PCLO BOX 1
 FT DOMAIN 603 674 PCLO BOX 2
 SQ SEQUENCE 682 AA; 77811 MW; 5860505BDE83D5F3 CRC64;
 Query Match 94.8%; Score 55; DB 1; Length 682;
 Best Local Similarity 90.9%; Pred. No. 0.011;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGRRPFFETS 11
 DB 270 MLGRRPFFET 280

RESULT 2
 SNK_RAT STANDARD; PRT; 682 AA.
 ID SNK_RAT STANDARD; PRT; 682 AA.
 AC Q90121;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine/threonine-protein kinase SNK (EC 2.7.1.1) (Serum inducible kinase).
 GN SNK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99452460; PubMed=12522972;
 RA Kaufmann G., Weller M., Wulff P., Jessberger S., Kortebein U.,
 RA Seifried G., Straub U., Reiterer Hahn J., Strothmann K., Kubi D.;
 RT "The polo-like protein kinases Fsk and Snk associate with a Galpha12 and regulate binding protein and are regulated dynamically with synaptic plasticity."
 RT EMBO J. 19:5528-5539 (1999).
 CC -- FUNCTION: MAY PLAY A ROLE IN THE DIVISION OF AT LEAST SOME CELL TYPES, SUCH AS FIBROBLASTS, AND COULD FUNCTION IN EMBRYOGENESIS, WOUND HEALING OR NEOPLASIA (BY SIMILARITY).
 CC -- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CC05/PCLO SUBFAMILY.
 CC -- SIMILARITY: CONTAINS 2 PCLO BOX 1/2.

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EMBL: AF136581; AACF0366.1;
 IP: WIPR0; IPRC03959; PCLO BOX 1;
 IP: WIPR0; IPRC03959; PCLO BOX 2;
 IP: WIPR0; IPRC03959; PCLO BOX 3;
 IP: WIPR0; IPRC03959; PCLO BOX 4;
 IP: WIPR0; IPRC03959; PCLO BOX 5;
 IP: WIPR0; IPRC03959; PCLO BOX 6;
 IP: WIPR0; IPRC03959; PCLO BOX 7;
 IP: WIPR0; IPRC03959; PCLO BOX 8;
 IP: WIPR0; IPRC03959; PCLO BOX 9;
 IP: WIPR0; IPRC03959; PCLO BOX 10;
 IP: WIPR0; IPRC03959; PCLO BOX 11;
 IP: WIPR0; IPRC03959; PCLO BOX 12;
 IP: WIPR0; IPRC03959; PCLO BOX 13;
 IP: WIPR0; IPRC03959; PCLO BOX 14;
 IP: WIPR0; IPRC03959; PCLO BOX 15;
 IP: WIPR0; IPRC03959; PCLO BOX 16;
 IP: WIPR0; IPRC03959; PCLO BOX 17;
 IP: WIPR0; IPRC03959; PCLO BOX 18;
 IP: WIPR0; IPRC03959; PCLO BOX 19;
 IP: WIPR0; IPRC03959; PCLO BOX 20;
 IP: WIPR0; IPRC03959; PCLO BOX 21;
 IP: WIPR0; IPRC03959; PCLO BOX 22;
 IP: WIPR0; IPRC03959; PCLO BOX 23;
 IP: WIPR0; IPRC03959; PCLO BOX 24;
 IP: WIPR0; IPRC03959; PCLO BOX 25;
 IP: WIPR0; IPRC03959; PCLO BOX 26;
 IP: WIPR0; IPRC03959; PCLO BOX 27;
 IP: WIPR0; IPRC03959; PCLO BOX 28;
 IP: WIPR0; IPRC03959; PCLO BOX 29;
 IP: WIPR0; IPRC03959; PCLO BOX 30;
 IP: WIPR0; IPRC03959; PCLO BOX 31;
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 IP: WIPR0; IPRC03959; PCLO BOX 36;
 IP: WIPR0; IPRC03959; PCLO BOX 37;
 IP: WIPR0; IPRC03959; PCLO BOX 38;
 IP: WIPR0; IPRC03959; PCLO BOX 39;
 IP: WIPR0; IPRC03959; PCLO BOX 40;
 IP: WIPR0; IPRC03959; PCLO BOX 41;
 IP: WIPR0; IPRC03959; PCLO BOX 42;
 IP: WIPR0; IPRC03959; PCLO BOX 43;
 IP: WIPR0; IPRC03959; PCLO BOX 44;
 IP: WIPR0; IPRC03959; PCLO BOX 45;
 IP: WIPR0; IPRC03959; PCLO BOX 46;
 IP: WIPR0; IPRC03959; PCLO BOX 47;
 IP: WIPR0; IPRC03959; PCLO BOX 48;
 IP: WIPR0; IPRC03959; PCLO BOX 49;
 IP: WIPR0; IPRC03959; PCLO BOX 50;
 IP: WIPR0; IPRC03959; PCLO BOX 51;
 IP: WIPR0; IPRC03959; PCLO BOX 52;
 IP: WIPR0; IPRC03959; PCLO BOX 53;
 IP: WIPR0; IPRC03959; PCLO BOX 54;
 IP: WIPR0; IPRC03959; PCLO BOX 55;
 IP: WIPR0; IPRC03959; PCLO BOX 56;
 IP: WIPR0; IPRC03959; PCLO BOX 57;
 IP: WIPR0; IPRC03959; PCLO BOX 58;
 IP: WIPR0; IPRC03959; PCLO BOX 59;
 IP: WIPR0; IPRC03959; PCLO BOX 60;
 IP: WIPR0; IPRC03959; PCLO BOX 61;
 IP: WIPR0; IPRC03959; PCLO BOX 62;
 IP: WIPR0; IPRC03959; PCLO BOX 63;
 IP: WIPR0; IPRC03959; PCLO BOX 64;
 IP: WIPR0; IPRC03959; PCLO BOX 65;
 IP: WIPR0; IPRC03959; PCLO BOX 66;
 IP: WIPR0; IPRC03959; PCLO BOX 67;
 IP: WIPR0; IPRC03959; PCLO BOX 68;
 IP: WIPR0; IPRC03959; PCLO BOX 69;
 IP: WIPR0; IPRC03959; PCLO BOX 70;
 IP: WIPR0; IPRC03959; PCLO BOX 71;
 IP: WIPR0; IPRC03959; PCLO BOX 72;
 IP: WIPR0; IPRC03959; PCLO BOX 73;
 IP: WIPR0; IPRC03959; PCLO BOX 74;
 IP: WIPR0; IPRC03959; PCLO BOX 75;
 IP: WIPR0; IPRC03959; PCLO BOX 76;
 IP: WIPR0; IPRC03959; PCLO BOX 77;
 IP: WIPR0; IPRC03959; PCLO BOX 78;
 IP: WIPR0; IPRC03959; PCLO BOX 79;
 IP: WIPR0; IPRC03959; PCLO BOX 80;
 IP: WIPR0; IPRC03959; PCLO BOX 81;
 IP: WIPR0; IPRC03959; PCLO BOX 82;
 IP: WIPR0; IPRC03959; PCLO BOX 83;
 IP: WIPR0; IPRC03959; PCLO BOX 84;
 IP: WIPR0; IPRC03959; PCLO BOX 85;
 IP: WIPR0; IPRC03959; PCLO BOX 86;
 IP: WIPR0; IPRC03959; PCLO BOX 87;
 IP: WIPR0; IPRC03959; PCLO BOX 88;
 IP: WIPR0; IPRC03959; PCLO BOX 89;
 IP: WIPR0; IPRC03959; PCLO BOX 90;
 IP: WIPR0; IPRC03959; PCLO BOX 91;
 IP: WIPR0; IPRC03959; PCLO BOX 92;
 IP: WIPR0; IPRC03959; PCLO BOX 93;
 IP: WIPR0; IPRC03959; PCLO BOX 94;
 IP: WIPR0; IPRC03959; PCLO BOX 95;
 IP: WIPR0; IPRC03959; PCLO BOX 96;
 IP: WIPR0; IPRC03959; PCLO BOX 97;
 IP: WIPR0; IPRC03959; PCLO BOX 98;
 IP: WIPR0; IPRC03959; PCLO BOX 99;
 IP: WIPR0; IPRC03959; PCLO BOX 100;

1 SIMILARITY: Contains 2 POLO box domains.

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EMBL: AF596177; AAC14573.1; ...
 EMBL: AF23574; AA962897.1; ...
 EMBL: U85755; AAC20575.1; ...
 EMBL: BC013849; AAH13873.1; ...
 XING: 607023; ...
 InterPro: IPR000959; POLO box.
 InterPro: IPR000719; Prot. kinase.
 InterPro: IPR02290; Ser. Thr. kinase.
 Pfam: PF00069; Kinase. 1
 Pfam: PF00653; POLO box; 2.
 Pfam: PF00653; POLO box; 1.
 PROSITE: PS00000; Prot. kinase; 1.
 SMART: SM00220; S_TKC; 1.
 PROSITE: PS00378; POLO BOX; 2.
 PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 PROSITE: PS00111; PROTEIN KINASE DOV; 1.
 PROSITE: PS00103; PROTEIN KINASE ST; 1.
 Transferrase: Serine/threonine-protein kinase: ATP binding: Repeat.
 FT DOMAIN 57 64 POLY-HIS.
 FT DOMAIN 82 334 PROTEIN KINASE.
 FT RE BIND 88 96 ATP (BY SIMILARITY).
 FT BINDING 111 111 ATP (BY SIMILARITY).
 FT ACT SITE 205 205 BY SIMILARITY.
 FT DOMAIN 510 573 POLO BOX 1.
 FT DOMAIN 666 677 POLO BOX 2.
 FT CONFLICT 28 28 A -> G (IN REF. 11).
 SQ SEQUENCE 455 AA; 78232 MW; 64295656FD8103433 CF 647

Query: VARCH 94.88; Score 55; DB 1; Length 645;
 Best Local Similarity 93.99; Pred. NC 0.811; Gaps 0;
 Matches 10; Conservative 1; Mismatches 0; Indels 0;

Cy J MLAGRPFFETS 11
 D 274 MLAGRPFFET 293

RESULT 4

EMBL: HUMAN STANDARD; PROT. NO. RA.
 AC P53360;
 DT 21-OCT-1996 (rel. 34, Created);
 DT 21-OCT-1996 (rel. 34, Last sequence update);
 DT 18-SEP-2003 (rel. 42, Last annotation update);
 DE Serine/threonine protein kinase PKA (p34) (catalytic) (Serine-
 DE threonine protein kinase 13) (SrpK1).
 GN PKA OR P.K1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eumammalia;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo;
 CX NCBI: TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 AC Tissue=Placenta;
 XC MEDLINE=94289293; PubMed=9018557;
 RA Hamada R., Maoid S., Smith M.A., O'Brien C.O., Longo D.L.,
 RA Ferris D.K.;
 RA "Cloning and characterization of human and murine homologues of the
 RA Drosophila polo serine-threonine kinase";
 RL Cell. Growth Differ. 5:249-257(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94067140; PubMed=7902533;
 RA Lake R.A., Jellinek W.R.;

RT "Cell cycle- and terminal differentiation-associated regulation of
 RL the mouse mRNA encoding a conserved mitotic protein kinase";
 RN Mol. Cell. Biol. 13:7793-7801(1993).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95051103; PubMed=7962193;
 RA Golsteyn R.M., Schultz S., Bartek J., Ziemiecki A., Ried T.,
 RA Nigg E.A.;
 RT "Cell cycle analysis and chromosomal localization of human p11, a
 RT putative homologue of the mitotic kinases Drosophila polo and
 RT Saccharomyces cerevisiae Cdc5";
 RL Cell Sci. 107:1509-1517(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC Tissue=Lung;
 RX MEDLINE=94173904; PubMed=127874;
 RA Holtrich U., Wolf G., Braeuninger A., Karn T., Boehme B.,
 RA Ruebsaenen-Waigmann H., Streibhardt K.;
 RT "Induction and down-regulation of PLK, a human serine/threonine
 RT kinase expressed in proliferating cells and tumors";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:1736-1740(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC Tissue=Colon, and Lung;
 RX MEDLINE=22398257; PubMed=12477932;
 RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Shtreitz T.H.,
 RA Raha S.S., Quellano N.A., Peters G.C., Abramson R.D., Mullaly S.J.,
 RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.X., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketteran V., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R., Madan A., Young A.C., Shevchenko Y., Bouffard G.S.,
 RA Blakesley R., Touchan J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RC [1] FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
 CC DURING G1 OR S PHASE.
 CC [2] SUBCELLULAR LOCATION: Nuclear.
 CC [3] TISSUE SPECIFICITY: PLACENTA AND COLON.
 CC [4] DEVELOPMENTAL STAGE: ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
 CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
 CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
 CC DURING S PHASE.
 CC [5] INDUCTION: BY GROWTH-STIMULATING AGENTS.
 CC [6] SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC COC5/POLO SUBFAMILY.
 CC [7] SIMILARITY: Contains 2 POLO box domains.
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EMBL: U01038; AAA56634.1; ...
 EMBL: L19559; AAA36659.1; ...
 EMBL: X73458; CAA51837.1; ...
 EMBL: X75932; CAA53536.1; ...
 EMBL: BC002369; AAH02469.1; ...
 EMBL: BC003002; AAH03002.1; ...
 EMBL: BC014946; AAH14946.1; ...

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DR PIR: S34130; S34130.
DR Genew: HGNC:9077; PLK.
DR GX: F53950.
DR MIM: 603232.
DR GC: G000004674; Eiprotein serine/threonine kinase activity; TAS.
DR GC: G000000067; Pinitosis; TAS.
DR GC: G000000048; P Oncogenesis; TAS.
DR GC: G000000074; P regulation of cell cycle; TAS.
DR InterPro: IPR000959; Polo box.
DR InterPro: IPR020719; Prot_kinase.
DR InterPro: IPR02290; Ser_thr_kinase.
DR Pfam: PF00469; Pkinase; 1.
DR Pfam: PF00459; Polo_box; 2.
DR Pfam: PF00000; Prot_kinase; 1.
DR SMART: SMC0220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00117; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00119; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00129; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP binding; Repeat;
Nucleotid protein.
FT DOMAIN 53 305 PROTEIN KINASE.
FT NP_BING 59 67 ATP (BY SIMILARITY).
FT BINDING 82 92 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 419 463 POLO BOX 1.
FT DOMAIN 515 584 POLO BOX 2.
FT CONFLICT 2 2 S -> T (IN REF. 1).
FT CONFLICT 11 11 A -> F (IN REF. 1).
FT CONFLICT 58 58 F -> L (IN REF. 1).
FT CONFLICT 60 60 F -> S (IN REF. 1).
FT CONFLICT 73 73 A -> V (IN REF. 2).
FT CONFLICT 141 141 C -> P (IN REF. 4).
FT CONFLICT 227 227 G -> E (IN REF. 4).
FT CONFLICT 301 301 N -> G (IN REF. 2).
FT CONFLICT 495 495 A -> G (IN REF. 2).
FT CONFLICT 501 501 E -> G (IN REF. 4).
DR SEQUENCE 601 AA: 68254 MW: 138013.02 Da (P34130)
Query Match 84.5% Score 49.0 E 1.0e-100
Pos: Local Similarity 72.7% Pred. No. 0.0
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
GV : M:DRPFPEETS 11
DV : 24; L:WGRPFPEETS 254
RESULT 1
PLOT Y-AXIS STANDARD.
ID PLOT Y-AXIS STANDARD.
AC Q78121.
DC 01 FEB 1994 (Ref. 31, Created)
DT 01 DEC 1999 (Ref. 34, Last sequence update)
DT 14 OCT 2001 (Ref. 40, Last annotation update)
DE Serine/threonine-protein kinase PLK (P34130) (Serine-
threonine protein kinase 13) (STPK13).
ON PLK.
CC Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CC NBI:Taxid:10090.
RN 1.
RP SOURCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Bone marrow.
RX MEDLINE=9321660; Pubmed=8099445.
RA Clay F.J., McEwen S.J., Bertonecchio L., Wilks A.F., Dunn A.R.
RT Identification and cloning of a protein kinase encoding mouse gene,
PT Plk, related to the polo gene of Drosophila.
RI Proc. Natl. Acad. Sci. U.S.A. 90:4482-4486(1993).
RN 1.
RP SOURCE FROM N.A.
RX SEQUENCE FROM N.A.
RP STRAIN=C57BL/6 X CBA; TISSUE=Try-ur.
RX MEDLINE=94289293; Pubmed=8018557.
RA Hamanaka R., Malooid S., Smith M.R., O'Connell C.D., Longo D.L.,
RA Ferris D.K.
RT Cloning and characterization of human and murine homologues of the
RL Drosophila polo serine-threonine kinase.
RN Cell Growth Differ. 5:249-257(1994).
RP SEQUENCE FROM N.A.
RC TISSUE=Testis.
RX MEDLINE=94067140; Pubmed=7902533.
RA Lake R.J., Celisnek W.R.
RT "Cell cycle- and terminal differentiation-associated regulation of
RL the mouse mENA encoding a conserved mitotic protein kinase."
RN Mol. Cell. Biol. 13:7793-7801(1993).
CC FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE
CC DURING G1 OR S PHASE.
CC SUBCELLULAR LOCATION: Nuclear.
CC TISSUE SPECIFICITY: NEWBORN AND ADULT SPLEEN, FETAL AND NEWBORN
CC KIDNEY, LIVER, BRAIN, THYMUS AND ADULT BONE MARROW, THYMUS,
CC OVARY AND TESTES.
CC DEVELOPMENTAL STAGE: IN THE THYMUS, LEVELS INCREASED DURING FETAL
CC DEVELOPMENT, WERE HIGHEST IN NEWBORN ANIMALS AND DECREASED IN THE
CC ADULT. IN THE TESTES, THE PLK LEVELS WERE HIGHER IN THE ADULT THAN
CC IN PREPUBESCENT MICE WHILE IN THE OVARY, THE LEVELS WERE HIGHER IN
CC THE PREPUBESCENT MICE. ACCUMULATES TO A MAXIMUM DURING THE G2 AND M
CC PHASES, DECLINES TO A NEARLY UNDETECTABLE LEVEL FOLLOWING MITOSIS
CC AND THROUGHOUT G1 PHASE, AND THEN BEGINS TO ACCUMULATE AGAIN
CC DURING S PHASE.
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDC5/POLO SUBFAMILY.
CC SIMILARITY: Contains 2 POLO box domains.
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CC or send an email to license@isb-sib.ch).
CC EMBL: L06144; AAA39949.1.
CC EMBL: J01063; AAA56635.1.
CC EMBL: L19558; AAA16071.1.
CC F02; A47545; A47545.
CC F02; A45936; A45936.
CC MGI:97621; Pk.
DR InterPro: IPR000959; POLO_box.
DR InterPro: IPR000719; Prot_kinase.
DR Pfam: PF00469; Pkinase; 1.
DR Pfam: PF00459; Polo_box; 2.
DR SMART: SMC0220; S_TKC; 1.
DR PROSITE: PS00078; POLO_BOX; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00117; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00119; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
Nuclear protein.
FT DOMAIN 53 305 PROTEIN KINASE.
FT NP_BING 59 67 ATP (BY SIMILARITY).
FT BINDING 82 92 ATP (BY SIMILARITY).
FT ACT_SITE 176 176 BY SIMILARITY.
FT DOMAIN 417 480 POLO BOX 1.
FT DOMAIN 515 584 POLO BOX 2.
FT CONFLICT 4 4 A -> V (IN REF. 1).
FT CONFLICT 15 15 A -> T (IN REF. 1).
FT CONFLICT 23 23 P -> L (IN REF. 1).
FT CONFLICT 27 27 V -> A (IN REF. 1).
FT CONFLICT 29 29 G -> S (IN REF. 1).
FT CONFLICT 41 41 P -> L (IN REF. 1).
FT CONFLICT 54 54 V -> L (IN REF. 1).
FT CONFLICT 495 495 A -> R (IN REF. 1).

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SQL SEQUENCE 603 AA; 68300 MW; 1B980646166EFA1C CR64;

Query March 84.5% Score 49; DB 1; Length 603;
Best Local Similarity 72.7%; Pred. No. 0.13;
Marches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLCGRPFETS 11

EE : 144 MLCGRPFETS 254

RESULT A

PK: RAC ID: PK: RAC STANDARD; PRT: 603 AA;
AC Q6243; DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase PKA (EC 2.7.1.1) (MCK-1)
ON FLK;
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
OX NCBI_TaxID=10116;
XP 1; RN 1; RP SEQUENCE FROM N.A.
RX MEDLINE=90025616; PubMed=9809744;
RA Tseng T.C., Chen S.H., Hsu Y.P., Tang T.K.;
RT "Protein Kinase profile of sperm and eggs: cloning and
RT characterization of two novel testis-specific protein kinases (AIE1,
RT AIE2) related to yeast and fly chromosome segregation regulators";
RL DNA Cell Biol. 19:679-688(2000);
CC -!- FUNCTION: May play a part in organizing microtubules in relation
CC to the function of the centrosome/spindle pole during mitosis.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to spindle pole from anaphase to
CC cytokinesis (BY similarity).
CC -!- TISSUE SPECIFICITY: Expressed only in testis.
CC -!- DEVELOPMENTAL STAGE: Expressed on day 14 dpc in prepubertal
CC testis, expression reached its plateau on day 21 dpc and remained
CC at a high level in adult.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL: AF054620; AAC25954.1;
CC EMBL: AF195272; AAF25638.1;
CC HSP: O63450; IAC6.
CC MGD: MGI:132119; Stk13.
CC InterPro: IPR000119; Prot_kinase.
CC InterPro: IPR002230; Ser_thr_kinase.
CC InterPro: IPR001245; Tyr_kinase.
CC Pfam: PF00069; Kinase; 1.
CC PRINTS: PR00139; TYRKINASE.
CC ProDom: PD000201; Prot_kinase; 1.
CC SMART: SM00229; S_TKc_1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
CC Cell cycle, transferase, Serine/threonine-protein kinase, ATP-binding.
KW DOMAIN 16 266 PROTEIN_KINASE
FT NP_BIND 22 30 ATP (BY SIMILARITY)
FT BINDING 45 45 ATP (BY SIMILARITY)
FT ACT_SITE 139 139 BY SIMILARITY
FT CONFLICT 74 74 P 10 P (IN REF. 21)

Query March 84.5% Score 49; DB 1; Length 603;
Best Local Similarity 72.7%; Pred. No. 0.13;
Marches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLCGRPFETS 11

EE : 144 MLCGRPFETS 254

RESULT 7
STKO_MOUSE ID: STKO_MOUSE STANDARD; PRT: 282 AA;
AC O88445; O9JLC2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Serine/threonine protein kinase 13 (EC 2.7.1.37) (Aurora/Ip11/Eg2
DE protein 1) (Aurora C)
GN STK13 OR AIE1;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OX NCBI_TaxID=10090;
RN 1; RP SEQUENCE FROM N.A.
RX MEDLINE=90025616; PubMed=9809744;
RA Tseng T.C., Chen S.H., Hsu Y.P., Tang T.K.;
RT "Protein Kinase profile of sperm and eggs: cloning and
RT characterization of two novel testis-specific protein kinases (AIE1,
RT AIE2) related to yeast and fly chromosome segregation regulators";
RL DNA Cell Biol. 19:679-688(2000);
CC -!- FUNCTION: May play a part in organizing microtubules in relation
CC to the function of the centrosome/spindle pole during mitosis.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to spindle pole from anaphase to
CC cytokinesis (BY similarity).
CC -!- TISSUE SPECIFICITY: Expressed only in testis.
CC -!- DEVELOPMENTAL STAGE: Expressed on day 14 dpc in prepubertal
CC testis, expression reached its plateau on day 21 dpc and remained
CC at a high level in adult.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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CC
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CC EMBL: AF195272; AAF25638.1;
CC HSP: O63450; IAC6.
CC MGD: MGI:132119; Stk13.
CC InterPro: IPR000119; Prot_kinase.
CC InterPro: IPR002230; Ser_thr_kinase.
CC InterPro: IPR001245; Tyr_kinase.
CC Pfam: PF00069; Kinase; 1.
CC PRINTS: PR00139; TYRKINASE.
CC ProDom: PD000201; Prot_kinase; 1.
CC SMART: SM00229; S_TKc_1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
CC Cell cycle, transferase, Serine/threonine-protein kinase, ATP-binding.
KW DOMAIN 16 266 PROTEIN_KINASE
FT NP_BIND 22 30 ATP (BY SIMILARITY)
FT BINDING 45 45 ATP (BY SIMILARITY)
FT ACT_SITE 139 139 BY SIMILARITY
FT CONFLICT 74 74 P 10 P (IN REF. 21)

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SQ SEQUENCE 282 AA: 32907 MW: 7038AEC9494B7881 CR:264;
Query Match: 77.6%; Score 45, DP 1; Length 282;
Best local similarity: 53.6%; Pred No. 334;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGRRPPT 10
DB 206 LLVGQPPPT 225

RESULT 9
STK6_XENLA STANDARD; PRT: 407 AA;
AC Q3282C;
DT 28-FEB-2003 (Rel. 41, Created);
DI 28-FEB-2003 (Rel. 41, Last sequence update);
DE 28-FEB-2003 (Rel. 41, Last annotation update);
DE Serine/threonine protein kinase P92 (EC 2.7.1.37) (p92) (p46B265);
GN B2;
OS Xenopus laevis (African clawed frog);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus;
CX NCBI_TaxID 9355;

RA Gibb R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster.";
CC Science 287:2185-2195(2000);
CC -!- FUNCTION: MAY PLAY A ROLE IN REGULATING BOTH NUCLEAR AND
CC CYTOPLASMIC ASPECTS OF THE MITOTIC CYCLE.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: LARVAL DISCS, BRAIN AND TESTIS.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: Contains 2 POLO box domains.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb.sib.ch).
CC
CC EMBL: X63361; CAA44963.1;
CC EMBL: AE003514; AAF42036.1;
CC PIR: S22127; S22127.
CC HSP: O61453; LA06.
CC FLYBase: FBem0003124; polo.
CC CG: CG0005813; Centrosome; IDA.
CC CG: CG0005819; Cspindie; IDA.
CC CG: CG0004674; F-protein; serine/threonine kinase activity; IDA.
CC CG: CG0007143; Pimale meiosis; IMP.
CC CG: CG0007067; Pimale meiosis; IMP.
CC CG: CG0000959; POLO box.
CC InterPro: IPR000019; Prot_Kinase.
CC InterPro: IPR002290; Ser_Thr_Kinase.
CC Pfam: PF00659; Pkinase; 1.
CC Pfam: PF00659; POLO box; 2.
CC ProDom: PD000033; Prot_Kinase; 1.
CC SMART: SMG0220; S_TK; 1.
CC
CC PROSITE: PS50078; POLO BOX; 2.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC TRANSferase; Serine/threonine-protein kinase; ATP-binding; Repeat.
CC DOMAIN 25 277 PROTEIN_KINASE.
CC NP_BIND 31 39 ATP (BY SIMILARITY).
CC BINDING 148 148 ATP (BY SIMILARITY).
CC ACT_SITE 398 461 POLO BOX 1.
CC DOMAIN 496 554 POLO BOX 2.
CC CONFLICT 187 187 P -> A (in Ref. 1).
CC
CC Query Match: 75.9%; Score 44; DP 1; Length 576;
CC Best local similarity: 70.0%; Pred No. 111;
CC Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 1 MLGRRPPT 10
DB 216 LLVGQPPPT 225

RESULT 9
STK6_XENLA STANDARD; PRT: 407 AA;
AC Q3282C;
DT 28-FEB-2003 (Rel. 41, Created);
DI 28-FEB-2003 (Rel. 41, Last sequence update);
DE 28-FEB-2003 (Rel. 41, Last annotation update);
DE Serine/threonine protein kinase P92 (EC 2.7.1.37) (p92) (p46B265);
GN B2;
OS Xenopus laevis (African clawed frog);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus;
CX NCBI_TaxID 9355;

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FT DOMAIN 455 518 POL BOX 1.
FT DOMAIN 553 623 POL BOX 2.
FT VARSPEC 373 373 L->LVSGMRSTSGHPURSE (in isoform 2).
FT 1734VSP_004927.1
FT CONFLICT 386 386 J -> V (IN REF. 2)
SQ SEQUENCE 631 AA: 70012 MW: 2085734.87005 DC QP164
Query Match: 70.7% Score 41; DB 1; Length 646;
Best Local Similarity 63.6%; Pred. No. 4.6;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

CY 1 MLGRRPPFFETS 11
DB 253 LDCGSPFFETA 263

RESULT 14
CNK_HUMAN STANDARD; PRT: 646 AA
AC Q9H4B4; Q15767;
FT 15 OCT-2001 (Rel. 40, Created;
FT 16 OCT-2001 (Rel. 40, Last sequence update;
DE 28-FEB-2003 (Rel. 41, Last annotation update;
DE Cytokine-inducible serine/threonine-protein kinase (EC 2.7.1.37) (FGF-
DE inducible kinase) (proliferation-related kinase).
CN CNK OR PKR OR PRK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID:9606;
RN 1;
RF SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX VEDLINE=20493044; PubMed=1039920;
RA Hestrich U., Wolf G., Yuan J., Berentzen-Hahn J., Rich T., Weller M.,
RA Kauselmann G., Rehl M., Andreessen M., Kaufmann M., Kuhl G.,
RA Strohhardt K.;
RT Adhesion induced expression of the serine/threonine kinase Pak in
RT human macrophages."
RL Oncogene 19:4632-4639(2000);
PK (1);
RP SEQUENCE OF 28-646 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94325053; PubMed=9704527;
RA Li B., Geyang B., Pan H., Reissmann P., Slamon D., Attoci R.,
RA Lu J., Dai W.;
FT "Pak, a cytokine-inducible human protein, contains threonine kinase whose
FT expression appears to be down-regulated in lung carcinomas."
RL Oncol. Chem. 571:19492-19498(1998);
RP CHARACTERIZATION;
RX MEDLINE=98019242; PubMed=9354331;
RA Geyang B., Pan H., Lu J., Slamon D., Attoci R., Dai W.;
FT "Human Pak is a conserved protein serine/threonine kinase involved in
FT regulation of phase functions."
RL Oncol. Chem. 572:28646-28651(1997);
RP CHARACTERIZATION;
RX MEDLINE=20027391; PubMed=10557094;
RA Geyang B., Li W., Pan H., Yeodows J., Hoffmann J., Dai W.;
RT "The physical association and phosphorylation of Cdc25C protein
RT phosphatase by Pak."
RL Oncogene 18:6029-6036(1999);
CC -1- FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN REGULATING M
CC PHASE FUNCTIONS DURING THE CELL CYCLE. MAY ALSO BE PART OF THE
CC SIGNALING NETWORK CONTROLLING CELLULAR ADHESION. IN VITRO, IS ABLE
CC TO PHOSPHORYLATE CDC25C AND CASEIN.
CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphorylated
CC SUBUNIT: BINDS TO THE CALCIUM/INTEGRIN-BINDING PROTEIN (CIB). THIS
CC INTERACTION PROBABLY OCCURS VIA THE POL-BOX DOMAIN.
CC -1- SUBCELLULAR LOCATION: Membrane-associated
CC -1- TISSUE SPECIFICITY: TRANSCRIPTS ARE HIGHLY DETECTED IN PLACENTA,
CC LUNG, FOLLOWED BY SKELETAL MUSCLE, HEART, PANCREAS, OVARIES AND

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CC KIDNEY AND WEAKLY DETECTED IN LIVER AND BRAIN. MAY HAVE A SHORT
CC HALF-LIFE IN CELLS OF HEMATOPOIETIC ORIGIN, STRONGLY AND
CC EXCLUSIVELY DETECTED IN TERMINALLY DIFFERENTIATED MACROPHAGES.
CC TRANSCRIPTS EXPRESSION APPEARS TO BE DOWN-REGULATED IN PRIMARY
CC LUNG TUMOR.
CC -1- INDUCTION: CYTOKINE AND CELLULAR ADHESION TRIGGER PKK INDUCTION.
CC -1- PTM: PHOSPHORYLATED AS CELLS ENTER MITOSIS AND DEPHOSPHORYLATED AS
CC CELLS EXIT MITOSIS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CDS/POLC SUPERFAMILY.
CC -1- SIMILARITY: Contains 2 POLC box domains.
CC This Swiss Prot entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; AC293866; CAC10659.1;
DR EMBL; U56998; AAC50637.1; AUT_INIT.
DR Genew; HGNC:2154; CNK.
DR GK; Q9H4B4;
DR MIM; 602913;
DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR GO; GO:0000734; P:regulation of cell cycle; TAS.
DR InterPro; IPR000959; POLC_BOX.
DR InterPro; IPR000191; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00669; PKinase; 1.
DR Pfam; PF00669; POLC_BOX; 2.
DR ProDom; PD020003; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00078; POLC_BOX; 2.
DR PROSITE; PS0107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS0001; PROTEIN KINASE DOM; 1.
DR PROSITE; PS0108; PROTEIN KINASE ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
KW phosphorylation.
FT DOMAIN 62 314 PROTEIN KINASE.
FT NP_BIND 68 74 ATP (BY SIMILARITY).
FT BINDING 91 91 ATP (BY SIMILARITY).
FT ACT_SITE 185 185 BY SIMILARITY.
FT DOMAIN 470 537 POLC_BOX_1.
FT DOMAIN 567 637 POLC_BOX_2.
FT CONFLICT 39 39 V -> A (IN REF. 2).
FT CONFLICT 353 353 V -> G (IN REF. 2).
FT CONFLICT 419 419 H -> C (IN REF. 2).
FT CONFLICT 464 470 FSEWGF -> VSKWVDY (IN REF. 2).
FT CONFLICT 522 522 R -> P (IN REF. 2).
SQ SEQUENCE 646 AA: 71789 MW: 620147030FC8A3B4 CRC64;
Query Match: 70.7%; Score 41; DB 1; Length 646;
Best Local Similarity 63.6%; Pred. No. 4.6;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

CY 1 MLGRRPPFFETS 11
DB 253 LDCGSPFFETA 263

RESULT 14
CNK_PIG STANDARD; PRT: 156 AA.
AC Q9NCX0.
DE 28-FEB-2003 (Rel. 41, Created;
DE 28-FEB-2003 (Rel. 41, Last sequence update;
DE 15-SEP-2003 (Rel. 42, Last annotation update;
DE Serine/threonine protein kinase 12 (EC 2.7.1.37) (Auroca-B)
DE (Fragment).
CN STK12.

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OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
 CX NCBI TaxID:9823;
 RN 1;
 RF SEQUENCE FROM N.A.
 RC TISSUE=small intestine;
 RX MEDLINE=223238; PubMed=12270407;
 RA Abram F., Hussein S.M., Hoff C., Danks S., Ringe B.,
 RT "Differential gene expression during intestinal ischemia-reperfusion
 injury".
 RL Transplant. Proc. 34:2303-2322(2002).
 RN 2;
 RF SEQUENCE FROM N.A.
 RC FUNCTION: May be directly involved in regulating the cleavage of
 polar spindle microtubules and is a key regulator for the onset of
 cytokinesis during mitosis by similarity;
 CC CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC SUBCELLULAR LOCATION: Localized to the midzone of central spindle
 in late anaphase and concentrated into the midbody in telophase
 and cytokinesis. Colocalized with gamma tubulin in the mid-body
 by similarity;
 CC SIMILARITY: BELONGS TO THE SEP/THR FAMILY OF PROTEIN KINASES.
 CC ANKRA SUBFAMILY.
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 CC
 DR EMBL AF244164; AAF61735;
 DR InterPro; IPRO00252; N6; Ntase;
 DR InterPro; IPRO00719; Prot_kinase;
 DR InterPro; IPRO02290; Ser_thr_kinase;
 DR InterPro; IPRO11245; Tyr_kinase;
 DR Pfam; PF00369; pkinase; 1;
 DR PRINTS; PR00109; TYRKINASE;
 DR PROSITE; PS00301; Prot_kinase; 1;
 DR PROSITE; PS00311; PROTEIN_KINASE_10; 1;
 DR PROSITE; PS0108; PROTEIN_KINASE_ST; 1;
 KW Cell cycle; Transferase, Serine/threonine-protein kinase, ATP-binding.
 FT NEM TER 1
 FT DOMAIN <1> 156 PROTEIN_KINASE
 FT ACT_SITE 51 51 BY SIMILARITY
 FT NEM TER 156 156
 SQ SEQUENCE 156 AA; 17487 BW; 12.4 kDa; 1000 amino acids.
 Query Match 69.0% Score 11.00 E-02 Domain: 100
 Best Local Similarity 54.5% Prot No: 156
 Matches 6; Conservative 4; Miscellaneous 1; Gaps 3;
 QY 1 VILGDPPEETS 11
 DE 11 VILGDPPEETS 127
 DE 11 VILGDPPEETS 127
 RESULT 1;
 STIC HUMAN
 ID STIC HUMAN STANDARD; REF. 144 AA
 AC 096354; 04610; 060446; 095083; 096055; 090046;
 LT 29-FEB-2003 (Ref. 41; Created)
 DT 29-FEB-2003 (Ref. 41; Last sequence update)
 DT 14-SEP-2003 (Ref. 42; Last annotation update)
 DE Serine/threonine protein kinase 12 (Ref. 2,7,11,30). Aurora- and Ipl-
 DE like midbody-associated protein 13 (AM13). Aurora-related kinase
 DE 21 (Aurora-related kinase 2) (STK13). Aurora B.
 GN STK13 OR AIM1 OR ARK2 OR Aik2.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catartiodactyla; Hominoidea;
 CX NCBI TaxID:9606;
 RN 1;
 RF SEQUENCE FROM N.A.
 RC TISSUE=Lung, lymph, and muscle;
 RX MEDLINE=2238857; PubMed=1477932;
 RA Strausberg R.D., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S., Wang J., Hsieh F.,
 RA Chachekso L., Matovina K., Farmer A.A., Rubin G.M., Hong D.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.J., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquelland N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatane P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.C., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN 17;
 RF REVIEW
 RX MEDLINE=21356577; PubMed=11413462;
 RA Nigg E.A.;
 RT "Mitotic kinases as regulators of cell division and its checkpoints.";
 RL Nat. Rev. Mol. Cell Biol. 2:21-32(2001).
 CC 1. FUNCTION: May be directly involved in regulating the cleavage of
 polar spindle microtubules and is a key regulator for the onset of
 cytokinesis during mitosis.
 CC CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC SUBCELLULAR LOCATION: Localized to the midzone of central spindle
 in late anaphase and concentrated into the midbody in telophase

RP SEQUENCE FROM N.A.
 RX MEDLINE=9818349; PubMed=9514916;
 RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
 RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
 RT "cDNA cloning, expression, subcellular localization, and chromosomal
 assignment of mammalian aurora homologues, aurora-related kinase (ARK)
 1 and 2".
 RL Biochem. Biophys. Res. Commun. 244:285-292(1998).
 RN 12;
 RF SEQUENCE FROM N.A.
 RX MEDLINE=99025855; PubMed=9409983;
 RA Tatsuta M., Katayama H., Ota T., Tanaka T., Odashima S., Suzuk F.,
 RA Terada Y.;
 RT "Multinuclearity and increased ploidy caused by overexpression of the
 RT aurora- and Ipl-1 like midbody-associated protein mitotic kinase in
 RT human cancer cells.";
 RL Cancer Res. 58:4811-4816(1998).
 RN 13;
 RF SEQUENCE FROM N.A.
 RC TISSUE=liver, and spleen;
 RX MEDLINE=99077743; PubMed=9958806;
 RA Kimura M., Matsuda Y., Yoshioaka T., Sumi N., Okano Y.;
 RT "Identification and characterization of STK12/Aik2: a human gene
 RT related to aurora of Drosophila and yeast IPl1".
 RL Cytogenet. Cell Genet. 82:147-152(1998).
 RN 14;
 RF SEQUENCE FROM N.A.
 RX MEDLINE=21364697; PubMed=1147245;
 RA Prigent C., Gail R., Trower M., Sarsneau P.;
 RT "In silico cloning of a new protein kinase, Aik2, related to
 RT Drosophila aurora using the new tool: EST Blast".
 RL In Silico Biol. 1:123-128(1999).
 RN 15;
 RF SEQUENCE FROM N.A.
 RX Zhang C., Yu L., Bi A.;
 RT "Cloning of a novel human gene homologous to mouse STK-1".
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN 16;
 RF SEQUENCE FROM N.A.
 RC TISSUE=Lung, lymph, and muscle;
 RX MEDLINE=2238857; PubMed=1477932;
 RA Strausberg R.D., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S., Wang J., Hsieh F.,
 RA Chachekso L., Matovina K., Farmer A.A., Rubin G.M., Hong D.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.J., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquelland N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatane P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.C., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN 17;
 RF REVIEW
 RX MEDLINE=21356577; PubMed=11413462;
 RA Nigg E.A.;
 RT "Mitotic kinases as regulators of cell division and its checkpoints.";
 RL Nat. Rev. Mol. Cell Biol. 2:21-32(2001).
 CC 1. FUNCTION: May be directly involved in regulating the cleavage of
 polar spindle microtubules and is a key regulator for the onset of
 cytokinesis during mitosis.
 CC CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC SUBCELLULAR LOCATION: Localized to the midzone of central spindle
 in late anaphase and concentrated into the midbody in telophase

SEQUENCE FROM N.A.
 TISSUE: Cervix, Colon, Kidney, and Muscle;
 PUBMED=22185257; PubMed=12477912;
 STAUDERBERG R.D., FEIGOLD E.A., GROUSE L.H., DERAG J.G.,
 KLAESER R.D., COLLINS P.S., WAGNER J., SHEPHERD C.M., SCHAFER G.,
 ALFORD S.F., ZIEBERG B., HUETW V.H., SCHAFER G., HAT R.K.,
 HARRIS R.F., JORDAN H., VOORE T., MAX S.L., WANG J., HARRIS F.,
 BRATCHEVSKO D., MARUSINA K., FARMER A., RUDIN S.M., HONG L.,
 STAPLETON M., SOARES M.B., BOZALCO N.F., CASAVANT C., SCHWARTZ T.E.,
 PETERS M., USIN T.E., TOSIYUKI S., GAZDAR C., FRANGE C.,
 PABA S., LUQUILLANO N.A., PETERS G., ABRAHAMSON K.C., MULLANEY S.J.,
 BOSUK S.A., MCGEEHAN P.J., MCKERRAN R.J., MALEK J.A., ZONATAROV B.H.,
 RICHARDS S., WOLLEY K.C., HALE S., BRIDGES A., SHY C., RALYK S.W.,
 VILLALBA L.K., KATZ D.M., SODERSTROM E.C., DE KLU, HARRIS E.A.,
 FAHEY J., HOLLON E., KETTERMAN M., MADAN A., FRIEDMAN J., SANCHEZ A.,
 WHITING M., MADAN A., YOUNG A.C., SHEVCHENKO Y., HOFFMANN G.G.,
 BRACKLEY R.W., TOUCHMAN J.W., SHEN E.D., DICKSON M.C.,
 RODRIGUEZ A.C., GRIMWOOD J., SCHMUTZ J., MYERS R.M.,
 BUTTERFIELD Y.S.N., KRZYWINSKI M., SKALSKA U., STALLUS D.E.,
 SCHROEDER A., SCHEIN J.E., JONES S.J., MATA V.A.,
 SCHROEDER A., SCHEIN J.E., JONES S.J., MATA V.A.,
 human and mouse cDNA sequences;
 J. Biol. Chem. 277:10719-10726(2002);
 [1]
 CELL-CYCLE REGULATION
 MELINSKI21995666; PubMed=1192777;
 TANAKA M., UEDA A., KANAMORI H., ITOYOSHII H., YAMU J., KITAHARA S.,
 KISHIMOTO Y.
 "Cell cycle dependent regulation of human aurora A transcription is
 mediated by periodic repression of bHLH."
 J. Biol. Chem. 277:10719-10726(2002);
 [2]
 REVIEW
 MELINSKI21995667; PubMed=11413442;
 TANAKA M., UEDA A., KANAMORI H., ITOYOSHII H., YAMU J., KITAHARA S.,
 KISHIMOTO Y.
 "Mitotic kinases as regulators of cell division and its checkpoints."
 Nat. Rev. Mol. Cell Biol. 2:223-232(2001);
 [3]
 FUNCTION: May play a role in cell cycle regulation during anaphase
 and/or telophase, in relation to the function of the
 centrosome/spindle pole region during chromosome segregation.
 May be involved in microtubule formation and/or stabilization. May
 play a key role during tumor development and progression.
 CATALYTIC ACTIVITY: ATP + a protein + H₂O → a phosphorylated
 protein + ADP + P_i.
 SUBCELLULAR LOCATION: Localized on centrosomes in interphase cells
 and at each spindle pole in mitosis.
 TISSUE SPECIFICITY: Highly expressed in testis and weakly in
 skeletal muscle, thymus and spleen. Also highly expressed in
 colon, ovary, prostate, and testis. Overexpression of this gene in
 cancer cell lines expresses a growth advantage to cells in culture.
 PUS: accumulates during G₂M. Localized on spindle pole.
 PUS: phosphorylated.
 DISEASE: Defects in STK6 are responsible for a form of centrosome
 aberrations including aneuploidy.
 SIMILARITY: BELONGS TO THE SER-THR FAMILY OF KINASES.
 AURORA SUBFAMILY.
 CAUTION: Ref 1: sequence differs from that shown due to frame-shifts
 in positions 105, 125, 129, 235 and 241.
 NOTE: Although authors have considered STK6 and STK6B as two
 different proteins, it is clear that they are the same protein.
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 EXP: A031146.1; AAC23448.1;
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CC MESSENGER, WHICH ACTIVATES THE TRANSCRIPTION OF A NUMBER OF GENES
 CC IN MULTIPLE TISSUES. THE INHIBITORY EFFECT OF I-KAPPA-B UPON
 CC NF-KAPPA-B IN THE CYTOPLASM IS EXERTED PRIMARILY THROUGH THE
 CC INTERACTION WITH P65. P65 SHOWS A WEAK DNA-BINDING SITE WHICH
 CC COULD CONTRIBUTE DIRECTLY TO DNA BINDING IN THE NF-KAPPA-B
 CC COMPLEX.
 CC SUBUNIT: ACTIVE NF-KAPPA-B IS A HETERODIMER OF AN ABOUT 50 kDa
 CC DNA-BINDING SUBUNIT AND THE WEAK DNA-BINDING SUBUNIT P65. TWO
 CC HETERODIMERS MIGHT FORM A LABILE TETRAMER.
 CC SUBCELLULAR LOCATION: NUCLEAR, BUT ALSO FOUND IN THE CYTOPLASM
 CC IN AN INACTIVE FORM COMPLEXED TO AN INHIBITOR (I-KAPPA-B).
 CC TISSUE SPECIFICITY: SPLEEN; LOWER LEVEL IN BRAIN.
 CC SIMILARITY: BELONGS TO THE REL/DORSAL FAMILY.
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 CC SMART: SM00229; IPT.1.
 CC PROSITE: PS01204; REL.1.
 CC PROSITE: PS0254; REL.2; 1.
 CC DNA binding: Transcription regulation; Activator; Nuclear protein;
 CC Phosphorylation.
 CC DOMAIN 25 311 REL_LIFE (RHD).
 CC DOMAIN 306 309 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC MOD_RES 281 281 PHOSPHORYLATION (BY PRK1 (POTENTIAL)).
 CC SEQUENCE 558 AA; 60371 MW; 052E159A4D47B36 CR664;
 CC
 CC Query Match 67.2%; Score 19; DB 1; Length 558;
 CC Best Local Similarity 77.8%; Pred No 9.5;
 CC Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC 3 LIGRPPEPT 10
 CC ||| |||
 CC 428 ILGPEPTDT 436
 CC
 CC RESULT 18
 CC PUX1_CAEEL STANDARD; PRT 449 AA
 CC AC P3433; G61-62; C76763;
 CC DT 01-FEB-1994 (rel. 28, Created;
 CC DT 28-FEB-2003 (rel. 41, Last sequence update;
 CC DT 28-FEB-2003 (rel. 41, Last annotation update;
 CC DE Serine/threonine-protein kinase plk1 (EC 2.7.11.1) (polo-like
 CC kinase-1).
 CC PLX-1 CR PDC1 CR C4B9.4.
 CC Caenorhabditis elegans.
 CC Eukaryota, Metazoa, Nematoda; Chromalvea; Rhaditida; Rhaditidaea;
 CC Rhaditidae; Pelodierinae; Caenorhabditis.
 CC KEGG TaxID:6239;
 CC [1]
 CC SEQUENCE FROM N.A. (ISOFORM B).
 CC YKELINE+9304501; Pubmed:10376213;
 CC Ouyang B., Wang Y., Dai W.;
 CC "Caenorhabditis elegans contains structural homologs of human prk and
 CC plx.",
 CC DNA Seq. 10:109-113(1999).
 CC
 CC SEQUENCE FROM N.A. (ISOFORM A), FUNCTION, AND SUBCELLULAR LOCATION.
 CC STRAIN-BRISTOL N2;
 CC

RX MEDLINE=20190108; Pubmed=10660671;
 RA Chase D., Serafinas C., Ahncroft N., Kosinski M., Longo D.,
 RA Ferris D.K., Golden A.;
 RT "The polo-like kinase PLK-1 is required for nuclear envelope breakdown
 RT and the completion of meiosis in *Caenorhabditis elegans*.";
 RL Genesis 26:26-41(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; Pubmed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton C., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Konstam L., Jones M., Kershaw J., Kirsten J., Laister N.,
 RA Laurrelle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkhen R.,
 RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 RA Woldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C*
 RT *elegans*.";
 RL Nature 368:32-38(1994).
 RN [4]
 RP REVISIONS, AND ALTERNATIVE SPLICING.
 RA Waterston R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 CC !- FUNCTION: Required for oocyte nuclear envelope breakdown before
 CC entry of oocyte into spermatheca. In mitotic cells, plays a role
 CC in spindle organization and centrosome maturation. In meiotic
 CC cells, required for spindle dynamics and probably for spindle
 CC attachment to the chromosomes. Zygotic role in the development of
 CC the germline and nerve cord.
 CC !- SUBCELLULAR LOCATION: In mitosis, remains associated with
 CC centrosomes entering prophase through to anaphase. During
 CC metaphase, found at the chromosomes of the metaphase plate. In
 CC meiosis, detected at centrosomes after pronuclear meeting in post-
 CC meiotic 2-cell embryos. Associated with chromatin during
 CC chromosome segregation of anaphase and in the region between the
 CC dividing chromosomes. Cytoplasmic in mature, unfertilized oocytes.
 CC !- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=b;
 CC IsoId=P34331-1; Sequence-D:displayed;
 CC Name=a;
 CC IsoId=P34331-2; Sequence-VSP 034928;
 CC !- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDC5/POLO SUBFAMILY.
 CC !- SIMILARITY: Contains 2 POLO box domains.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: AF057165; AAC:4129.1; ..
 CC EMBL: AF080581; AAC34661.1; ..
 CC EMBL: L15188; AAC27947.2; ..
 CC EMBL: L15188; AAC2825.1; ..
 CC PIR: T43337; T43337.
 CC HSSP: O63450; 1A06.
 CC WormPep: C14B9.4a; CE266649.
 CC WormPep: C14B9.4b; CE30602.
 CC GO:0005634; C:nucleus; IEPI.
 CC GO:0005524; F:ATP binding activity; ISS.
 CC GO:0004674; F:protein serine/threonine kinase activity; ISS.
 CC GO:0007417; P:central nervous system development; IMP.
 CC GO:0007098; P:cell cycle; IMP.
 CC GO:0007077; P:mitotic nuclear envelope breakdown; IMP.

EMSL; XC5279; CAZ28893.2; JOINED.
EMSL; XC5280; CAZ28893.2; JOINED.
EMSL; XC5281; CAZ28893.2; JOINED.
EMSL; XC5282; CAZ28893.2; JOINED.
EMSL; XC5283; CAZ28893.2; JOINED.
EMSL; AEC03855; AAF57932.1; -
EMSL; AEC03855; AAF57933.1; -
EMSL; AYC35003; AAM1131.1; -
HSSP; P05597; 17N.

Query Match 65.5%; Score 38, CB 1; Length 634;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGSRPPE 9
 ID 495 MWAGRPPE 503

RESULT 24

ID PKN COREP STANDARD; PRT; 683 AA;
 AC QP015;
 DT 15-SEP-2003 (Rel. 42, Created);
 DT 15-SEP-2003 (Rel. 42, Last sequence update);
 DE Probable serine/threonine protein kinase (EC 2.7.1.37);
 GN CE033;
 OS Corynebacterium efficiens;
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium;
 CC NCBI_TaxID=152794;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
 RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
 RA Ikeda K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
 RA Usuda Y., Sugimoto S.;
 RT "The entire genomic sequence of Corynebacterium efficiens YS-314,"
 RT Submitted (MAY-2002) to the EMBL/GenBank/DSJ databases.
 CC 1 CATALYTIC ACTIVITY: ATP -> a protein + ADP - a phosphoprotein.
 CC 1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC 1 SIMILARITY: Contains 3 PASTA domains.

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EMBL: AF035214; BAC16843.1;
 InterPro: IPR00543; PASTA;
 InterPro: IPR00719; Prot_Kinase
 InterPro: IPR00290; Ser_Thr_Kinase
 InterPro: IPR01245; Tyk_Proteinase
 Pfam: PF01733; PASTA_3
 Pfam: PF00661; Kinase4; 1;
 ProDom: PRO0001; Prot_Kinase; 1;
 SMART: SM00742; PASTA_3;
 SMART: SM00223; S_TKc; 1;
 SMART: SM00119; TyKc; 1;
 SMART: PS00127; PROTEIN_KINASE_ATP; 1;
 SMART: PS00129; PROTEIN_KINASE_DOM; 1;
 PRS1: PRS00129; PROTEIN_KINASE_ST; 1;
 KW Hydrophobic protein; Transferase; Serine/threonine protein kinase;
 FT ATP-binding; Repeat; Complete proteome;
 FT DOMAIN 9 278
 FT PASTA 1;
 FT DOMAIN 377 443
 FT PASTA 1;
 FT DOMAIN 444 512
 FT PASTA 1;
 FT DOMAIN 513 577
 FT NP-BIND 15 23
 FT NP-BIND 38 38
 FT ACT_SITE 136 136
 FT ACT_SITE 136 136
 BY SIMILARITY;
 SEQUENCE 660 AA; 69646 MW; D31079EB025449; CDS(44)

Query Match 65.5%; Score 38, CB 1; Length 660;
 Best Local Similarity 66.7%; Pred. No. 18;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGSRPPE 9

DB 207 LVTGRPPE 215

RESULT 25

ID PKN COREP STANDARD; PRT; 683 AA;
 AC P50528;
 DT 01-OCT-1996 (Rel. 34, Created);
 DT 01-OCT-1996 (Rel. 34, Last sequence update);
 DT 15-SEP-2003 (Rel. 42, Last annotation update);
 DE Serine/threonine-protein kinase p101 (EC 2.7.1.37);
 GN P101 OR SPAC23C11.16
 OS Schizosaccharomyces pombe (Fission Yeast);
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomycetes;
 CC NCBI_TaxID=4896;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=95262899; PubMed=7744248;
 RA Okura H., Hagan I.M., Glover D.M.;
 RT "The conserved Schizosaccharomyces pombe kinase p101, required to form a bipolar spindle, the actin ring, and septum, can drive septum formation in G1 and G2 cells";
 RT Genes Dev. 9:1059-1073(1995);
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Brooks K., Peat N., Hayles J., Baker S., Basham D., Bowman S., Collins M., Brown D., Brown S., Challinor T., Churcher C.M., Collins M., Connor P., Cronin A., Davis P., Fellwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Jolley K., Jones S., Jones M., Leather S., McDaniel D., McEwan J., McInerney P., Meule S., Mungall K., Murphy L., Niblett D., Odeh C., Oliver K., O'Neill S., Pearson C., Quail M.A., Rabinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skilton J., Simmonds M., Squares R., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward C., Volkart G., Aert R., Robben J., Grynolprez B., Weijters I., Vansireels E., Plegier M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Pitz C., Holzer E., Moestl D., Hilbert H., Bozzym K., Langer T., Beck A., Lehtach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gallardou C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado C., Jimenez J., Sanchez M., del Rey F., Benito M., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Spakovski G.V., Ussery D., Barrett B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe";
 RL Nature 415:871-880(2002);
 CC 1-1 FUNCTION: REQUIRED TO FORM A BIPOLAR SPINDLE, THE ACTIN RING AND SEPTUM. FUNCTIONS 'UPSTREAM' OF THE WHOLE SEPTUM FORMATION PATHWAY, INCLUDING ACTIN RING FORMATION (REGULATED BY LATE SEPTATION GENES) AND SEPTAL MATERIAL DEPOSITION (REGULATED BY EARLY SEPTATION GENES). BEHAVES AS A "SEPTUM-PROMOTING FACTOR", AND COULD ALSO BE INVOLVED IN INDUCING OTHER LATE EVENTS OF CELL DIVISION.
 CC 1-1 CATALYTIC ACTIVITY: ATP -> a protein + ADP + a phosphoprotein.
 CC 1-1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CDC5/POLO SUBFAMILY.
 CC 1-1 SIMILARITY: Contains 2 POLO box domains.

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FT MCD_RES 702 702 PHOSPHORYLATION (AUTO-) (POTENTIAL);
 FT MCD_RES 709 709 PHOSPHORYLATION (AUTO-) (POTENTIAL);
 SQ SEQUENCE 236 AA: 2634PE59E98FEB CRC64;
 Query Match 65.5%; Score 38; DS 1; Length 737;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGRPPE 9
 DE 599 NYAGQPPPE 607
 RESULT 29
 KPCF HUMAN STANDARD; PRT: 737 AA.
 ID C02156; Q9J581;
 DT 01-JUL-1993 (Rel. 26, last sequence update);
 DT 28-FEB-2003 (Rel. 41, last annotation update);
 DE Protein kinase C, epsilon type IEC 2.7.1.1 (nPKC-epsilon);
 GN PKCE OR PKCE;
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
 OX NCBI_TaxID:9606;
 RN 1;
 RE SEQUENCE FROM N.A.
 RX MEDLINE 9100319; PubMed1382605;
 RA Pasta P., Stricklund M.B., Holmes W., Morris C.R., Ballas L.N.,
 RA Burns D.J.;
 RA Sequence and expression of human protein kinase C epsilon 1;
 RA J. Biol. Chem. 268:11321-11327 (1993);
 RA Protein. Biochem. Acta 113:1154-1160 (1992);
 RA
 RA SEQUENCE OF 1-116 FROM N.A.
 RA Waterston R.
 RA Submitted (JAN 1999) to the EMBL/GenBank/DDB databases.
 CC FUNCTION: THIS IS CALCIUM INDEPENDENT, PROSTHETIC INDEPENDENT,
 CC SERINE- AND THREONINE-SPECIFIC ENZYME.
 CC 1 FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
 CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
 CC THE RECEPTOR FOR PHORBOL ESTERS. A CLASS OF TUMOR PROMOTERS,
 CC 1. SIMILARITY: Contains 2 zinc-dependent phospho-ester and DAG
 CC binding domains.
 CC 1. SIMILARITY: Contains 1 C2 domain.
 CC 1. SIMILARITY: BELONGS TO THE SERINE/THREONINE KINASES.
 CC PKC SUBFAMILY.
 CC
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 CC
 DR EM2L; X65293; CAA46388.1;
 DR EMBL; U51244; AAC08955.1;
 DR F01; S28942;
 DR HSPF; P28867; 1PFC
 DR GenBank; F01; S28942;
 DR X01; 176975;
 DR GO; GO:0005624; C:membrane fraction; TAS
 DR GO; GO:0004697; P:protein kinase C activity; TAS
 DR GO; GO:0004871; P:signal transducer activity; TAS
 DR GO; GO:0006917; P:induction of apoptosis; TAS
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS
 DR InterPro; IPR000008; C2
 DR InterPro; IPR002219; DAG-PE-bind
 DR InterPro; IPR000961; PKinase C
 DR InterPro; IPR000219; Prot_kinase
 DR InterPro; IPR000220; Ser_Thr_kinase
 DR InterPro; IPR000169; C2_1

DR Pfam; PF00130; DAG-PE-bind; 2.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF00433; Kinase_C; 1.
 DR PRINTS; PR00008; DAGPEDOMAIN.
 DR ProDom; PD003001; Prot_kinase; 1.
 DR SMART; SM0109; C1; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00133; S-TK_X; 1.
 DR SMART; SM00220; S-TK; 1.
 DR PROSITE; PS00004; C2_DOMAIN; 2; 1.
 DR PROSITE; PS00479; DAG-PE-BIND_DOM; 1; 2.
 DR PROSITE; PS00081; DAG-PE-BIND_DOM; 2; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR Repeat; ATP-binding; Transferase; Phosphorylation;
 KW Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
 FT DOMAIN 1 99 C2 DOMAIN.
 FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1.
 FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2.
 FT DOMAIN 408 568 PROTEIN KINASE.
 FT NP_BIND 414 422 ATP (BY SIMILARITY).
 FT BINDING 437 437 ATP (BY SIMILARITY).
 FT ACT_SITE 532 532 BY SIMILARITY.
 FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 FT MOD_RES 720 720 PHOSPHORYLATION (AUTO-) (POTENTIAL).
 SQ SEQUENCE 737 AA: 83573 MW: 850320091ALFTF CRC64;
 Query Match 65.5%; Score 38; DS 1; Length 737;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLLGRPPE 9
 DE 600 NYAGQPPPE 608
 RESULT 30
 KPCF MOUSE STANDARD; PRT: 737 AA.
 ID KPCF_MOUSE STANFAPR; PRT: 737 AA.
 AC P16554;
 DT 01-APR-1993 (Rel. 14, Created);
 DT 01-APR-1993 (Rel. 14, last sequence update);
 DT 28-FEB-2003 (Rel. 41, last annotation update);
 DE Protein kinase C, epsilon type IEC 2.7.1.1 (nPKC-epsilon);
 GN PKCE OR PKCE OR PKCEA;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sauriognathi; Muridae; Mus;
 OX NCBI_TaxID:10090;
 RN 1;
 RE SEQUENCE FROM N.A.
 RX MEDLINE 89137541; PubMed=2917656;
 RA Schaad D., Parker P.J., Bristol A., Kriz R., Knopf J.;
 RA "Unique substrate specificity and regulatory properties of
 RA PKC-epsilon: a rationale for diversity";
 RA FEBS Lett. 243:351-357 (1999);
 RN 121
 RN SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99127436; PubMed=9467942;
 RA Wang Q.J., Acs P., Seidnight J., Blumberg P.M., Mischak H.,
 RA Mushinski J.F.;
 RA "The catalytic domain of PKC-epsilon, in reciprocal PKC-delta and
 RA epsilon chimeras, is responsible for conferring tumorigenicity to
 RA NIH3T3 cells, whereas both regulatory and catalytic domains of
 RA PKC-epsilon contribute to in vitro transformation";
 RL Oncogene 16:53-61 (1998);
 RN 13;
 RN SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Wheeler F.L.;
 RL Submitted (JAN 1999) to the EMBL/GenBank/DDB databases.


```

FT NP BIND 414 422 ATP (BY SIMILARITY)
FT BINDING 437 437 ATP (BY SIMILARITY)
FT ACT SITE 532 532 BY SIMILARITY
FT MOD RES 703 703 PHOSPHORYLATION AUTO INHIBITION
FT MOD RES 710 710 PHOSPHORYLATION AUTO INHIBITION
SQ SEQUENCE 437 AA: 83478 MW: 6AD63999FDD2648F CP 744,
Query Match 65.5% Score 187 DB 1 Length 437
Best Local Similarity 66.7% Pred. No. 20
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
DE 600 NNAAGPPPE 608
RESULT 32
KPCP APLCA STANDARD; PRT; 743 AA.
AC Q6945;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Calcium-independent protein kinase C IEC 2.7.1.1 (APC 11).
GN PKC2
OR Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Aniscombranchia; Anaspidea;
OC Aplysioidae; Aplysiidae; Aplysia.
CX NCBI TaxID:6500;
PP SEQUENCE FROM N.A.
RX MEDLINE:91332620; PubMed:1869917;
RA Krüger K.E., Sossin W.S., Sacktor T.C., Bergold P.J., Buehhausen S.,
RA Schwartz J.H.
RA "Cloning and characterization of Ca2+-dependent and Ca2+-
PT independent PKCs expressed in Aplysia sensory cells."
PL J. Neurosci. 11:2303-2313(1991).
RN [2]
EP CHARACTERIZATION:
RX MEDLINE 93194577; PubMed:8449941;
RA Sossin W.S., Diaz-Arastia R., Schwartz J.H.
RA "Characterization of two isoforms of protein kinase C in the nervous
RT system of Aplysia californica."
RC J. Biol. Chem. 268:5761-5768(1993).
RF C2 DOMAIN [2].
RX MEDLINE-92344440; PubMed-834856.
RA Sossin W.S., Schwartz J.H.
RA "Ca2+-independent protein kinase C isoform 1 contains a conserved domain
RT similar to the C2 consensus sequence."
RC Trends Biochem. Sci. 18:209-205(1993).
RN [4]
EP CHARACTERIZATION:
RX MEDLINE-98334616; PubMed:9666285;
RA Peipo A.V., Fan X., Sossin W.S.
RA "The role of C2 domains in Ca2+-activated and Ca2+-independent protein
RT kinase C in Aplysia."
RC J. Biol. Chem. 273:19040-19049(1998).
RN [5]
EP ERRATUM
RA Peipo A.V., Fan X., Sossin W.S.
RL J. Biol. Chem. 273:22856-22858(1998).
RN [6]
EP CHARACTERIZATION:
RX MEDLINE-98138438; PubMed:9477951;
RA Peipo A.V., Sossin W.S.
RA "The C2 domain of the Ca2+-independent protein kinase C Apl II
RT inhibits photolysis of ester binding to the C2 domain in a phosphatidic
RT acid-sensitive manner."
RC Biochemistry 37:1256-1263(1998).
CC FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
SERINE AND THREONINE-SPECIFIC ENZYME.

```

```

CC FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
CC SIMILARITY).
CC ENZYME REGULATION: REQUIRES HIGH LEVELS OF PHOSPHATIDYL-SERINE TO
CC BE ACTIVATED. THE PRESENCE OF THE C2 DOMAIN LOWERS THE AFFINITY OF
CC PROTEIN KINASE C ACTIVATORS FOR THE C2 DOMAINS AND THIS INHIBITION
CC CAN BE REMOVED BY PHOSPHATIDYL-SERINE. PHOSPHATIDIC ACID, HOWEVER,
CC IS MUCH MORE POTENT THAN PHOSPHATIDYL-SERINE IN REDUCING C2 DOMAIN-
CC MEDIATED INHIBITION, SUGGESTING THAT PHOSPHATIDIC ACID MAY BE A
CC REQUIRED COFACTOR FOR THE ACTIVATION OF APC 11.
CC SUBCELLULAR LOCATION: Membrane-associated.
CC TISSUE SPECIFICITY: EXPRESSED IN NERVOUS TISSUES, OVOTESTIS AND
CC GUT.
CC SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG
CC binding domains.
CC SIMILARITY: Contains 1 C2 domain.
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC or send an e-mail to license@isb-sib.ch).
CC
CC EMBL: N94884; AAA27771.1;
CC HSP: P28867; IPTG.
CC InterPro: IPR000308; C2.
CC InterPro: IPR02219; DAG_PE_bind.
CC InterPro: IPR033961; PKinase_C.
CC InterPro: IPR033719; Prot_Kinase.
CC InterPro: IPR002290; Ser_Thr_Pkinase.
CC Pfam: PFC0168; C2; 1.
CC Pfam: PFC0130; DAG_PE_bind; 2.
CC Pfam: PFC0369; PKinase; 1.
CC Pfam: PFC433; PKinase; C; 1.
CC PRINTS: PR00038; DAGPECDOMAIN.
CC ProDom: P000031; Prot_Kinase; 1.
CC SMART: SM00109; C1; 2.
CC SMART: SM00239; C2; 1.
CC SMART: SM00133; S_TK_X; 1.
CC SMART: SM00223; S_TK; 1.
CC PROSITE: PS00499; C2_DOMAIN_1; FALSE_NEG.
CC PROSITE: PS00004; C2_DOMAIN_2; 1.
CC PROSITE: PS0479; DAG_PE_BIND_DOM; 2.
CC PROSITE: PS02081; DAG_PE_BIND_DOM; 2; 2.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS02108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Transferase; Serine/threonine-protein kinase;
KW Phorbol-ester binding; Zinc; Repeat.
FT DOMAIN 1 128 C2 DOMAIN.
FT DOMAIN 177 226 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 248 297 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 403 663 PROTEIN KINASE.
FT NP BIND 403 417 ATP (BY SIMILARITY).
FT BINDING 432 432 ATP (BY SIMILARITY).
FT ACT SITE 527 527 BY SIMILARITY.
SQ SEQUENCE 743 AA: 84413 MW: 4C982C563CA2B659 CRC64;
Query Match 65.5% Score 38; DB 1; Length 743;
Best Local Similarity 66.7% Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGRPPPE 9
DE 595 VVAGOPPE 603
RESULT 33

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DPOL THEG8
ID DPOL THEG8 STANDARD; PRT: 1699 AA.
AC 39HH84.
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase (EC 2.7.7.7) [Contains: Endonuclease P1-TspG81]
DE (EC 3.1.1.1) [Tsp-G8A pol-1 intein]; Endonuclease P1-TspG81;
DE (EC 3.1.1.1) [Tsp-G8A pol-2 intein];
GN POL OR POL1.
CS Thermococcus sp. (strain G8A).
CC Archaea: Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
CC Ther: Thermococcus.
CX NCBI_TaxID=10553.
RN 1.
SEQUENCE FROM N.A.
RA Querolacu J.J.E., Cambon M.A., Jongsomjit P., Barbier G.
RT "Thermococcales taxonomy and phylogeny based on the comparative use of
RT 16S rDNA, 16S-23S rRNA intergenic spacer and family B DNA polymerase
RT genes".
RI Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE
CC EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY (BY SIMILARITY).
CC FUNCTION: P1 TSPG81 AND P1-TSPG81 ARE ENDONUCLEASES
CC (POTENTIAL).
CC CATALYTIC ACTIVITY: N deoxyribonucleoside triphosphate + N diphosphate
CC + H2O = NMP + H2O.
CC 1. THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
CC A POST-TRANSCRIPTIONAL EXCISION OF THE INTERVENING REGION (INTEIN)
CC FOLLOWED BY PEPTIDE LIGATION.
CC SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE B FAMILY.
CC 1. SIMILARITY: IN THE INTEIN SECTION, BELONGS TO THE HOMING
CC ENDONUCLEASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch.)
CC
CC EMBL: A225333; CAC:2850.1;
CC IPI: B567; P56689; ITGO.
CC InterPro: IPR006122; ENA_pol_B
CC InterPro: IPR006134; ENA_pol_B
CC InterPro: IPR006133; DNA_pol_B_exo
CC InterPro: IPR003586; Hedgehog_hinh
CC InterPro: IPR003587; Hedgehog_hinh
CC InterPro: IPR003541; Intein
CC InterPro: IPR003542; Intein_endom
CC InterPro: IPR003578; POL2.
CC Pfam: PF00126; ENA_pol_B_3.
CC Pfam: PF00104; ENA_pol_B_exo_1.
CC PRINTS: PR00379; INTEIN_
CC SMART: SM03305; HINLC_2.
CC SMART: SM03306; HINLN_2.
CC SMART: SM03486; POLB_1.
CC TIGRfam: TIGR01443; Intein_Cterm_1.
CC TIGRfam: TIGR01445; Intein_Nterm_1.
CC TIGRfam: TIGR00592; pol2_2.
CC PROSITE: PS00116; DNA_POLYMERASE_B_FALSE_NUC
CC PROSITE: PS00818; INTEIN_CTERM_2.
CC PROSITE: PS00819; INTEIN_ENDONUCLEASE_2.
CC PROSITE: PS00817; INTEIN_NTERM_2.
CC Transferase; DNA-directed DNA polymerase; DNA replication.
CC DNA-binding; Hydroxylase; Nuclease; Exonuclease; Multifunctional enzyme;
CC Protein splicing; Autocatalytic cleavage; Endonuclease; Intein homing.
CC CHAIN 1 491 DNA POLYMERASE, 1ST PART.
CC CHAIN 492 1026 ENDONUCLLEASE P1 TSPG81.
CC CHAIN 1027 1075 DNA POLYMERASE, 2ND PART.
CC CHAIN 1076 1464 ENDONUCLLEASE P1-TSPG81.1.

SQ CHAIN 1465 1699 DNA POLYMERASE, 3RD PART.
SQ SEQUENCE 1699 AA; 197323 MW; F389B4351F0B12D3 CRC64;

Query Match 65.5%; Score 38; DB 1; Length 1699;
Best Local Similarity 72.7%; Pred. No. 48;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLIGRPPEETS 1:
DB 629 ILGLPPEETS 639

RESULT 34
NHAB PSECL STANDARD; PRT: 220 AA.
AC P27783;
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nitrile hydratase subunit beta (EC 4.2.1.84) (Nitrilase) (NHase);
GN NTHB.
CS Pseudomonas chlororaphis (Pseudomonas aureofaciens).
CC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
CC Pseudomonadaceae; Pseudomonas.
CX NCBI_TaxID=333.
RN 1.
SEQUENCE FROM N.A.; AND SEQUENCE OF 1-23 AND 158-170.
RC STRAIN=B23;
RX MEDLINE=91193202; PubMed=2013568;
RA Nishiyama M., Horinouchi S., Kobayashi M., Nagasawa T., Yamada H.,
RA Beppu T.
RT "Cloning and characterization of genes responsible for metabolism of
RT nitrile compounds from Pseudomonas chlororaphis B23."
RL J. Bacteriol. 173:2465-2472(1991).
CC FUNCTION: NHASE CATALYZES THE HYDRATION OF VARIOUS NITRILE
CC COMPOUNDS TO THE CORRESPONDING AMIDES. INDUSTRIAL PRODUCTION OF
CC ACRYLAMIDE IS NOW BEING DEVELOPED USING SOME OF THESE ENZYMES.
CC CATALYTIC ACTIVITY: An aliphatic amide + a nitrile + H2O.
CC SUBUNIT: Heterodimer of an alpha and a beta chain.
CC SIMILARITY: BELONGS TO THE NITRILE HYDRATASE SUBUNIT BETA FAMILY.
CC
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CC or send an email to license@isb-sib.ch.)
CC
CC EMBL: D90216; BAA1434.1;
CC IPI: B42725; B42725.
CC HSP: P13449; 2AHJ.
CC InterPro: IPR001168; NHase_beta.
CC Pfam: PF02211; NHase_beta_1.
CC KW Lyase.
SQ SEQUENCE 220 AA; 24545 MW; 151AE1C5F14C4864 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 220;
Best Local Similarity 75.0%; Pred. No. 8.5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLGRPPE 9
DB 118 LIGRPPE 125

RESULT 15
STKC RAT STANDARD; PRT: 343 AA.
AC Q55C99;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 43, Last annotation update)

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DE Serine/threonine protein kinase 12 (EC 2.7.1.37) (Aurora and Ipl-
DE like midbody-associated protein 1) (AIM 1) (Aurora-B).
GN STK12 OR AIM1
OS Rattus norvegicus (rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; T-SSUE=Testis;
RX MEDLINE=98119810; PubMed=9455992;
RA Terada Y., Tatsuka M., Suzuki F., Yasuda Y., Fujita S., Inoue M.;
PT "AIM 1, a mammalian midbody-associated protein required for
RT cytokinesis";
RL EXPC J. 17:663-676(1998);
CC -!- FUNCTION: Maybe directly involved in regulating the cleavage of
CC polar spindle microtubules and is a key regulator for the onset of
CC cytokinesis during mitosis (by similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to the midzone of central spindle
CC in late anaphase and concentrated into the midbody in telophase
CC and cytokinesis. Colocalized with gamma tubulin in the mid-body
CC (by similarity).
CC -!- TISSUE SPECIFICITY: High level expression seen in the testis. It
CC is also expressed in the spleen, lung and heart. Expressed in the
CC G2/M phase of the cell cycle.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC
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CC
CC EM551 D89731; BAA23794.1;
DR HSP67 C63450.1; NC6
DR InterPro: IPR002052; N6_Mtase.
DR InterPro: IPR003719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF03569; kinase_1.
DR Pfam: PF03601; Prot_kinase_1.
DR SMART: SM02220; STKC_1.
DR PROSITE: PS00107; PROTEIN KINASE ATP_1.
DR PROSITE: PS00108; PROTEIN KINASE ST_1.
DR PROSITE: PS00117; PROTEIN KINASE D_1.
KW Cell cycle; Transferase; Serine/threonine protein kinase; ATP binding.
FT DOMAIN 60 330 PROTEIN KINASE
FT NP_BIND 86 94 ATP (BY SIMILARITY)
FT BINDING 109 109 ATP (BY SIMILARITY)
FT ACT_SITE 203 203 BY SIMILARITY
SQ SEQUENCE 433 AA; 39234 MW; 27E740D0E2A7598 CEM44;
Query March 63.8%; Score 17; DB 1; Length 393;
Best local similarity 50.0%; Pred. No. 14;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLLGRPPFET 10
DQ 269 LNVGNPPFES 278
RESULT 36
STKC_MOUSE
ID STKC_MOUSE STANDARD; PRT; 345 AA.
AC Q70126; Q61892;
DT 28-FEB-2003 (rel. 41, Created)
DT 28-FEB-2003 (rel. 41, Last sequence update)
DT 15-SEP-2003 (rel. 42, Last annotation update)
DE Serine/threonine protein kinase 12 (EC 2.7.1.37) (Aurora-related

DE kinase 2) (Serine/threonine protein kinase 5) (STK-1) (Aurora-B).
GN STK12 OR STK5 OR ARK2 OR STK1.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; T-SSUE=Testis;
RX MEDLINE=96194801; PubMed=9647446;
RA Niwa H., Abe K., Kimisada T., Yamamura K.;
PT "Cell-cycle-dependent expression of the STK-1 gene encoding a novel
RL murine putative protein kinase";
RL Gene 169:197-201(1998);
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RX MEDLINE=98184339; PubMed=9514916;
RA Shindo M., Nakano H., Kuroyanagi H., Shirasawa T., Mihara M.,
RA Gilbert D.J., Jenkins N.A., Copeland N.G., Yagita H., Okumura K.;
PT "cDNA cloning, expression, subcellular localization, and chromosomal
RT assignment of mammalian aurora homologues, aurora-related kinase (ARK)
RT 1 and 2";
RL Biochem. Biophys. Res. Commun. 244:285-292(1998);
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Collins B., Buetow K.H., Buetow C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Sapetchno M., Soares X.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
RA Bosak S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunatane P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay J.J., Huys S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey C., Helton E., Ketteran M., Maman A., Rodrigues S., Sanchez A.,
RA Whitting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki Y.I., Skalska U., Smalusz D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra V.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May be directly involved in regulating the cleavage of
CC polar spindle microtubules and is a key regulator for the onset of
CC cytokinesis during mitosis (by similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBCELLULAR LOCATION: Localized to the midzone of central spindle
CC in late anaphase and concentrated into the midbody in telophase
CC and cytokinesis. Colocalized with gamma tubulin in the mid-body
CC (by similarity).
CC -!- TISSUE SPECIFICITY: Expressed in testis, intestine and spleen. All
CC of them are tissues that contain a large number of proliferating
CC cells. Expressed during S phase, in a cell-cycle-
CC dependent fashion.
CC -!- DEVELOPMENTAL STAGE: Strongly expressed in 8.5 and 12.5 dpc.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC AURORA SUBFAMILY.
CC
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CC EMBL; D31099; BAA04658.1; ..

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DR EMBL: U69107; AAC12483.1; 1;
DR EMBL: BC003262; AA03262.1; 1;
DR HSSP: Q63450; A06
DR MGD: NC0107188; Stk12.
DR InterPro: IPR002052; N6_Mtase.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR002290; Ser_Thr_Kinase
DR InterPro: IPR001245; Tyros_Pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD00001; Prot_Kinase; 1.
DR SMART: SM0225; S_TK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR Cell Cycle: Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 82 332 PROTEIN KINASE.
FT NP_BIND 84 96 ATP (BY SIMILARITY).
FT BINDING 111 111 ATP (BY SIMILARITY).
FT ACT_SITE 205 205 BY SIMILARITY.
FT CONFLICT 44 44 R -> W (IN REF. 1).
SQ SEQUENCE 345 AA; 39124 MW; C1CD8B6BDEA0AC CR664;

Query Match 63.8%; Score 37; DB 1; Length 380;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPFET 10
DI 201 LNVGPRPFS 280

RESULT 38
PK3 CAPEL STANDARD; PRT; 380 AA.
AC P54317
DT 01-OCT-1998 (Ref. 34, Created)
DI 01-OCT-1998 (Ref. 34, Last sequence update)
DI 16-SEP-2003 (Ref. 42, Last annotation update)
DE Serine/threonine-protein kinase ptk3 EC 2.7.1.1.
GN PTK3
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; Deltaaproteobacteria; Myxococcaceae.
OC Cystobacteriaceae; Myxococcaceae; Myxococcus
CX NCBI:TaxID=14.
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=9304501;
RA Zhang W., Inouye M., Inouye S.
RT "Regulation of the differentiation of Myxococcus xanthus
by Ptk5 and Ptk6, eukaryotic-like serine protein kinases."
Mol. Microbiol. 25:435-447(1998).
CC FUNCTION: Ptk5 and ptk6 may have reciprocal roles in growth and
development. Ptk5 may be a kinase that negatively regulates
development.
CC CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphorylated
protein.
CC SUBCELLULAR LOCATION: Cytoplasmic.
CC DEVELOPMENTAL STAGE: Expressed constitutively throughout the life
cycle, with slight increases at an early stage of development.
CC PTM: Autophosphorylated at serine residues.
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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CC EMBL: U69107; AAC12483.1; 1;
CC EMBL: U58750; AA03642.1; 1;
CC PIR: T29221; T29223.
CC HSSP: Q63450; A06.
CC WormPep: P55014; P507285.
CC GO: GO:0005634; Cytoplasm; ISS.
CC GO: GO:0005624; ATP binding activity; ISS.
CC GO: GO:0004674; Protein serine/threonine kinase activity; ISS.

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DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_Thr_kinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD00001; Prot_Kinase; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 9 376 PROTEIN KINASE.
FT NP_BIND 15 23 ATP (BY SIMILARITY).
FT BINDING 38 38 ATP (BY SIMILARITY).
FT ACT_SITE 244 244 BY SIMILARITY.
SQ SEQUENCE 380 AA; 41924 MW; DC3ADFB2420C1F1 CR664;

Query Match 63.8%; Score 37; DB 1; Length 380;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPFET 9
DI 314 LNSGRPFED 222

RESULT 38
PLK3 CAPEL STANDARD; PRT; 615 AA.
AC Q20845;
DI 28-FEB-2003 (Ref. 41, Created)
DI 28-FEB-2003 (Ref. 41, Last sequence update)
DI 28-FEB-2003 (Ref. 41, Last annotation update)
DE Serine/threonine-protein kinase plk-3 EC 2.7.1.1. (Polo-like
kinase 3).
GN PLK-3 OR PLC2 OR P55G1.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Pelodoriace; Caenorhabditis.
CX NCBI:TaxID=6219;
RN 11
RP SEQUENCE FROM N.A.
RC MEDLINE=99304501; PubMed=10376213;
RA Qiyang B., Wang Y., Dai W.
RT "Caenorhabditis elegans contains structural homologs of human plx and
Plx "1".
RL DNA Seq. 10:109-111(1993).
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol; N2;
RA Murray J., Lee T.
RT Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC FUNCTION: May be required for cell division and may have a role
during G1 or S phase (by similarity).
CC SUBCELLULAR LOCATION: Nuclear (by similarity).
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CC05/PCLO SUBFAMILY.
CC SIMILARITY: Contains 2 PCLO box domains.
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or send an email to license@sib-sib.ch.)
CC EMBL: AF59024; AAC14425.1; 1;
CC EMBL: U58750; AA03642.1; 1;
CC PIR: T29221; T29223.
CC HSSP: Q63450; A06.
CC WormPep: P55014; P507285.
CC GO: GO:0005634; Cytoplasm; ISS.
CC GO: GO:0005624; ATP binding activity; ISS.
CC GO: GO:0004674; Protein serine/threonine kinase activity; ISS.

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DR GO: 00-060468; P:protein amino acid phosphorylation; ISS.
DR InterPro: IPR000659; PLOC box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00669; pkinase; 1.
DR Pfam: PF00659; PLOC box; 2.
DR Pfam: PF00659; PLOC box; 1.
DR SMART: SM00229; S_TK; 1.
DR PROSITE: PS00137; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00137; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00139; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00139; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00139; PLOC BOX; 2.
DR PROSITE: PS00139; PLOC BOX; 1.
KW ATP-binding; Serine/threonine-protein kinase; Disordered; Repeat;
KW Nuclear protein.
FT DOMAIN 35 286 PROTEIN_KINASE
FT BINDING 41 49 ATP BY SIMILARITY.
FT BINDING 64 64 ATP BY SIMILARITY.
FT ACT_SITE 158 158 BY SIMILARITY
FT DOMAIN 402 463 PLOC BOX 1.
FT DOMAIN 525 573 PLOC BOX 2.
SQ SEQUENCE 615 AA; 70436 MW; D510727329C4P26 CR644;

Query Match 63.8%; Score 37; DB 1; Length 644;
Best Local Similarity 60.8%; Pred No. 27;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 1 MLCGRPFEE 10
DB 245 MLCGRPFEE 234

RESULT 37
KPC: APLCA STANDARD; PRT; 349 AA.
AC Q16974;
DT 30-MAY-2000 (Ref. 39, Created);
DT 30-MAY-2000 (Ref. 39, Last sequence update);
DT 28-FEB-2003 (Ref. 41, Last annotation update);
DE Calcium-dependent protein kinase C (EC 2.7.1.1) (AFL 1)
PKCS.
GN Aplysia californica (California sea hare).
OS Aplysia californica (Mollusca: Gastropoda); Orthogastropoda;
OC Acanthogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
OC Aplysiidae; Aplysiidae; Aplysia.
CX RPT: TaxID=6500;
PM 11;
RF MEDLINE:91132620; Pubmed:1869917;
RA Kruger K.E., Sossin W.S., Sacktor T.C., Fagan J.F., Sacktor T.C.,
Schwartz J.H.
PT Cloning and characterization of Ca2+-dependent protein kinase C
independent PKCs expressed in Aplysia sensory cells.
RI J. Neurosci. 11:2193-2199;1991.
RN 12;
RP CHARACTERIZATION.
EX MEDLINE:9119487; Pubmed:8449941;
SA Sossin W.S., Diaz-Arreola R., Schwartz J.H.;
PT Characterization of two isoforms of protein kinase C in the nervous
system of Aplysia californica.
RI J. Biol. Chem. 268:5763-5768(1993).
RN 13;
RP CHARACTERIZATION.
EX MEDLINE:95334636; Pubmed:9668035;
SA Peipo A.X., Pan X., Sossin W.S.;
PT The role of C2 domains in Ca2+-activated and Ca2+-independent protein
kinase Cs in Aplysia.
RI J. Biol. Chem. 273:19040-19048(1998).
RN 14;
RP ERATUM.
SA Peipo A.X., Pan X., Sossin W.S.;
RI J. Biol. Chem. 273:22856-22856(1998).
CC FUNCTION: THIS IS CALCIUM-DEPENDENT, PHOSPHORYLATION-DEPENDENT,
SERINE AND THREONINE-SPECIFIC KINASE. ACTIVATION OF PKC BY

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CC SEROTONIN RESULTS IN PRESYNAPTIC FACILITATION OF DEPRESSED
CC SENSORY-TO-MOTOR NEURON SYNAPSES, WHICH IS THOUGHT TO UNDERLIE
CC BEHAVIORAL DISHABITUATION.
CC FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS (BY
CC SIMILARITY).
CC ENZYME REGULATION: ACTIVATED BY PHOSPHATIDYLSELINE.
CC SUBCELLULAR LOCATION: CYTOSOL; CYTOSOL; TRANSLOCATED TO NEURONAL
CC MEMBRANES.
CC SIMILARITY: Contains 2 zinc dependent phorbol-ester and DAG
CC binding domains.
CC SIMILARITY: Contains 1 C2 domain.
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M94983; AAA27770.2;
CC HSP; P05497; ITEN
CC InterPro: IPR000008; C2
CC InterPro: IPR002219; DAG_PE_bind.
CC InterPro: IPR000361; Pkinase_C.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam: PF00168; C2; 1.
CC Pfam: PF00130; DAG_PE_bind; 2.
CC Pfam: PF00069; pkinase; 1.
CC Pfam: PF0433; pkinase_C; 1.
CC PRINTS: PR0360; C2DOMAIN.
CC PRINTS: PR00008; DAGPECDOMAIN.
CC ProDom: PD00001; Prot_kinase; 1.
CC SMART: SM00109; C1; 2.
CC SMART: SM00239; C2; 1.
CC SMART: SM00133; S_TK; 1.
CC SMART: SM00220; S_TK; 1.
CC PROSITE: PS00499; C2_DOMAIN_1; 1.
CC PROSITE: PS00004; C2_DOMAIN_2; 1.
CC PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
CC PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Transferrase; Serine/threonine protein kinase;
KW Phorbol ester binding; Zinc; Repeat;
KW PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 22 71 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 96 135 C2 DOMAIN.
FT DOMAIN 157 244 C2 DOMAIN.
FT DOMAIN 320 578 PROTEIN_KINASE.
FT NF_BIND 326 334 ATP (BY SIMILARITY).
FT BINDING 349 349 ATP (BY SIMILARITY).
FT ACT_SITE 444 444 BY SIMILARITY.
SQ SEQUENCE 649 AA; 74075 MW; A53253399284E330 CR664;

Query Match 63.8%; Score 37; DB 1; Length 649;
Best Local Similarity 60.7%; Pred No. 27;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 1 MLCGRPFEE 9
DB 512 MLCGRPFEE 520

RESULT 40
KPC: LYTP1 STANDARD; PRT; 656 AA.
AC Q25378;

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GenCore version 5.1.6
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CV proteins Protein search, using sw model

Run on: November 14, 2003, 14:34:38 ; Search time 15 seconds

(without alignments)

81,102 Million cell updates/sec

Title: US-09-736-076-19

Perfect score: 58

Sequences: 1 MULGRPPPTS 11

Scoring table: HIGSUN62

Gapop 10.0 ; Gapext 0.5

Searched: 810525 seqs, 258052654 residues

Total number of hits satisfying chosen parameters: 810525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTREXBL 231:
1: sp_archea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organeller:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacterioph:
17: sp_archea:

Pred. No. is the number of results predicted by the model to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total search distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	94.8	316	Q9BDK4	Q9BDK4 sus scrofa
2	55	94.8	372	Q8N7M6	Q8N7M6 homo sapien
3	55	94.8	666	Q90XS4	Q90XS4 xenopus lae
4	55	94.8	682	Q8K226	Q8K226 mus musculu
5	49	84.5	526	Q9BDK8	Q9BDK8 sus scrofa
6	49	84.5	598	Q8K232	Q8K232 xenopus lae
7	49	84.5	623	Q8L035	Q8L035 asterina pe
8	48	82.8	769	Q97143	Q97143 drosophila
9	46	79.3	324	Q9CV86	Q9CV86 mus musculu
10	46	79.3	925	Q8R015	Q8R015 mus musculu
11	46	79.3	925	Q64702	Q64702 mus musculu
12	46	79.3	970	Q36Q95	Q36Q95 homo sapien
13	46	79.3	970	Q30444	Q30444 homo sapien
14	46	79.3	970	Q81Y60	Q81Y60 homo sapien
15	45	77.6	568	Q8MX06	Q8MX06 caenorhabd:
16	45	77.6	592	Q5GRE7	Q5GRE7 centricentri:

17	45	77.6	749	5	Q8MXG7	Q8MXG7 caenorhabdi
18	45	77.6	780	5	Q76360	Q76360 caenorhabdi
19	44	75.9	485	13	Q90XS2	Q90XS2 xenopus lae
20	44	75.9	557	13	Q90XS3	Q90XS3 xenopus lae
21	44	75.9	767	5	Q15882	Q15882 trypanosoma
22	43	74.1	80	13	Q91891	Q91891 xenopus lae
23	43	74.1	673	5	Q62567	Q62567 suberites d
24	43	74.1	677	5	Q96997	Q96997 godia cydo
25	42	72.4	456	5	Q8MYF1	Q8MYF1 dictyosteli
26	42	70.7	346	13	Q8C0S8	Q8C0S8 brachydiano
27	41	70.7	504	11	Q8K0J7	Q8K0J7 mus musculu
28	41	70.7	646	4	Q96CV1	Q96CV1 homo sapien
29	39	67.2	153	16	Q84342	Q84342 chlamydia t
30	39	67.2	235	5	Q9GP07	Q9GP07 leishmania
31	39	67.2	358	5	Q00872	Q00872 leishmania
32	39	67.2	690	16	Q8G6P9	Q8G6P9 blattobacte
33	39	67.2	1337	2	Q9KCN7	Q9KCN7 myxococcus
34	38	65.5	240	11	Q63432	Q63432 rattus norv
35	38	65.5	256	16	Q9EPA6	Q9EPA6 campylobact
36	38	65.5	256	16	Q9KXT3	Q9KXT3 thermotoga
37	38	65.5	257	16	Q8Y2AC	Q8Y2AC ralstonia s
38	38	65.5	305	5	Q01427	Q01427 caenorhabdi
39	38	65.5	332	16	Q9AZ29	Q9AZ29 streptomyce
40	38	65.5	434	16	Q8EM12	Q8EM12 oceanobacil
41	38	65.5	536	17	Q8Z2C9	Q8Z2C9 pyrobaculum
42	38	65.5	554	5	Q95778	Q95778 drosophila
43	38	65.5	605	10	Q932C9	Q932C9 arabidopsis
44	38	65.5	656	10	Q95770	Q95770 arabidopsis
45	38	65.5	660	16	Q9FC15	Q9FC15 corynebacte

ALIGNMENTS

RESULT 1

Q9BDK4 PRELIMINARY; PRT; 316 AA.

AC Q9BDK4;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Serum-inducible Kinase (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CX NCBI TaxID:9823;
RN 11;
RP SEQUENCE FROM N.A.
RA Anger M., Kues W.A., Klima W., Motlik J., Carnwath J.W., Niemann H.;
RT "Porcine serum-inducible Kinase."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF348424; AAK27154.1;
DR InterPro; IPR000959; POLO box.
DR InterPro; IPR000719; Prot_Kinase.
DR Pfam; PF00669; pkinase; 1;
DR Pfam; PF00659; POLO box; 1;
DR ProDom; PD000503; Prot_Kinase; 1;
DR PROSITE; PS00078; POLO_BOX; 1;
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1;
KW ATP-binding; Kinase; Transferase.
FT NON_TER 1;
FT NON_TER 316;
SQ SEQUENCE 316 AA; 35330 MW; F63B8E4A2691D62F CRC64;

Query Match 94.8%; Score 55; DB 6; Length 316;
Best Local Similarity 90.9%; Pred. No. 0.029;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MULGRPPPTS 11

DB 25 MULGRPPPTS 35

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DR EMBL: AF357840; AAL30175.1; -.
DR InterPro: IPR000959; POLO_box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_Thr_pkinase.
DR Pfam: PF00659; pkinase.1
DR Pfam: PF00659; POLO_box.2.
DR ProDom: PDC00001; Prot_kinase.1.
DR SMART: SM0220; S_TKc.1.
DR PROSITE: PS50078; POLO_BOX; 2.
DR PROSITE: PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW SEQUENCE 666 AA; 76322 MW; AB4D8F83D5B5D4FC CRC64;

Query Match 94.8%; Score 55; DB 13; Length 666;
Best Local Similarity 90.9%; Pred.No.0.063;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : MLGRRPPFFTS 1:
|||||
DB 254 MLGRRPPFFET 264

RESULT 4
CRX226 PRELIMINARY; PRT; 682 AA.
ID Q8K226
AC Q8K226;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Serine-inducible kinase.
DE Serum-inducible kinase.
GN SNK.
GS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
CX NCBI_TaxID:10090;
CC [1]_TaxID:10090;
RN SEQUENCE FROM N.A.
RA Strausberg R.;
RJ Submitted (JUL-2002) to the EMBL/GenBank/DBC databases.
RJ EMBL: BC034513; AAL34513.1; -.
DR MGD: MGI:129979c; Ssk.
DR InterPro: IPR000959; POLO_box.
DR InterPro: IPR002719; Prot_kinase.
DR InterPro: IPR002290; Ser_Thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00659; pkinase.1.
DR Pfam: PF00659; POLO_box.2.
DR ProDom: PDC00001; Prot_kinase.1.
DR SMART: SM0220; S_TKc.1.
DR SMART: SM0219; TyPKc.1.
DR PROSITE: PS50078; POLO_BOX; 2.
DR PROSITE: PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Transferase.
KW SEQUENCE 682 AA; 77777 MW; 89BA65C8DFAFFD95 CRC64;

Query Match 94.8%; Score 55; DB 11; Length 682;
Best Local Similarity 90.9%; Pred.No.0.063;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY : MLGRRPPFFTS 1:
|||||
DB 270 MLGRRPPFFET 280

RESULT 5
CRX6P9 PRELIMINARY; PRT; 526 AA.
ID Q9B0P9
AC Q9B0P9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

```

DT 01-MAR-2003 (TREMBlrel. 17, Last sequence update);
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update);
 DE Polio-like protein kinase (Fragment);
 OS Sus scrofa (Pig);
 CC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae, Sus;
 CX NCBI_TaxID=9823;
 RN 1;
 RP SEQUENCE FROM N.A.
 RA Anger, M., Kues W.A., Kiria J., Wielenz M., Votlik M., Garavito J.M.,
 RA Krumm H.,
 RT "Expression of polio-like kinase in cell cycle synchronized porcine
 RT fetal fibroblasts";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 CC 1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 EP EMBL: AF359221; AAK28550.1; ...
 DE HSP: Q63450; I406.
 DR InterPro: IPR000959; POLC box.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR Pfam: PF00069; Pkinase; 2.
 DR Pfam: PF00659; POLC_box; 2.
 DR Pfam: PF00069; Prot_kinase; 1.
 DR SMART: SW00220; S_TKC; 1.
 DR PROSITE: PS0075; POLC_BOX; 2.
 DR PROSITE: PS0101; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS0211; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS0188; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NCN_TPR 526 526
 FT NCN_TPR 526 526
 SQ SEQUENCE 526 AA, 60399 MW, 126185309820RPI CR:64;

 Query Match 84.5%; Score 49; DB 4; Length 526;
 Best Local Similarity 72.7%; Pred. No. 0.74;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

 QY 1 MLCGRPPPTS 11
 DB 149 LLVGRPPPTS 203

 RESULT #
 ID C97143 PRELIMINARY; PRT; 149 AA
 AC C97143;
 DT 01-FEB-1997 (TREMBlrel. 22, Created);
 DT 01-FEB-1997 (TREMBlrel. 22, Last sequence update);
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update);
 DE P1X1;
 OS Xenopus laevis (African clawed frog);
 CC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 CC Amphibia; Anura; Mesobatrachia; Pipididae; Pipidae;
 CC Xenophodidae; Xenopus;
 CX NCBI_TaxID=8355;
 RN 1;
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96355660; PubMed=8703070;
 RA Kumada A., Lumphry W.G.;
 RT "Purification and molecular cloning of P1X1, a cAMP-dependent kinase
 RT from Xenopus egg extracts";
 RL Science 273:1377-1380(1996);
 CC 1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 EP EMBL: U58205; AAC60017.1; ...
 DE HSP: Q63450; I406.
 DR InterPro: IPR000959; POLC box.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00659; POLC_box; 2.
 DR Pfam: PF00069; Prot_kinase; 1.
 DR SMART: SW00220; S_TKC; 1.
 DR PROSITE: PS0075; POLC_BOX; 2.

DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 598 AA, 68211 MW, 246719591122556 CRC64;

 Query Match 84.5%; Score 49; DB 13; Length 598;
 Best Local Similarity 72.7%; Pred. No. 0.74;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MLCGRPPPTS 11
 DB 235 LLVGRPPPTS 245

 RESULT #
 ID Q81U35 PRELIMINARY; PRT; 623 AA
 AC Q81U35;
 DT 01-MAR-2003 (TREMBlrel. 23, Created);
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update);
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update);
 DE Polio-like kinase.
 GN PLX.
 OS Asterina pectinifera (Starfish);
 CC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
 CC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina;
 CC NCBI_TaxID=7594;
 RN 11;
 RP SEQUENCE FROM N.A.
 RA Uchida T.O., Tachibana K., Kishimoto T.;
 RT "Starfish PLX";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB084455; BAC22692.1; ...
 KW Kinase;
 SQ SEQUENCE 623 AA, 70329 MW, CFCDI9008020724A CRC64;

 Query Match 84.5%; Score 49; DB 5; Length 623;
 Best Local Similarity 72.7%; Pred. No. 0.78;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MLCGRPPPTS 11
 DB 223 LLVGRPPPTS 243

 RESULT #
 ID C97143 PRELIMINARY; PRT; 769 AA
 AC C97143;
 DT 01-MAY-1999 (TREMBlrel. 10, Created);
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update);
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update);
 DE SAK protein.
 GN SAK OR CG7186.
 OS Drosophila melanogaster (Fruit fly);
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila;
 CX NCBI_TaxID=7227;
 RN 11;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., J. P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vande L.M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blaze R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Batley R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Berni P.V., Berntson P.P., Bhandari D., Bolshakov S.,

PA Borkava S., Botchan M.R., Bonck C., Bruckstein P., Brothier F.,
 RA Butts K.C., Busam D.A., Butler H., Cadieux E., Center A., Chandra I.,
 RA Cherry G.M., Clarke S., Danke S., Davenport L.B., Davis P.,
 RA De Fabros B., Decker Z., Deng Z., Doyle A.D., Dow J., Dierckx S.M.,
 RA Dodson K., Doup B.E., Downes M., Duran Rocha S., Duvoy R., Dunn P.,
 RA Duttin K.J., Evangelista A.C., Furrer M., Furtado S., Fleckenmann W.,
 RA Eberhart C., Evangelista A.C., Garg M.S., Gallati W., Glasner K.,
 RA Glodok A., Gora F., Gorrell J.H., Gu Z., Guan F., Harlin V.,
 RA Harris M.D., Harvey D., Heiman T., Hernandez J.P., Hock J.,
 RA Heaton D., Hendon D., Howland T., Wei Y.H., Ikegami C.,
 RA Jafari M., Kalish F., Karpen R.H., Ku Z., Kunkin S.A., Kunkin K.A.,
 RA Kimmel B.E., Kodara C.D., Kraft T., Kravitz S., Krip C., Lai G.,
 RA Lasko P., Lee Y., Levitsky A.A., Li J., Li X., Ling Y., Lin X.,
 RA Liu X., Muller B., McIntosh T.C., Mead M.F., Schneider Z.,
 RA Markov G., Milshina N.V., Mohary G., Morris C., Moshroff A.,
 RA Mouni S.M., Myer M., Murphy A., Murphy B., Nazzari B., Nelson D.L.,
 RA Nelson S.M., Nelson K.A., Nixon K., Nussken D.P., Paele C.M.,
 RA Pakizlo Y., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Rebertus K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden Klamis I., Simpson V., Skupski M.P., Smith T.,
 RA Spies E., Spadling A.C., Stalderon X., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Massarman D.A., Weintraub G.M., Weissbach J.,
 RA Williams S.Y., Woodage T., Wolley K.C., Wu D., Yang S., Yan Q.A.,
 RA Ye C., Yeh R., Zaveri G.S., Zhao X., Zhang G., Zhao G., Zheng L.,
 RA Zhou X.H., Zhou F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of Drosophila melanogaster",
 RA Science 287:2185-2195 (2000).
 RA "Functional annotation of a full-length mouse cDNA collection",
 RA Nature 409:695-697 (2001).
 RA EMBL: AK006827; BAE24759.1; ...
 RA HSSP: C00534; 1B18.
 RA XCD: MG1101783; SK18.
 RA InterPro: IPR000719; Prot_kinase.
 RA InterPro: IPR002290; Ser_thr_kinase.
 RA Pfam: PF00069; pkcinase; 1.
 RA PRINTS: PR0109; TYRKINASE.
 RA ProDom: PD000001; Prot_kinase; 1.
 RA SMART: SV00220; S_TKc; 1.
 RA PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 RA PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 RA PROSITE: PS0109; PROTEIN_KINASE_TYR; 1.
 RA ATP-binding; Transferase.
 RA NON_TER 324 324
 RA SEQUENCE 324 AA; 46488 MW; 04347065DFE196CC CRC64;

Query Match 82.8% Score 46; DP 11; Length 324;
 Best Local Similarity 80.0% Pred. NO 1.5;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VLGGSTPEET 10
 DI 246 LGGSTPEET 215

RESULT 0
 QY005 PRELIMINARY; PRT: 324 AA
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Serine/threonine kinase 18 (Frag 40
 SK18)
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN (1)_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RX MEDLINE21055660; PubMed=11217851;
 RA Kawai C., Shitagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,
 RA Akawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamana K.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Asburner K., Baralov S., Casavari T.,
 RA Fletschmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuch P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush C.,
 RA Schiri L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli P., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Butt C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kariya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Morbiers P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyono O., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection",
 RA Nature 409:695-697 (2001).
 RA EMBL: AK006827; BAE24759.1; ...
 RA HSSP: C00534; 1B18.
 RA XCD: MG1101783; SK18.
 RA InterPro: IPR000719; Prot_kinase.
 RA InterPro: IPR002290; Ser_thr_kinase.
 RA Pfam: PF00069; pkcinase; 1.
 RA PRINTS: PR0109; TYRKINASE.
 RA ProDom: PD000001; Prot_kinase; 1.
 RA SMART: SV00220; S_TKc; 1.
 RA PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 RA PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 RA PROSITE: PS0109; PROTEIN_KINASE_TYR; 1.
 RA ATP-binding; Transferase.
 RA NON_TER 324 324
 RA SEQUENCE 324 AA; 46488 MW; 04347065DFE196CC CRC64;

Query Match 79.1% Score 46; DP 11; Length 324;
 Best Local Similarity 70.0% Pred. NO 1.5;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLGGSTPEET 10
 DI 246 LGGSTPEET 215

RESULT 10
 QY005 PRELIMINARY; PRT: 325 AA
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical: 103.9 kDa protein.
 SK18.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN (1)_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RA Strausberg P.;
 RA Submitted (Apr 2002) to the EMBL/GenBank/CDJ databases.
 RA EMBL: B026785; AAB026785.1; ...
 RA XCD: MG1101783; SK18.
 RA InterPro: IPR000719; Prot_kinase.
 RA InterPro: IPR002290; Ser_thr_kinase.
 RA Pfam: PF00069; pkcinase; 1.
 RA PRINTS: PR0109; TYRKINASE.
 RA ProDom: PD000001; Prot_kinase; 1.
 RA SMART: SV00220; S_TKc; 1.
 RA PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 RA PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 RA PROSITE: PS0109; PROTEIN_KINASE_TYR; 1.
 RA ATP-binding; Transferase.
 RA NON_TER 324 324
 RA SEQUENCE 324 AA; 46488 MW; 04347065DFE196CC CRC64;


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DR InterPro: IPR000959; POLD box.
DR InterPro: IPR000119; Prot_kinase.
DR InterPro: IPR02293; Ser_thr_kinase.
DR InterPro: IPR01245; Tyr_kinase.
DR Pfam: PF00769; pkinase; 1.
DR PRINTS: PR0109; TYRKINASE.
DR PROSITE: PS02001; Prot_kinase.
DR SMART: SM0228; S_TKc; 1.
DR PROSITE: PS0019; POLD_BOX; 1.
DR PROSITE: PS0107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS0109; PROTEIN_KINASE_TYR; 1.
KW ATP binding; Kinase; Transferase.
SQ SEQUENCE 970 AA; 10895 MW; 1521456.558FRRERPS QH4.4.

Query Match: 79.3%; Score 46; DB 4; Length 970;
Best Local Similarity 70.0%; Pred. No. 4;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLGPPPET 10
DE : 204 LLIGRPPT 213

RESULT 14
QY10 PRELIMINARY; PRT: 970 AA.
AC QY10;
DT 01-VAR-2001 (TrEMBLrel. 23, Created.
DT 01-VAR-2001 (TrEMBLrel. 23, Last sequence update)
DT 01-VAR-2001 (TrEMBLrel. 23, Last annotation update)
DE Similar to serine/threonine protein kinase.
DE Hsp90 superfamily.
DE Eukaryota; Metazoa; Chordata; Chelonia; Vertebrata; Reptilia;
DE Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homin.
CX KCB: T01D-9656;
FN [1]
SQ SEQUENCE FROM N.A.
AC Straussberg R.;
DT Submitted JUN-2002; AAH16023.1;
DR EMBL: E036023; TrEMBLrel. 23.
KW Kinase; Serine/threonine-protein kinase.
SQ SEQUENCE 970 AA; 10897 MW; 42565F098111A6 QH4.4.

Query Match: 79.3%; Score 46; DB 4; Length 970;
Best Local Similarity 70.0%; Pred. No. 4;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY : MLGPPPET 10
DE : 204 LLIGRPPT 213

RESULT 14
QY10 PRELIMINARY; PRT: 569 AA.
AC QY10;
DT 01-VAR-2001 (TrEMBLrel. 22, Created.
DT 01-VAR-2001 (TrEMBLrel. 22, Last sequence update)
DT 01-VAR-2001 (TrEMBLrel. 23, Last annotation update)
DE Euk-4 protein, corresponding sequence Pf0A8.2d.
CX P55A4.2 OR EG-4;
FN Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematozoa; Chordata; Phlebotomina; Statiditidae;
OC Rhaditidae; Pelodierinae; Caenorhabditis.
CX KCB: T01D-6239;
FN [1]
SQ SEQUENCE FROM N.A.
AC STRAIN-ERISTOL N2;
DT Submitted MAY-1996; Pubmed:9851916;
DR Waterston R.;
DE Genome sequence of the nematode C. elegans, a pioneer in

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R: Investigating biology. The C. elegans Sequencing Consortium."
R: Science 282:2312-2318(1998).
RN [2]
RC STRAIN=Bristol N2.
RA Langston Y., Wohlmann P., Duckels G.,
R: "The sequence of C. elegans cosmid P55A8",
RL Submitted JUN-1999, to the EMBL/GenBank/CCDB databases.
RN [3]
RC SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted AUG-2002, to the EMBL/GenBank/CCDB databases.
DR EMBL: AF067612; AAH98011.1;
DR Wormpep; F55A8.2d; CE1542.
DR InterPro: IPR002373; CAMP_kin.
DR InterPro: IPR002374; GMP_kin.
DR InterPro: IPR000595; CNMP_binding.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR02289; Ser_thr_kinase.
DR InterPro: IPR01245; Tyr_kinase.
DR Pfam: PF00027; CNMP_binding; 2.
DR Pfam: PF00049; Pkinase; 1.
DR Pfam: PF00433; Pkinase_C; 1.
DR PRINTS: PR0103; CAMPKINASE.
DR PRINTS: PR0104; GMPKINASE.
DR ProDom: PD003001; Prot_kinase; 1.
DR SMART: SM00100; CNMP; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00886; CNMP_BINDING_1; 1.
DR PROSITE: PS00889; CNMP_BINDING_2; 1.
DR PROSITE: PS00042; CNMP_BINDING_3; 2.
DR PROSITE: PS0107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS0108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 568 AA; 65094 MW; 423AB3BD652ACE4 CRC64;

Query Match: 77.6%; Score 45; DB 5; Length 568;
Best Local Similarity 63.6%; Pred. No. 4;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGPPPET 11
DE 448 LLIGPPPEQS 458

RESULT 16
QYGPB7 PRELIMINARY; PRT: 592 AA.
AC QYGPB7;
DT 01-VAR-2001 (TrEMBLrel. 16, Created)
DT 01-VAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-VAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Polo-like kinase.
GN UP2K.
OS Hemicotritus pulcherrimus (sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinozoa; Echinozoa; Echinacea; Echinacea; Strongylocentrotidae;
OC Hemicotritus.
CX KCB: T01D-7650;
FN [1]
SQ SEQUENCE FROM N.A.
RA Yonemura I., Fujimoto H., Mabuchi I.;
R: "Cloning of sea urchin plx.",
RL Submitted MAY-2000, to the EMBL/GenBank/CCDB databases.
RN [2]
RC SEQUENCE FROM N.A.
RA Yonemura I., Fujimoto H., Mabuchi I.;
R: "Cloning of sea urchin polo-like kinase.",

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PL Submitted (MAY-2000) to the EMBL/GenBank/DBSJ databases.
 CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AB043997; BAB18588.1; .
 DR InterPro: IPR000195; AIdoc/Kec_red.
 DR InterPro: IPR000959; POLO_box.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF03659; POLO_box; 2.
 DR ProDom: PDC00001; Prot_Kinase; 1.
 DR SMART: SM0220; S_TK; 1.
 DR PROSITE: PS0063; ALCKETO_REDUCTASE; 1.
 DR PROSITE: PS03078; POLO_BOX; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS0108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine protein kinase; Transferrase.
 SQ SEQUENCE 582 AA; 66429 MW; A4774ACCAACFDESD CRC64.

Query Match 77.6%; Score 45; DB 5; Length 582;
 Best Local Similarity 70.0%; Pred. No. 5.3;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLGSRPFET 10
 DQ 218 TLVGKPFET 227

RESULT 17
 ID Q6XG7 PRELIMINARY; PRT; 749 AA.
 AC Q6XG7
 DT 01-OCT-2002 (TREMBLrel_22, Created)
 DT 01-OCT-2002 (TREMBLrel_22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel_23, Last annotation update)
 DE EG5-4 protein [corresponding sequence F55A8.2]
 GN F55A8.2 OR EG5-4
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 EV MEDLINE=99069613; PubMed=9851916;
 RA Waterston R.
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology, the C. elegans sequencing consortium
 RT Science 242:2012-2018 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Langston Y., Wohldmann P., Duckels G.
 RT "The sequence of C. elegans cosmid F55A8."
 RC Submitted (JUN-1998) to the EMBL/GenBank/DBSJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.
 RL Submitted (AUG 2002) to the EMBL/GenBank/DBSJ databases.
 DR EMBL: AF067612; AAM990.0.1; .
 DR WormPep: F55A8.2; CE31541.
 DR InterPro: IPR002373; cAMP_kin.
 DR InterPro: IPR002374; cGMP_kin.
 DR InterPro: IPR000595; cAMP_binding.
 DR InterPro: IPR000961; Pkinase_C.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF03659; POLO_box; 2.
 DR PRINTS: PR00103; CAMPKINASE.

DR PRINTS: PR00104; CGMPKINASE.
 DR ProDom: PDC00001; Prot_Kinase; 1.
 DR SMART: SM0100; cGMP; 2.
 DR SMART: SM00220; S_TK; 1.
 DR SMART: SM00133; S_TK_X; 1.
 DR SMART: SM00219; TyK; 1.
 DR PROSITE: PS00888; cAMP_BINDING; 1; 2.
 DR PROSITE: PS00889; cAMP_BINDING; 2; 2.
 DR PROSITE: PS00842; cAMP_BINDING; 3; 2.
 DR PROSITE: PS0007; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS0108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Transferrase.
 SQ SEQUENCE 749 AA; 84497 MW; ADE089F6354D93C6 CRC64.

Query Match 77.6%; Score 45; DB 5; Length 749;
 Best Local Similarity 63.6%; Pred. No. 5.3;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGSRPFET 11
 DQ 629 LMLGRPFQAS 639

RESULT 18
 ID Q76360 PRELIMINARY; PRT; 780 AA.
 AC Q76360
 DT 01-NOV-1998 (TREMBLrel_08, Created)
 DT 01-NOV-1999 (TREMBLrel_12, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel_23, Last annotation update)
 DE Hypothetical 86.7 kDa protein. F55A8.2 in chromosome IV.
 GN F55A8.2
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Langston Y., Wohldmann P., Duckels G.
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBSJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBSJ databases.
 CC -1 ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; MAY BE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF067612; AAD36954.1; .
 DR EMBL: AF067612; AAD36953.1; .
 DR KSP: P05132; IAPM.
 DR WormPep: F55A8.2a; CE19897.
 DR WormPep: F55A8.2b; CE19898.
 DR InterPro: IPR002374; cGMP_kin.
 DR InterPro: IPR000595; cAMP_binding.
 DR InterPro: IPR000961; Pkinase_C.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR002290; Ser_Thr_kinase.
 DR Pfam: PF00027; cAMP_binding; 2.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00433; Pkinase_C; 1.
 DR PRINTS: PR00104; CGMPKINASE.
 DR ProDom: PDC00001; Prot_Kinase; 1.
 DR SMART: SM0100; cGMP; 2.
 DR SMART: SM00220; S_TK; 1.
 DR SMART: SM00133; S_TK_X; 1.
 DR PROSITE: PS00888; cAMP_BINDING; 1; 2.
 DR PROSITE: PS00889; cAMP_BINDING; 2; 2.
 DR PROSITE: PS00842; cAMP_BINDING; 3; 2.
 DR PROSITE: PS0007; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.

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DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
KW Hypothetical protein; ATP-binding; Alternative splicing; Kinase.
KW Serine/threonine protein kinase; Transferase.
FT VARSPLOC 1 52
SQ SEQUENCE 780 AA; 86741 MW; 556CFAF5626DC2 CRC64;

Query Match 77.6%; Score 44; DB 5; Length 485;
Best Local Similarity 72.7%; Pred. No. 5;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 MLLGRPEFFS 11
DB 660 LMGTRPEFFS 670

RESULT 19
Q90XS2 PRELIMINARY; PRT; 485 AA.
AC Q90XS2
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Polo like kinase 3 (Fragment).
GN PLK3.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Arthropoda; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae.
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355.
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=21481843; PubMed=11597129;
RA Duncan P.I., Pollet N., Niehrs C., Nigg E.A.;
RT "Cloning and Characterization of Plx2 and Plx3, Two Additional Polo-
R1 Like Kinases from Xenopus laevis."
RC Exp. Cell Res. 270:78-87(2001).
CC 1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF357841; AAL30177.1.
DR InterPro: IPR000959; Polo_box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00659; Ekinase; 1.
DR Pfam: PF00659; Polo_box; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PSS0078; POLO_BOX; 1.
DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PSS0108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 557
SQ SEQUENCE 557 AA; 62501 MW; 852212418FAE8E78 CRC64;

Query Match 75.9%; Score 44; DB 13; Length 557;
Best Local Similarity 72.7%; Pred. No. 6;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MLLGRPEFFS 11
DB 252 LMGTRPEFFS 262

RESULT 21
Q15882 PRELIMINARY; PRT; 767 AA.
AC Q15882
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Polo-like protein kinase (Fragment).
GN PLK.
OS Trypanosoma brucei
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OC NCBI_TaxID=5691.
RN 1
RP SEQUENCE FROM N.A.
RX STRAIN=STIB247.
RX MEDLINE=98172736; PubMed=9511745;
RA Graham T.M., Tait A., Hyde G.;
RT "Characterisation of a polo-like protein kinase gene homologue from an
R1 evolutionary divergent eukaryote, Trypanosoma brucei."
RC Gene 207:71-77(1998).
CC 1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: Y13968; CAA74301.1.
DR InterPro: IPR000959; Polo_box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00659; Ekinase; 1.
DR Pfam: PF00659; Polo_box; 2.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PSS0078; POLO_BOX; 2.
DR PROSITE: PSS0107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PSS0111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PSS0108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 767
SQ SEQUENCE 767 AA; 86923 MW; 8960E253FF64D41 CRC64;

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OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355.
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=21481843; PubMed=11597129;
RA Duncan P.I., Pollet N., Niehrs C., Nigg E.A.;
RT "Cloning and Characterization of Plx2 and Plx3, Two Additional Polo-
R1 Like Kinases from Xenopus laevis."
RC Exp. Cell Res. 270:78-87(2001).
CC 1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF357841; AAL30177.1.
DR InterPro: IPR000959; Polo_box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00659; Ekinase; 1.
DR Pfam: PF00659; Polo_box; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PSS0078; POLO_BOX; 1.
DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PSS0108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 557
SQ SEQUENCE 557 AA; 62501 MW; 852212418FAE8E78 CRC64;

Query Match 75.9%; Score 44; DB 13; Length 557;
Best Local Similarity 72.7%; Pred. No. 6;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MLLGRPEFFS 11
DB 252 LMGTRPEFFS 262

RESULT 21
Q15882 PRELIMINARY; PRT; 767 AA.
AC Q15882
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Polo-like protein kinase (Fragment).
GN PLK.
OS Trypanosoma brucei
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OC NCBI_TaxID=5691.
RN 1
RP SEQUENCE FROM N.A.
RX STRAIN=STIB247.
RX MEDLINE=98172736; PubMed=9511745;
RA Graham T.M., Tait A., Hyde G.;
RT "Characterisation of a polo-like protein kinase gene homologue from an
R1 evolutionary divergent eukaryote, Trypanosoma brucei."
RC Gene 207:71-77(1998).
CC 1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: Y13968; CAA74301.1.
DR InterPro: IPR000959; Polo_box.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00659; Ekinase; 1.
DR Pfam: PF00659; Polo_box; 2.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PSS0078; POLO_BOX; 2.
DR PROSITE: PSS0107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PSS0111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PSS0108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 767
SQ SEQUENCE 767 AA; 86923 MW; 8960E253FF64D41 CRC64;

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-1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC EMBL: Y13099; CAA73553.1;
DR HSP; P28867; IPTQ.
DR InterPro: IPR000009; C2.
DR InterPro: IPR001064; CRYSTALLIN.
DR InterPro: IPR022219; DAG_PE_BIND.
DR InterPro: IPR000961; PKINASE_C.
DR InterPro: IPR007019; Prot_Kinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00168; C2.
DR Pfam: PF00133; DAG_PE_BIND; 2.
DR Pfam: PF00059; pkinase; 1.
DR Pfam: PF00433; pkinase_C; 1.
DR PRINTS: PR03360; C2DOMAIN.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR ProDom: PDC00001; Prot_Kinase; 1.
DR SMART: SMC0109; C1; 2.
DR SMART: SMC0219; C2; 1.
DR SMART: SMC0220; STKX; 1.
DR SMART: SW00133; STKX; 1.
DR PROSITE: PSC0499; C2_DOMAIN; 1.
DR PROSITE: PSC0004; C2_DOMAIN; 2; 1.
DR PROSITE: PSC0225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE: PSC0479; DAG_PE_BIND_DOM; 2.
DR PROSITE: PSC0081; DAG_PE_BIND_DOM; 2.
DR PROSITE: PS00081; DAG_PE_BIND_DOM; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_S; 1.
DR PROSITE: PS00108; Ser/threonine-protein_kinase; Transferase.
KW ATP-binding; Kinase; Ser/threonine-protein_kinase; Transferase.
SQ SEQUENCE 673 AA; 77344 MW; 96D24E554970C293 CRC64;

Query Match: 74.1%; Score 43; DB 5; Length 673;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps

Cy 1 MLLGRPFPE 9
D6 535 MLVGRPFPE 543

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RESULT 24
O96997      PRELIMINARY;          PRT;    577 AA.
AC          O96997
DT          01-MAY-1999   TREMBLEUR 13. Created
LT          01-MAY-1999   TREMBLEUR 13. Last sequence update)
ET          01-MAR-2003   TREMBLEUR 23. Last annotation update;
DE          Protein Kinase C
GN          PKC2
CS          Geodia cydonium (Spongia).
CC          Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
CC          Asporoporida; Geodiidae; Geodia
OX          NCBI_TaxID=6047;
RN          [1]
RP          SEQUENCE FROM N.A.
RX          MEDLINE=99147839; PubMed=12023072;
RA          Sack J., Kruse X., Mueller I.M., Mueller W.B.G.;
RT          "Promoter and exon-intron structure of the protein kinase C gene from
Rt          the marine sponge Geodia cydonium: Evolutionary considerations and
RL          promoter activity";
RL          Biochim. Biophys. Acta 1444:241-253(1999).
CC          - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC          - SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR          ENBL; Y17882; CAA36911...
DR          HSPB; P28867; IPTQ
DR          InterPro: IPRO00008; C2
DR          InterPro: IPRO01064; Crystallin
DR          InterPro: IPRO02259; BAG PE-binding
DR          InterPro: IPRO02981; Kinase C
DR          InterPro: IPRO03011; Prot Kinase
DR          InterPro: IPRO03284; Ser Thr Kinases
DR          Fam119; F00000; F00001
DR          Fam119; F00000; F00001

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DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00669; kinase; 1.
DR Pfam: PF00659; POLO box; 1.
DR ProDom: PD000011; Prot_kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; T_YKc; 1.
DR PROSITE: PS00378; POLO_BOX; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Transferase.
SQ SEQUENCE 554 AA; 5594 MW; F48D79BD273D59 C544.

Query Match 70.7%; Score 41; DB 11; Length 644;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLCGRPPFETS 11
DB 253 LCGSPPFETA 263

RESULT 29
Q96CV:
ID Q96CV1 PRELIMINARY; PRT; 546 AA.
AC Q96CV1.
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DI 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
FT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo
CX NCBI_TaxID:9606;
LN 1;
GN SEQUENCE FROM N.A.
RC TISSUE: Brain;
RA Strausberg A.;
RL Submitted (SEP 2001) to the EMBL/GenBank/DBJ databases.
CC 1 - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR InterPro: IPR000359; POLO_BOX.
DR InterPro: IPR000719; Prot_Kinase.
DR Pfam: PF00669; kinase; 1.
DR Pfam: PF00659; POLO box; 1.
DR ProDom: PD000011; Prot_kinase; 1.
DR SMART: SM00219; S_TKc; 1.
DR PROSITE: PS00378; POLO_BOX; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_ST; 1.
KW Hypothetical protein; ATP-binding; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 646 AA; 15420 MW; 342AD03C086538 C6047.

Query Match 70.7%; Score 41; DB 4; Length 644;
Best Local Similarity 63.6%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MLCGRPPFETS 11
DB 253 LCGSPPFETA 263

RESULT 29
Q94342
ID Q94342 PRELIMINARY; PRT; 151 AA.
AC Q94342.
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DI 01-NOV-1998 (TRENBLrel. 08, Last sequence update)

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DT 01-MAR-2002 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein Cn338.
GN Cn338.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
CX NCBI_TaxID=813;
LN 1;
GN SEQUENCE FROM N.A.
RC STRAIN=D/JM-3/Cx;
RX MEDLINE=98000809; PubMed=9784116;
RA Stephens R.S., Kaiman S., Lammel C.J., Fan C., Marathe R., Aravind L.,
RA Mitchell W.P., Olinier L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis".
RL Science 282:754-759 (1998).
RL EMBL; AE001307; AAC67933.7.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 153 AA; 17828 MW; DAE9E4E28F8B17C CRC64;

Query Match 67.2%; Score 39; DB 16; Length 153;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LGRPPFET 10
DB 11 LGAPPFET 18

RESULT 30
Q9GP07
ID Q9GP07 PRELIMINARY; PRT; 235 AA.
AC Q9GP07.
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DI 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DI 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Putative mitogen-activated protein kinase (Fragment).
GN WPK1.
OS Leishmania amazonensis.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
CX NCBI_TaxID=5659;
LN 1;
GN SEQUENCE FROM N.A.
RC STRAIN=LV73;
RA Wiese M., Goercke I.;
RT "Homologues of LMPK, a mitogen-activated protein kinase from
RT Leishmania mexicana, in different leishmania species".
RL Submitted (NOV 2000) to the EMBL/GenBank/DBJ databases.
CC 1 - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ258321; CAC17612.1; 1.
DR HSSP; P24941; IHC.
DR InterPro: IPR003527; MAP_Kin.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00669; kinase; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR PROSITE: PS00351; MAPK; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 235
FT NON_TER 235
SQ SEQUENCE 235 AA; 26791 MW; 7FEDF167C0FB03B7 CRC64;

Query Match 67.2%; Score 39; DB 5; Length 235;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLCGRPPFET 9
DB 192 MLCGRPFET 200

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RESULT 31
Q63872
ID Q63872 PRELIMINARY: PRT: 358 AA.
AC Q63872
DT 01-JUL-1997 (TrEMBLrel. 24, Created)
DT 01-JUL-1997 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE VAB-kinase homologue.
GN VABK.
OS Leishmania mexicana.
CC Eukaryota; Eucaryozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID:5665;
RN [1]
RC STRAIN:NMN/702/62/M379;
RX MEDLINE:98232507; PubMed:9564044;
RA Wiese M.;
RT "A mitogen-activated protein (MAP) kinase homologue of Leishmania mexicana is essential for parasite survival in the infected host.";
RL EMBL J0172619-2628(1998);
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: Z95887; CAB093071;
DR HSSP: Q00534; IB18.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR022290; Ser_thr_kinase.
DR Pfam: PF00369; Pkinase; 1.
DR PROSITE: P000001; Prot_kinase; 1.
DR SMART: SMC0220; S_TK; 1.
DR PROSITE: PS01351; MARK; 1.
DR PROSITE: PS0107; PROTEIN_KINASE_ATH; 1.
DR PROSITE: PS0211; PROTEIN_KINASE_GLY; 1.
DR PROSITE: PS0108; PROTEIN_KINASE_SER; 1.
DR ATP-binding; Kinase; Serine/threonine protein kinase; Transferase.
SQ SEQUENCE 358 AA; 41131 MW; 70204060570D4F PRK4;

Query Match 67.2%; Score 39; DB 5; Length 365;
Best Local Similarity 88.9%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY : MLLGRPPF 9
DB 232 MLLGRPPF 220

RESULT 32
Q63879
ID Q63879 PRELIMINARY: PRT: 358 AA.
AC Q63879
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Probable serine/threonine-protein kinase FRK5.
GN FRK5 OR BL3895.
OS Bifidobacterium longum.
CC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
CC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID:216216;
RN [1]
RC STRAIN:NAACC 2705;
RX MEDLINE:22294977; PubMed:12381787;
RA Schell M.A., Karmarantzou M., Snel P., Vilanova D., Berger B.,
RA Pessi G., Zwaalen M.-C., Desiere F., Work F., Cellery M.,
RA Pridmore R.D., Aragoni F.;
RA "The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14428(2002);
FP ENEM: AEC14680; AAN24413;
KW Kinase; Complete proteome.
SQ SEQUENCE 690 AA; 72243 MW; 6A19EACED5D92D CR264;

Query Match 67.2%; Score 40; DB 16; Length 493;

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Best Local Similarity 87.5%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPF 8
DB 217 MLLGRPPF 234

RESULT 33
Q9KJN7
ID Q9KJN7 PRELIMINARY: PRT: 1337 AA.
AC Q9KJN7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative serine/threonine protein kinase.
GN PKND2.
OS Myxococcus xanthus.
CC Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
CC Cystobacteriales; Myxococcaceae; Myxococcus.
OX NCBI_TaxID:34;
RN [1]
RC STRAIN:FROM N.A.
RC STRAIN:DZ2;
RX MEDLINE:20032045; PubMed:12564511;
RA Cho K., Zusman D.R.;
RT "Sporeulation timing in Myxococcus xanthus is controlled by the espAB locus.";
RL Mol. Microbiol. 34:714-725(1999);
RN [2]
RC STRAIN:FROM N.A.
RC STRAIN:DZ2;
RX Submitted (JUL-2000) to the EMBL/GenBank/DBSJ databases.
RL EMBL: AF163841; AAF87930.1;
DR InterPro: IPR00719; Prot_kinase.
DR InterPro: IPR031440; TPR_
DR Pfam: PF03069; Pkinase; 1.
DR Pfam: PF03151; TPR_4;
DR PROSITE: P000001; Prot_kinase; 1.
DR SMART: SMC0028; TPR; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW SEQUENCE 1337 AA; 144738 MW; 6056E8CA4C92499D CRC64;

Query Match 67.2%; Score 39; DB 2; Length 1337;
Best Local Similarity 87.5%; Pred. No. 13e-02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLLGRPPF 8
DB 242 MLLGRPPF 249

RESULT 34
Q63432
ID Q63432 PRELIMINARY: PRT: 240 AA.
AC Q63432
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rat protein kinase C-family related (fragment).
OS Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID:10116;
RN [1]
RC STRAIN:FROM N.A.
RX MEDLINE:87147193; PubMed:3469647;
RA Husey G.M., O'Brian C.A., Johnson M.D., Kirschmeier P.,
RA Weinstein I.B.;
RT "Isolation of cDNA clones encoding protein kinase C: Evidence for a protein kinase C-related gene family.";

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RJ Proc. Natl. Acad. Sci. U.S.A. 94:1065-1069(1997).
CC 1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: X15923; AA41877.1;
DR HSP: Q64502; I206.
DR InterPro: IPR000719; Prot_kinase
DR Pfam: PF00069; pkinase; 1.
DR PROSITE: PS00001; Prot_kinase; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1 240
FT NON_TER 240 240
SQ SEQUENCE 240 AA; 26842 MW; 2899148257E4762 CR; 0;

Query Match 65.5%; Score 14; DB 16; Length 240;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLGPPPF 9
PRT: 256 AA.
||| |||
DR 204 MNAQCPPE 212

RESULT 15
Q892AC PRELIMINARY; PRT: 256 AA.
AC Q892AC
RX MEDLINE:20150912; PubMed:10688204;
RA Parkhill J., Wren B.W., Mangani K., Kerley C.M., Churcher C.,
RA Rastam D., Chillingworth T., Davies R.M., Feltwell T., Holtby S.,
R. Jørgensen K., Karyshev A.V., Meade S., Paulsen M., Park C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Bartell B.G.;
PT whole genome sequence of the food-borne pathogen Listeria;
PT reveals hypervariable sequences;
RT Nature 403:665-668(2000);
DR EMBL: AJ139076; CAB7382.1;
DR HSP: P10344; IWDN.
DR InterPro: IPR01311; SBP/glu receptor;
DR InterPro: IPR01638; SBP_bac_3;
DR Pfam: PF00497; SBP_bac_3; 1.
DR SWART: SMO0862; PRPb; 1.
KW Complete proteome.
SQ SEQUENCE 256 AA; 28913 MW; 6CE440856AFC13CF CR; 0;

Query Match 65.5%; Score 14; DB 16; Length 240;
Best Local Similarity 72.7%; Pred. No. 37;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLGPPPF 11
PRT: 256 AA.
||| |||
DR 25 YELGPPPF 35

RESULT 16
Q892AC PRELIMINARY; PRT: 256 AA.
ID Q892AC
AC Q892AC
RX MEDLINE:21681879; PubMed:11921952;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brothier P., Camy J.-C., Cattolico L.,
RA Chardier M., Choisme N., Claude-Renard C., Cunac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siguer P., Theault P., Whalen M., Wincker P., Levy M.,
RA Weissbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
RT Nature 415:497-502(2002);
DR EMBL: AL646059; CAB13964.1;
DR InterPro: IPR001173; Glyco_trans_2;
DR Pfam: PF00535; Glycos_transf_2; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 257 AA; 28452 MW; DE8F0AC694090A25 CR; 0;

Query Match 65.5%; Score 38; DB 16; Length 257;
Best Local Similarity 63.6%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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DT 01-NOV-1999 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE IRON(III) ABC transporter, ATP-binding protein.
GN TM0078.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2316;
RV [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99253126; PubMed=10165517;
RA Nelson K.E., Clayton R.A., Gill S.R., Swinn M.D., Dodson R.J.,
RA Haft D.H., Hickey E.K., Petersen J.C., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Wank J.A., Zanker K.D., Garrett M.V.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richards D.,
RA Salzberg S.L., Smith H.O., Venter C.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima";
RL Nature 399:323-329(1999);
DR EMBL: AE001694; AAC35172.1;
DR TIGR: TM0078.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR004339; ABC_transporter.
DR Pfam: PF00005; ABC_tran; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 256 AA; 28723 MW; 725DA5365C84E156 CR; 0;

Query Match 65.5%; Score 38; DB 16; Length 256;
Best Local Similarity 80.0%; Pred. No. 37;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLGRPPPF 11
PRT: 257 AA.
||| |||
DR 62 LLGR:PWST 71

RESULT 37
Q892AC PRELIMINARY; PRT: 257 AA.
ID Q892AC
AC Q892AC
RX MEDLINE:21681879; PubMed:11921952;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brothier P., Camy J.-C., Cattolico L.,
RA Chardier M., Choisme N., Claude-Renard C., Cunac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siguer P., Theault P., Whalen M., Wincker P., Levy M.,
RA Weissbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
RT Nature 415:497-502(2002);
DR EMBL: AL646059; CAB13964.1;
DR InterPro: IPR001173; Glyco_trans_2;
DR Pfam: PF00535; Glycos_transf_2; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 257 AA; 28452 MW; DE8F0AC694090A25 CR; 0;

Query Match 65.5%; Score 38; DB 16; Length 257;
Best Local Similarity 63.6%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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CV 1 MLCGRPPFE 11
 ID 001427 PRELIMINARY: PPT: 332 AA
 AC 001427
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE C. ELEGANS AUFORA/IPD related protein KINASE 2 (AIR 2) (AB AF011207).
 DE CONTAINS SIMILARITY TO PFAM 0069 (KINASE1, E-VALUE: 295.1,
 DE E-VALUE 2.8E-85, N=1 (AIR-2) (KINASE)).
 GN AIR 2
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Peliceridae; Caenorhabditis.
 CX NCBI_TaxID 6239;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE:95069613; PubMed:9851916;
 RA Nemoy
 RT Complete sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.
 RT Science 281:2212-2018(1998).
 RN 12;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Hunkeler C., Weidmann P.;
 RT "The sequence of C. elegans cosmid P07.11"
 RT Submitted (APR 1997) to the EMBL/GenBank/DBJ databases.
 RN 13;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Watkinson R.J.
 RT Submitted APR 1997 to the EMBL/GenBank/DBJ databases.
 RN 14;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Watkinson R.J.
 RT Submitted AUG 1999 to the EMBL/GenBank/DBJ databases.
 RN 15;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Watkinson R.J.
 RT Submitted JAN 2000 to the EMBL/GenBank/DBJ databases.
 RN 16;
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Schracher J.M., Golden A., Dorova P.;
 RT "AIR 2: An Aurora/Ipki-related protein kinase associated with
 RT chromosomes and midbody microtubules is required for polar body
 RT extrusion and cytokinesis in C. elegans embryos".
 RT J. Cell Biol. 150:101-110(1998).
 CC 1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR ENH1_097196; AAB52459.2;
 DR ENH2_097197; AAC71207; AAC73945.1;
 DR HSP1_P49411; IAO1.
 DR InterPro: IPR00719; Prot kinase.
 DR InterPro: IPR02290; Ser/Thr kinase.
 DR Pfam: PF00699; Kinase; I
 DR Pfam: PF00001; Prot kinase; I
 DR SMART: SMART001; S_TKc1.
 DE SWISS-PROT: P50307, PROTEIN KINASE AIR 2

DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS0108; PROTEIN KINASE ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 305 AA; 34749 MW; 1635B6C02E14C11 CRC64;
 Query Match 65.5%; Score 38; DB 5; Length 305;
 Best Local Similarity 75.0%; Pred. No. 45;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QV 2 MLCGRPPFE 4
 ID 001427 PRELIMINARY: PPT: 332 AA
 AC 001427
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein SC07729.
 GN SC07729 OR SC8011.20.
 OS Streptomyces coelicolor.
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Streptomycineae; Streptomycetaceae; Streptomycetes.
 CX NCBI_TaxID:1902;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Saunders D.C., Harris D.;
 RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN 12;
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Cerdeno A.M., Parkhill J., Bartell B.G., Raftandream M.A.;
 RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN 13;
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE:97000451; PubMed:8843436;
 RA Rederbach M., Kieser H.M., Derapalte D., Eichner A., Cullum G.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosids and a detailed genetic and physical map for
 RT the R Xb Streptomyces coelicolor A3(2) chromosome";
 RT Mol. Microbiol. 21:77-96(1996).
 RN 14;
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2); / M145;
 RX MEDLINE:21996410; PubMed:12000933;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.M., Challis G.D.,
 RA Thomson N.B., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Baraman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hida-go J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Lake J., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Raftandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J., Bartell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2)".
 RT Nature 417:141-147(2002).
 RC EMBL; AL391332; CAC2737.1;
 DR InterPro: IPR001829; DUF209.
 DR Pfam: PF02678; DUF209; I
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 332 AA; 36974 MW; 7E05869A938680ED CRC64;
 Query Match 65.5%; Score 38; DB 16; Length 332;
 Best Local Similarity 77.8%; Pred. No. 49;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QV 1 MLCGRPPFE 4

